

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 ; Search time 479.47 Seconds
(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-1

Perfect score: 2587

Sequence: 1 ggaagggcagcggcagctcc.....tgatataatatacttctt 2587

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2565	99.1	2627	3	US-09-404-879A-391
2	2565	99.1	2627	4	US-09-667-857-391
3	1543	59.6	1567	3	US-09-404-879A-74
4	1543	59.6	1567	4	US-09-338-933-74
5	1543	59.6	1567	4	US-09-215-681-74
6	1543	59.6	1567	4	US-09-215-681-74
7	1543	59.6	1567	4	US-09-667-857-74
8	958.8	37.1	1046	4	US-09-799-451-332
9	532.2	20.6	541	3	US-09-404-879A-28
10	532.2	20.6	541	4	US-09-338-933-28
11	532.2	20.6	541	4	US-09-215-681-28
12	532.2	20.6	541	4	US-09-215-681-28
13	532.2	20.6	541	4	US-09-667-857-28
14	448.2	17.3	461	4	US-09-404-879A-27
15	448.2	17.3	461	4	US-09-338-933-27
16	448.2	17.3	461	4	US-09-215-681-27
17	448.2	17.3	461	4	US-09-215-681-27
18	448.2	17.3	461	4	US-09-215-681-27
19	412	15.9	695	3	US-09-667-857-27
20	412	15.9	695	3	US-09-404-879A-15
21	412	15.9	695	3	US-09-123-912-15
22	412	15.9	695	3	US-09-643-597-15
23	412	15.9	695	4	US-09-480-884A-15
24	412	15.9	695	4	US-09-542-615A-15
25	412	15.9	695	4	US-09-606-421B-15
26	412	15.9	695	4	US-09-221-107-15
27	412	15.9	695	4	US-09-466-396A-15

28	412	15.9	695	4	US-09-630-940B-15	Sequence 15, Appl
29	412	15.9	695	4	US-09-285-479-15	Sequence 15, Appl
30	320	12.4	335	4	US-09-513-999C-30680	Sequence 30680, A
31	74	2.9	247299	4	US-09-949-016-17590	Sequence 17590, A
32	72.6	2.8	59828	4	US-09-949-016-16238	Sequence 16238, A
33	70.6	2.7	10610	4	US-09-949-016-15967	Sequence 15967, A
34	70.2	2.7	132438	4	US-09-949-016-14349	Sequence 14349, A
35	70.2	2.7	132438	4	US-09-949-016-14350	Sequence 14350, A
36	70.2	2.7	151089	4	US-09-949-016-14348	Sequence 14348, A
37	70.2	2.7	524032	4	US-09-949-016-16328	Sequence 16328, A
38	70.2	2.7	524032	4	US-09-949-016-16329	Sequence 16329, A
39	70.2	2.7	524032	4	US-09-949-016-16330	Sequence 16330, A
40	70.2	2.7	524032	4	US-09-949-016-16331	Sequence 16331, A
41	70.2	2.7	529885	4	US-09-949-016-14340	Sequence 14340, A
42	70.2	2.7	529885	4	US-09-949-016-14341	Sequence 14341, A
43	70.2	2.7	529885	4	US-09-949-016-14342	Sequence 14342, A
44	70.2	2.7	529885	4	US-09-949-016-14343	Sequence 14343, A
45	70.2	2.7	529885	4	US-09-949-016-14344	Sequence 14344, A

ALIGNMENTS

RESULT 1									
US-09-404-879A-391									
Sequence 391, Application US/09404879A									
Patent No. 6468546									
GENERAL INFORMATION:									
APPLICANT: Mitcham, Jennifer L.									
APPLICANT: King, Gordon E.									
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND									
FILE REFERENCE: 210121.462C2									
CURRENT APPLICATION NUMBER: US/09/404,879A									
CURRENT FILING DATE: 1999-09-24									
NUMBER OF SEQ ID NOS: 393									
SOFTWARE: FASTSEQ for Windows Version 3.0									
SEQ ID NO 391									
LENGTH: 2627									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-404-879A-391									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;									
QY	12	GGAGCTCAGTCAGCAGTACCCAGATAGCGTGGAGACCTTCCCGACATGGCTTCC	71						
DB	33	GGAGCTCAGTCAGCAGTACCCAGATAGCGTGGAGACCTTCCCGACATGGCTTCC	92						
QY	72	TGGGGAGATCTCTTCTGAGCATTAATGATCATCTTAATTCTGCTGAGCAATTG	131						
DB	93	TGGGGAGATCTCTTCTGAGCATTAATGATCATCTTAATTCTGCTGAGCAATTG	152						
QY	132	CAGTATCATTTGGCTTGGTATTTTCAGGAGACATCTTCATCAGTCACTAGTGTGCT	191						
DB	153	CAGTATCATTTGGCTTGGTATTTTCAGGAGACATCTTCATCAGTCACTAGTGTGCT	212						
QY	192	CAGCTGGAGAACTTGGGGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC	251						
DB	213	CAGCTGGAGAACTTGGGGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC	272						
QY	252	TTTCTGATATCGTATACATGCTGGAAGAGGTGTTTAACTTGTGTCATGACTTCA	311						
DB	273	TTTCTGATATCGTATACATGCTGGAAGAGGTGTTTAACTTGTGTCATGACTTCA	332						
QY	312	AAGAGGCAAAAGATGAGCTGTGAGAGCAGATGAATTTTCAGAGCCGGAACAGCTGT	371						
DB	333	AAGAGGCAAAAGATGAGCTGTGAGAGCAGATGAATTTTCAGAGCCGGAACAGCTGT	392						
QY	372	TTCGTATCAAGTATGATTGGCAATGCTTTTGGGCTGAAAGAACTGCAATCAGAG	431						

|||||
Db 393 TTGGATGATGAAGTATAGTTGGCAATGCTCTTTGGGCTGAAAAACGTGCAACTCACAG 452
Qy 432 ATGCTGGCACTTACAAATGTTATATCATCACTTTAAAGGCAAGGGAAATGCTAACTTG 491
Db 453 ATGCTGGCACTTACAAATGTTATATCATCACTTTAAAGGCAAGGGAAATGCTAACTTG 512
Qy 492 AGTATAAACTGAGGCTTCAGCATGCCGGAAGTGAATGTGACTATATGTCAGCTGAG 551
Db 513 AGTATAAACTGAGGCTTCAGCATGCCGGAAGTGAATGTGACTATATGTCAGCTGAG 572
Qy 552 AGACCTTGGGATGTGAGGCTCCCGATGGTTCCCGAGCCCAAGTGTCTGGGCAATCCC 611
Db 573 AGACCTTGGGATGTGAGGCTCCCGATGGTTCCCGAGCCCAAGTGTCTGGGCAATCCC 632
Qy 612 AAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATCCAGCTTTGAGCTGAACTG 671
Db 633 AAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATCCAGCTTTGAGCTGAACTG 692
Qy 672 AGAATGTGACATGAAGTTGTGTCTGTCTCAATGTTTACATGATCAACACATACT 731
Db 693 AGAATGTGACATGAAGTTGTGTGTCTGTCTCAATGTTTACATGATCAACACATACT 752
Qy 732 CCTGTATGATTGAAAAATGACATTTGCCAAAGCAAGGGGATATCAAAATGACAGAAATCG 791
Db 753 CCTGTATGATTGAAAAATGACATTTGCCAAAGCAAGGGGATATCAAAATGACAGAAATCG 812
Qy 792 AGATAAAAAGGGAGTCACTTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTCT 851
Db 813 AGATAAAAAGGGAGTCACTTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTCT 872
Qy 852 CTTTCTTTGGCATCAGCTGGGACCTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 911
Db 873 CTTTCTTTGGCATCAGCTGGGACCTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 932
Qy 912 GTGCTTTGGCCACAAAAAAGCATGCAAGTCAATTTGTACACAGGATCTACAGAACTAT 971
Db 933 GTGCTTTGGCCACAAAAAAGCATGCAAGTCAATTTGTACACAGGATCTACAGAACTAT 992
Qy 972 TTCACACACAGATATGACCTAGTTTATATTTCTGGAGGAATGAATATCATATCTAGAA 1031
Db 993 TTCACACACAGATATGACCTAGTTTATATTTCTGGAGGAATGAATATCATATCTAGAA 1052
Qy 1032 GTCTGAGTGAAGCAAAACAGACAGAAACAAAGAAAGCCAAAGCAGAAAGCTCTCAAT 1091
Db 1053 GTCTGAGTGAAGCAAAACAGACAGAAACAAAGAAAGCCAAAGCAGAAAGCTCTCAAT 1112
Qy 1092 ATGAAACAAGATTAATCTATCTTCAAGACATATTAAGAGTTGGAAATATTAATTCATGTA 1151
Db 1113 ATGAAACAAGATTAATCTATCTTCAAGACATATTAAGAGTTGGAAATATTAATTCATGTA 1172
Qy 1152 ACTTAACAAGTGTGTAAGAGTATTAAGTAAGTAAGTCAAGTGAACAAGTGAATCCCAAG 1211
Db 1173 ACTTAACAAGTGTGTAAGAGTATTAAGTAAGTAAGTCAAGTGAACAAGTGAATCCCAAG 1232
Qy 1212 ATCTCAGGAGCTCCCTGCTGTCACTGAGGAGTGAAGAGACAGATATGATGATTT 1271
Db 1233 ATCTCAGGAGCTCCCTGCTGTCACTGAGGAGTGAAGAGACAGATATGATGATTT 1292
Qy 1272 CTTTGTCTCTGAATTTTATAGTATATGCTGTATATTTGCTGTAGAGAAAGCCCTGGA 1331
Db 1293 CTTTGTCTCTGAATTTTATAGTATATGCTGTATATTTGCTGTAGAGAAAGCCCTGGA 1352
Qy 1332 AGTATATCCCAACATATCCACATCTTATATTTCCACAAATTAAGCTGTATATGTAACCTTA 1391
Db 1353 AGTATATCCCAACATATCCACATCTTATATTTCCACAAATTAAGCTGTATATGTAACCTTA 1412
Qy 1392 AGACGCTGTATATGACTGCACTTGCAGAACTCAGGGGCGGCTGCATTTTATGTAATGGT 1451
Db 1413 AGACGCTGTATATGACTGCACTTGCAGAACTCAGGGGCGGCTGCATTTTATGTAATGGT 1472
Qy 1452 CAAATGATTTCACTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1511
|||||

Db 1473 CAAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGGCTTCTTCCCAACTGACA 1532
Qy 1512 AATGCCAAAGTTGAAAAATGATCATATTTTATGCAATTAACAGAGCAGTGGGACACC 1571
Db 1533 AATGCCAAAGTTGAAAAATGATCATATTTTATGCAATTAACAGAGCAGTGGGACACC 1592
Qy 1572 GATTTTATTAATTAACCTGAGCCTTCTTTTAAACAAACAAATGCGGGTTATATTTCTCA 1631
Db 1593 GATTTTATTAATTAACCTGAGCCTTCTTTTAAACAAACAAATGCGGGTTATATTTCTCA 1652
Qy 1632 GATGATGTTCAATCCGTGAATGCTCAAGGAAAGACCTTTCACTTTGACTATATGCAATTA 1691
Db 1653 GATGATGTTCAATCCGTGAATGCTCAAGGAAAGACCTTTCACTTTGACTATATGCAATTA 1712
Qy 1692 TGTCATCAACAAGCTCTGAGGCTTCTCTTTCATCTGCGAGGACAGCTAAGACCTCAGT 1751
Db 1713 TGTCATCAACAAGCTCTGAGGCTTCTCTTTCATCTGCGAGGACAGCTAAGACCTCAGT 1772
Qy 1752 TTTCAATAGCATCTAAGACAGTGGGACCTCAGCTGGGGTGAATTTGGCCCCCATCTCGGG 1811
Db 1773 TTTCAATAGCATCTAAGACAGTGGGACCTCAGCTGGGGTGAATTTGGCCCCCATCTCGGG 1832
Qy 1812 GGAATGTCTGAAGACAAATTTTGTGTTAATCTCAATAGAGGAGTGAAGAGATACAGTGTCTA 1871
Db 1833 GGAATGTCTGAAGACAAATTTTGTGTTAATCTCAATAGAGGAGTGAAGAGATACAGTGTCTA 1892
Qy 1872 CTACCAACTAGTGAATAAAGGCAAGGAGTGTGCTCAACTCTTACATGATACAGAGACGT 1931
Db 1893 CTACCAACTAGTGAATAAAGGCAAGGAGTGTGCTCAACTCTTACATGATACAGAGACGT 1952
Qy 1932 CTCCCATTTACACCTAACCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTTGGT 1991
Db 1953 CTCCCATTTACACCTAACCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTTGGT 2012
Qy 1992 TTTGAGTGAAGAAAGGGCTGGAAGAGAGGAGCCAAACAAATCTGTCTTCTTCACTT 2050
Db 2013 TTTGAGTGAAGAAAGGGCTGGAAGAGAGGAGCCAAACAAATCTGTCTTCTTCACTT 2072
Qy 2051 AGTCATTTGGCAAAATTAAGCAATCTGTCTTGGCTGTGCTCAGACAGAGAGCCAGAA 2110
Db 2073 AGTCATTTGGCAAAATTAAGCAATCTGTCTTGGCTGTGCTCAGACAGAGAGCCAGAA 2132
Qy 2111 CTATATCGGGACCAAGATTAACATCTCTCACTGAAACAGATTTGAACAAGGCTTATGGGAA 2170
Db 2133 CTATATCGGGACCAAGATTAACATCTCTCACTGAAACAGATTTGAACAAGGCTTATGGGAA 2192
Qy 2171 TGCCGTATGGGATATATCTTCAAGCTTTGAGCTTCTAAGTTCTTCCCTTCACTTACCC 2230
Db 2193 TGCCGTATGGGATTAATCTTCAAGCTTTGAGCTTCTAAGTTCTTCCCTTCACTTACCC 2252
Qy 2231 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTCTAAGCTCAGGTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTCTAAGCTCAGGTTTCTTACTCTGA 2312
Qy 2291 ATTTAGATCTCAGACCTTCTTGCCCAATTTCAATTAAGGCAACAACATATACCTT 2350
Db 2313 ATTTAGATCTCAGACCTTCTTGCCCAATTTCAATTAAGGCAACAACATATACCTT 2372
Qy 2351 CCAATGAACAACAACAGACTTTTGAAGACAGACAAATGACTGCTTGAATTAAGGCTTGG 2410
Db 2373 CCAATGAACAACAACAGACTTTTGAAGACAGACAAATGACTGCTTGAATTAAGGCTTGG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAAAGAAATPCTTTGTTTCCAGGCCCTTCCACACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAAAGAAATPCTTTGTTTCCAGGCCCTTCCACACTCTTCA 2492
Qy 2471 TGTGTTAAACAATGCTTCTGACCTTGAACCTTGAAGCAAGGCTGACTGTATTAATGTTGTTAT 2530
Db 2493 TGTGTTAAACAATGCTTCTGACCTTCTGACCTTGAAGCAAGGCTGACTGTATTAATGTTGTTAT 2552
Qy 2531 AGAAAACGATTTTATAGATTTCTGATGCTTCAAGAGAAATGATTAATATACATTTTCT 2587
Db 2553 AGAAAACGATTTTATAGATTTCTGATGCTTCAAGAGAAATGATTAATATACATTTTCT 2609
|||||


```
RESULT 2
US-09-667-857-391
; Sequence 391, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-667-857-391

Query Match      99.1%; Score 2565; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      12 GGCAGCTCCACTGACCCAGTACCCAGATACGCTGGGAACTTCCCAAGCCATGCTTCCC 71
DB      33 GGCAGCTCCACTGACCCAGTACCCAGATACGCTGGGAACTTCCCAAGCCATGCTTCCC 92
QY      72 TGGGGAGAGATCCCTTCTGGAGCATATTTAGCATTCATTTCTGGGAGCAATTG 131
DB      93 TGGGGAGATCCCTTCTGGAGCATATTTAGCATTCATTTCTGGGAGCAATTG 152
QY      132 CACTCATCATTTGGCTTGTATTTCAAGGAGACACTCCATCAGATCAGTACCTGCGCT 191
DB      153 CACTCATCATTTGGCTTGTATTTCAAGGAGACACTCCATCAGATCAGTACCTGCGCT 212
QY      192 CAGCTGGGAACTTTGGGAGATGGAATCTGAGCTGCACTTTTGAACCTGACATCAAC 251
DB      213 CAGCTGGGAACTTTGGGAGATGGAATCTGAGCTGCACTTTTGAACCTGACATCAAC 272
QY      252 TTTCTGATATCGGATACATATGGCTGAAGAGAGTGTTTAGGCTTGTCCATGAGTTCA 311
DB      273 TTTCTGATATCGGATACATATGGCTGAAGAGAGTGTTTAGGCTTGTCCATGAGTTCA 332
QY      312 AAGAAGCAAAAGATGAGCTGTGGAGAGAGATGAAATGTTCAAGAGCCGGAAGAGAGTGT 371
DB      333 AAGAAGCAAAAGATGAGCTGTGGAGAGAGATGAAATGTTCAAGAGCCGGAAGAGAGTGT 392
QY      372 TTGCTGATCAAGTATGATTGGCAATGCTTTTGGCGCTGAAGAAAGTGAACCTCAG 431
DB      393 TTGCTGATCAAGTATGATTGGCAATGCTTTTGGCGCTGAAGAAAGTGAACCTCAG 452
QY      432 ATGCTGGCACTCAAAATGTTATATCATCACTTTAAAGGCAAGGGGAATGCTAACCTTG 491
DB      453 ATGCTGGCACTCAAAATGTTATATCATCACTTTAAAGGCAAGGGGAATGCTAACCTTG 512
QY      492 AGTATTAATCTGAGAGCTTCCAGATGCGGAGATGGAATGATGATTAATGCCAGCTCAG 551
DB      513 AGTATTAATCTGAGAGCTTCCAGATGCGGAGATGGAATGATGATTAATGCCAGCTCAG 572
QY      552 AGACCTTGGCGGTGAGAGCTTCCCGATGTTCCCGCAAGCCCAAGTGTGTGGCATGCC 611
DB      573 AGACCTTGGCGGTGAGAGCTTCCCGATGTTCCCGCAAGCCCAAGTGTGTGGCATGCC 632
```

```
QY      612 AAGTTGACCGAGGAGCCAACTTCTCGAAGTCTCCAAATACAGACTTTGAGCTGAACCTTG 671
DB      633 AAGTTGACCGAGGAGCCAACTTCTCGAAGTCTCCAAATACAGACTTTGAGCTGAACCTTG 692
QY      672 AGAATGACCAATGAAGGTTGTCTGTCTCTACAAATGTTACGATCAACAACATTAAT 731
DB      693 AGAATGACCAATGAAGGTTGTCTGTCTCTCTACAAATGTTACGATCAACAACATTAAT 752
QY      732 CCTGTATGATTTGAAAATGACATTTGCCAAGCAACAGGGATTTCAAAAGTGAAGATCCG 791
DB      753 CCTGTATGATTTGAAAATGACATTTGCCAAGCAACAGGGATTTCAAAAGTGAAGATCCG 812
QY      792 AGATCAAAAGGCGAGTCACTACCTACAGCTGCTAACTCAAGAGCTTCTGTGTCTCTT 851
DB      813 AGATCAAAAGGCGAGTCACTACCTACAGCTGCTAACTCAAGAGCTTCTGTGTCTCTT 872
QY      852 CTTTCTTTGCCATCAGCTGGGCACTTCTGCTCTGAGCCCTTAAGCTGATGCTAAATTAAT 911
DB      873 CTTTCTTTGCCATCAGCTGGGCACTTCTGCTCTGAGCCCTTAAGCTGATGCTAAATTAAT 932
QY      912 GTGCTTGGCCCAAAAAAAGCATGCAATGCTATTTGTAACAAGGATCTACAGAACTAT 971
DB      933 GTGCTTGGCCCAAAAAAAGCATGCAATGCTATTTGTAACAAGGATCTACAGAACTAT 992
QY      972 TTCACCAACAGATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCAATCTAGAA 1031
DB      993 TTCACCAACAGATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCAATCTAGAA 1052
QY      1032 GTCTGAGTGAAGCAAAACAAGACAGAAACAACAAAGAGCCAAAGCAGAGGCTCAAT 1091
DB      1053 GTCTGAGTGAAGCAAAACAAGACAGAAACAACAAAGAGCCAAAGCAGAGGCTCAAT 1112
QY      1092 ATGAACAATATTAATTTATCTTCAAGAATATTAAGTGGGAAATTAATTCATGTA 1151
DB      1113 ATGAACAATATTAATTTATCTTCAAGAATATTAAGTGGGAAATTAATTCATGTA 1172
QY      1152 ACTAGACAAGTGTGTTAAGATGATTAAGTAAATGACCTGAGACAAATGATGCCAG 1211
DB      1173 ACTAGACAAGTGTGTTAAGATGATTAAGTAAATGACCTGAGACAAATGATGCCAG 1232
QY      1212 ATCTCAGGAGACCTCCCTGCTGTCACTGAGGAGTGAAGAGACAGATATGATGTT 1271
DB      1233 ATCTCAGGAGACCTCCCTGCTGTCACTGAGGAGTGAAGAGACAGATATGATGTT 1292
QY      1272 CTTTGTCTGGAATTTTATGATTAATGCTGTAATGTTGCTCTGAGAGAGCCCTGGA 1331
DB      1293 CTTTGTCTGGAATTTTATGATTAATGCTGTAATGTTGCTCTGAGAGAGCCCTGGA 1352
QY      1332 AGTCTATCCCAACATATCCACATCTTAATATTCACAAATTAAGCTGTAGTATCCCTA 1391
DB      1353 AGTCTATCCCAACATATTCACATCTTAATATTCACAAATTAAGCTGTAGTATCCCTA 1412
QY      1392 AGACGCTGCTAAATGACCTGCACTTGCACACTCAAGGAGGCGCTGCAATTTAGTATG 1451
DB      1413 AGACGCTGCTAAATGACCTGCACTTGCACACTCAAGGAGGCGCTGCAATTTAGTATG 1472
QY      1452 CAAATGATTCATCTTTTATGATGCTTCCAAAGTGTCTTCTCTCCCACTGAACA 1511
DB      1473 CAAATGATTCATCTTTTATGATGCTTCCAAAGTGTCTTCTCTCCCACTGAACA 1532
QY      1512 AATGCCAAAGTTGAGAAAATGATCATATTTTAAAGATTAACAGAGAGTGGCGACACC 1571
DB      1533 AATGCCAAAGTTGAGAAAATGATCATATTTTAAAGATTAACAGAGAGTGGCGACACC 1592
QY      1572 GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGCTTATTTCTCA 1631
DB      1593 GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGCTTATTTCTCA 1652
QY      1632 GATGATGTTCAATCCGTAATGCTTCCAGGAGAGAGACCTTTCACTTGAATATGATTA 1691
DB      1653 GATGATGTTCAATCCGTAATGCTTCCAGGAGAGAGACCTTTCACTTGAATATGATTA 1712
QY      1692 TGTATCATCAAGCTGTGAGGCTTCTCTTCAATCTGCTGAGACAGTAAACCTCACT 1751
```

```

Db      1713 TTTTCAATGACAGCTGTGAGGCTTCTCTTCCATCTCTGTGAGACAGTAAACCTCAGT 1772
Qy      1752 TTTTCAATGACATCTGTAGAGCAGTGGAGCTAGCTGGGGTATTTCCGCCCCCATCTCCGGG 1811
Db      1773 TTTTCAATGACATCTGTAGAGCAGTGGAGCTAGCTGGGGTATTTCCGCCCCCATCTCCGGG 1832
Qy      1812 GGAATGTCGAAAGACAAATTTGGTTACCCCAATGAGGAGTGAAGAGGATCAGTGTCTA 1871
Db      1833 GGAATGTCGAAAGACAAATTTGGTTACCCCAATGAGGAGTGAAGAGGATCAGTGTCTA 1892
Qy      1872 CTACCACTAGTGTGATTAAGAGCCAGGAGTGTCTCAACCTCTCAACATGTACAGACCT 1931
Db      1893 CTACCACTAGTGTGATTAAGAGCCAGGAGTGTCTCAACCTCTCAACATGTACAGACCT 1952
Qy      1932 CTCCCATTTACAACTACCAATCCGAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1991
Db      1953 CTCCCATTTACAACTACCAATCCGAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2012
Qy      1992 TTTTGTAGTAAAGAGGCTGTGAAAGAGGAGGAGCAACAAATCTGTCTGTCTGTCTGTCTGTCT 2050
Db      2013 TTTTGTAGTAAAGAGGCTGTGAAAGAGGAGGAGCAACAAATCTGTCTGTCTGTCTGTCTGTCT 2072
Qy      2051 AGTCATTTGCAATTAAGCAATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2110
Db      2073 AGTCATTTGCAATTAAGCAATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2132
Qy      2111 CTCTATCGGGCACACAGATTAACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2170
Db      2133 CTCTATCGGGCACACAGATTAACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2192
Qy      2171 TGCCTGATGGGATTTATCTTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2230
Db      2193 TGCCTGATGGGATTTATCTTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2252
Qy      2231 CTGCAAGCCAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2290
Db      2253 CTGCAAGCCAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2312
Qy      2291 ATTTAGATCTCCAGACCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
Db      2313 ATTTAGATCTCCAGACCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2372
Qy      2351 CCATGAGACACACAGACCTTTTGAAGCAAGACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2410
Db      2373 CCATGAGACACACAGACCTTTTGAAGCAAGACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2432
Qy      2411 AGGAATGAAGCTTTGAAGAAAGAAATTAATCTTTTCCAGCCCTTCCACACCTCTTCA 2470
Db      2433 AGGAATGAAGCTTTGAAGAAAGAAATTAATCTTTTCCAGCCCTTCCACACCTCTTCA 2492
Qy      2471 TGTGTTAACCACTGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2530
Db      2493 TGTGTTAACCACTGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2552
Qy      2531 AGAAAACTGATTTTAGATTTGATGTTCAAGAGATGATTAATATACATTTCT 2587
Db      2553 AGAAAACTGATTTTAGATTTGATGTTCAAGAGATGATTAATATATACATTTCT 2609

```

```

RESULT 3
US-09-404-879A-74
; Sequence 74, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24

```

```

; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-74

Query Match      59.6%; Score 1543; DB 3; Length 1567;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 2; Gaps 2;
Matches 1565; Conservative 0;

Qy      1022 ATATCTAGAAGCTGTGAGTGAAGCAACAAAGAGCAAGAAACAAAGAGCCAAAGCAGA 1081
Db      1 ATATCTAGAAGCTGTGAGTGAAGCAACAAAGAGCAAGAAACAAAGAGCCAAAGCAGA 60
Qy      1082 AGGCTCCATATGAAACAAAGATTAATCTATCTTCAAGACATATTGAAAGTTGGGAAATA 1141
Db      61 AGGCTCCATATGAAACAAAGATTAATCTATCTTCAAGACATATTGAAAGTTGGGAAATA 120
Qy      1142 ATTCATGTGAAGCTGACAAAGTGTGTGTAGAGTGAATGAATGAATGAATGAATGAATGAATGAAT 1201
Db      121 ATTCATGTGAAGCTGACAAAGTGTGTGTAGAGTGAATGAATGAATGAATGAATGAATGAATGAAT 180
Qy      1202 GCATCCCGAGATCTCAGGAGACCTCCCTGCTGTCACTGTGGAGTGAAGAGAGAT 1261
Db      181 GCATCCCGAGATCTCAGGAGACCTCCCTGCTGTCACTGTGGAGTGAAGAGAGAT 240
Qy      1282 AGTGATGTTCTTGTGTCTGTGAATTTTGTATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1321
Db      241 AGTGATGTTCTTGTGTCTGTGAATTTTGTATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Qy      1322 GCCCTGGAAGAGTCTATCCCAACATATCCATCTTATTTCAACAATTAAGCTGTAGT 1381
Db      301 GCCCTGGAAGAGTCTATCCCAACATATCCATCTTATTTCAACAATTAAGCTGTAGT 360
Qy      1382 ATGTACCCCTAAGACGCTCTAATGTGACGTGCACTTGGCACTCAGGGGCGGCTGCATTTT 1441
Db      361 ATGTACCCCTAAGACGCTCTAATGTGACGTGCACTTGGCACTCAGGGGCGGCTGCATTTT 420
Qy      1442 AGTAATGGGTCAATGATTTCACTTTTATGATGCTTCCAAAGTGTCTTGTCTTCTTC 1501
Db      421 AGTAATGGGTCAATGATTTCACTTTTATGATGCTTCCAAAGTGTCTTGTCTTCTTC 480
Qy      1502 CCAACTGACAAATGCAAGTTGAGAAATATGATCATTAATTTAGCATTAACAGAGCAGT 1561
Db      481 CCAACTGACAAATGCAAGTTGAGAAATATGATCATTAATTTAGCATTAACAGAGCAGT 540
Qy      1562 CGGCGACACCGATTTTAAATAACTGAGACCTTCTTTTAAACAAACAAATGCGGGT 1621
Db      541 CGGCGACACCGATTTTAAATAACTGAGACCTTCTTTTAAACAAACAAATGCGGGT 600
Qy      1622 TTAATTTCAAGATGATTTTCACTCGGTGAATGTCCAGGAAAGACCTTTCACCTTGACTA 1681
Db      601 TTAATTTCAAGATGATTTTCACTCGGTGAATGTCCAGGAAAGACCTTTCACCTTGACTA 660
Qy      1682 TATGGCATTTAGTCAACAAGCTGTGAGCTTCTCTTCCATCTCTGCTGAGCAGCTA 1741
Db      661 TATGGCATTTAGTCAACAAGCTGTGAGCTTCTCTTCCATCTCTGCTGAGCAGCTA 720
Qy      1742 AGACCTCAGTTTCAATAGCATTAAGACAGTGGAGCTCAGCTGGGTGATTTGCGCCCC 1801
Db      721 AGACCTCAGTTTCAATAGCATTAAGACAGTGGAGCTCAGCTGGGTGATTTGCGCCCC 780
Qy      1802 CATCTCCGGGGGAATGTCTGAAGACAAATTTTGTGTCTCAATGAGGAGTGGAGGAGA 1861
Db      781 CATCTCCGGGGGAATGTCTGAAGACAAATTTT-GTTAATCTCAATGAGGAGTGGAGGAGA 839
Qy      1862 TACAGTGTACTACCAACTAGTGAATGAAGGAGGAGTGTGCTCAACTCTCTACATG 1921
Db      840 TACAGTGTACTACCAACTAGTGAATGAAGGAGGAGTGTGCTCAACTCTCTACATG 899
Qy      1922 TACAGAGCTCTCCCATTAACAATCAACCAATCCGAAAGTGTCAACTGTGTGAGACTAAG 1981

```

Db	900	TACGAGCGTCTCCCACTTACACTACCAATCCGAGTGTCACTGTGACGACTAAG	959
Qy	1982	AAACCTGGTTTTAGTAGAAAAGGSCCTGGAAAAGAGGAGCCAACTCTGTCTCT	2041
Db	960	AAACCTGGTTTTAGTAGAAAAGGSCCTGGAAAAGAGGAGCCAACTCTGTCTCT	1019
Qy	2042	T-CTCACAATTAGCTTAGTGGCAATTAAGACTTCTGTCTCTTTGGCTGCTGCTCAGCAG	2100
Db	1020	TCCTCACATTTAGTCAATTTGGCAAAATTAAGACTTCTGTCTTTGGCTGCTGCTCAGCAG	1079
Qy	2101	AGAGCGAACACTCATATGGGGACCAAGGATTAATCTCTCAGTGAACAGAGTTGCAAGGC	2160
Db	1080	AGAGCGAACACTCATATGGGGACCAAGGATTAATCTCTCAGTGAACAGAGTTGCAAGGC	1139
Qy	2161	CTAATGGGAAATGCGCTGATGGGATTAATCTTCACTGTGTGAAGCTTCTAAGTTCTTCCCT	2220
Db	1140	CTAATGGGAAATGCGCTGATGGGATTAATCTTCACTGTGTGAAGCTTCTAAGTTCTTCCCT	1139
Qy	2221	TCATTTCAACCTGCAGAACCAAGTTCTGTAGAAGAAATGCTGAGTTCTAGCTCAGTTTT	2280
Db	1200	TCATTTCAACCTGCAGAACCAAGTTCTGTAGAAGAAATGCTGAGTTCTAGCTCAGTTTT	1259
Qy	2281	CTTACTCTGCAATTTAGATCTCAGACCCCTTCTGCGCCCAATTTCAATTAAGGACAA	2340
Db	1260	CTTACTCTGCAATTTAGATCTCAGACCCCTTCTGCGCCCAATTTCAATTAAGGACAA	1319
Qy	2341	CATATACCTTCATGAGACACACACAGACTTTTGAAGCAAGACAATGATGCTGTAAT	2400
Db	1320	CATATACCTTCATGAGACACACACAGACTTTTGAAGCAAGACAATGATGCTGTAAT	1379
Qy	2401	TGAGGCGCTTGAGGAATGAAGCTTTGAAAGAAAAGATACTTTGTTCCAGGCCCTTCC	2460
Db	1380	TGAGGCGCTTGAGGAATGAAGCTTTGAAAGAAAAGATACTTTGTTCCAGGCCCTTCC	1439
Qy	2461	ACACTCTTCATGTGTAACTCACTGCTTCTCTGAGACTTTGAGCCACGCTGACTGATTAAC	2520
Db	1440	ACACTCTTCATGTGTAACTCACTGCTTCTCTGAGACTTTGAGCCACGCTGACTGATTAAC	1499
Qy	2521	ATGTTGTATAGAAAACCTGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTAATATAC	2580
Db	1500	ATGTTGTATAGAAAACCTGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTAATATAC	1559
Qy	2581	ATTTCCT 2587	
Db	1560	ATTTCCT 1566	
RESULT 4			
	US-09-338-933-74		
	; Sequence 943, Application US/09338933		
	; Patent No. 6488931		
	GENERAL INFORMATION:		
	APPLICANT: Mitcham, Jennifer Lynn		
	APPLICANT: King, Gordon E.		
	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF		
	FILE OF INVENTION: OVARIAN CANCER		
	FILE REFERENCE: 210121.462CI		
	CURRENT APPLICATION NUMBER: US/09/338,933		
	CURRENT FILING DATE: 1999-06-23		
	NUMBER OF SEQ ID NOS: 312		
	SOFTWARE: FastSeq for Windows Version 3.0		
	SEQ ID NO 74		
	LENGTH: 1567		
	TYPE: DNA		
	ORGANISM: Homo sapien		
	US-09-338-933-74		
Query Match 59.6%; Score 1543; DB 4; Length 1567;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1565; Conservative 0; Mismatches 0; Indels 2; Gaps 2;			
Qy	1022	ATATCTAGAGTCTGAGTGAGCAAAACAAAGACAGAAAACAAAAGAACCAAGCAGA	10811

Db	1	ATATCTGAAGACTCTGGAGTGAAGCAACAGAGCAAGAAACAAAAGAAAGCCAAAGCAG	60
Qy	1082	AGGCTCCAAATATGAAACAAGATAAATCTATCTTCACAAGACATATTAGAGTTGGGAAAAATA	11411
Db	61	AGGCTCCAAATATGAAACAAGATAAATCTATCTTCACAAGACATATTAGAGTTGGGAAAAATA	120
Qy	1142	ATTATGATGAACTTGAACAAGTGTGTAAAGATGAATAAGTAAATATGCATGTGAGACAAAGT	12012
Db	121	ATTATGATGAACTTGAACAAGTGTGTAAAGATGAATAAGTAAATATGCATGTGAGACAAAGT	180
Qy	1202	GCATCCCCAGATCTCAGGGACCTCCCTGCTGTCACTCGGGGAGTGAAGACAGGAT	12612
Db	181	GCATCCCCAGATCTCAGGGACCTCCCTGCTGTCACTCGGGGAGTGAAGACAGGAT	240
Qy	1262	AGTGCATGTTCTTTGTCTCTGCAATTTTAAAGTAAATGCTGAATGTTGCTCTGAGGAA	13212
Db	241	AGTGCATGTTCTTTGTCTCTGCAATTTTAAAGTAAATGCTGAATGTTGCTCTGAGGAA	300
Qy	1322	GCCCCCTGAAAAGTCTATCCCAACATATCCATCTTATATTCACAATAATTAAGCTATAGT	13812
Db	301	GCCCCCTGAAAAGTCTATCCCAACATATCCATCTTATATTCACAATAATTAAGCTATAGT	360
Qy	1382	ATGTAACTTGAAGAGCTGTATATGACCTGCACCTCGCACTCGAGGGGGGGCTGCATTTT	14412
Db	361	ATGTAACTTGAAGAGCTGTATATGACCTGCACCTCGCACTCGAGGGGGGGCTGCATTTT	420
Qy	1442	AGTATAGGGTCAAAATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTGCTCTCTTC	15012
Db	421	AGTATAGGGTCAAAATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTGCTCTCTTC	480
Qy	1502	CCAACTGACAAATGCCAAAGTTGAGAAAATGATCATATATTATTAAGCATAAACAGAGCAGT	15612
Db	481	CCAACTGACAAATGCCAAAGTTGAGAAAATGATCATATATTATTAAGCATAAACAGAGCAGT	540
Qy	1562	CGGGGACACCGATTTTATTAATACTGAGACCTTCTTTTAAACAACAAATGCGGGT	16212
Db	541	CGGGGACACCGATTTTATTAATACTGAGACCTTCTTTTAAACAACAAATGCGGGT	600
Qy	1622	TTATTTTCTCAGATGATGTTCACTCCGTAAATGCTCAAGGAGAGACCTTTCACTTGACTA	16812
Db	601	TTATTTTCTCAGATGATGTTCACTCCGTAAATGCTCAAGGAGAGACCTTTCACTTGACTA	660
Qy	1682	TATGGCATTTATGTCATGACAAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAACAAGTA	17412
Db	661	TATGGCATTTATGTCATGACAAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAACAAGTA	720
Qy	1742	AGACCTCAGTTTCAATATGCACTTAAGAGCATGTGGGACTCAGCTTGGGGTGAATTTGGCCCC	18012
Db	721	AGACCTCAGTTTCAATATGCACTTAAGAGCATGTGGGACTCAGCTTGGGGTGAATTTGGCCCC	780
Qy	1802	CATCTCCGGGGGAATGCTGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGAGA	18612
Db	781	CATCTCCGGGGGAATGCTGAAGACAAATTTGGTTACTCAATGAGGAGTGAAGAGAGA	839
Qy	1862	TACAGTGTACTACCAACTAGTGATTAAGGCCAGGATGCTGTCAACCTCTTACCAATG	19212
Db	840	TACAGTGTACTACCAACTAGTGATTAAGGCCAGGATGCTGTCAACCTCTTACCAATG	899
Qy	1922	TACAGAGCTTCTCCCATTTACACTACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAG	19812
Db	900	TACAGAGCTTCTCCCATTTACACTACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAG	959
Qy	1982	AAACCCGTGGTTTGAATGAGAAAAGGGCTGGAAAAGAGGGGAGCCAAACAAATCTGTGCT	20412
Db	960	AAACCCGTGGTTTGAATGAGAAAAGGGCTGGAAAAGAGGGGAGCCAAACAAATCTGTGCT	10119
Qy	2042	T-CTACATTAGTATGGCAATATAGCATTTCTCTTTGGCTGTGCTCAGACAG	21002
Db	1020	TCCTCAACTTATAGTATGGCAATATAGCATTTCTCTTTGGCTGTGCTCAGACAG	10719
Qy	2101	AGAGCCAGAACTTATGGGGCACAGATTAACATCTCTCACTGAACAAGTTGACAGGC	21602

Db	1080	AGAGCGAGAACTCATTCGGGCAACGAGTAACATCTCTCATGAACAGAGTTGACAAAGC	1139
Qy	2161	CTATGGGAAATGCCCTGATGGGATTAATCTTCAGCTTTGAGCTTCTAAATTTCTTCTCCCT	2220
Db	1140	CTATGGGAAATGCCCTGATGGGATTAATCTTCAGCTTTGAGCTTCTAAATTTCTTCTCCCT	1199
Qy	2221	TCATTTCTACCCCTGCAGCGCAAGTCTGTAAAGAAATGCCCTGAGTTCTAGCTCAGGTTTT	2280
Db	1200	TCATTTCTACCCCTGCAGCGCAAGTCTGTAAAGAAATGCCCTGAGTTCTAGCTCAGGTTTT	1259
Qy	2281	CTTACTCTGAATTTAGATCTTCAGACCCCTTCCTGGCCACATTCGAAATTAAGCAACAA	2340
Db	1260	CTTACTCTGAATTTAGATCTTCAGACCCCTTCCTGGCCACATTCGAAATTAAGCAACAA	1319
Qy	2341	CATATACCTTCATGAGACACACACAGCTTTGAAAGCAGACATGACTCTTGAT	2400
Db	1320	CATATACCTTCATGAGACACACACAGCTTTGAAAGCAGACATGACTCTTGAT	1379
Qy	2401	TGAGGCCCTTGAGGATGAAGCTTTGAAGAAAAGATCTTGTTCCAGGCCCTTCCC	2460
Db	1380	TGAGGCCCTTGAGGATGAAGCTTTGAAGAAAAGATCTTGTTCCAGGCCCTTCCC	1439
Qy	2461	ACACTCTTCATGTGTTAAACAATGCTTCTCTGAGCCTTGAAGCACAAGGTGACTGATTAAC	2520
Db	1440	ACACTCTTCATGTGTTAAACAATGCTTCTCTGAGCCTTGAAGCACAAGGTGACTGATTAAC	1499
Qy	2521	ATGTTGTTATGAAAAATCGATTTTAGATTTCTGATCTTCAAGAGAAATGATTAATATAC	2580
Db	1500	ATGTTGTTATGAAAAATCGATTTTAGATTTCTGATCTTCAAGAGAAATGATTAATATAC	1559

RESULT 5
US-09-215-681-74

```

: Sequence 74, Application US/09215681A
: Patent No. 6528253
:
: GENERAL INFORMATION:
:
: APPLICANT: Matcham, Jennifer L.
: APPLICANT: Frudakis, Tony N.
: APPLICANT: King, Gordon B.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
: OF INVENTION: OF OVARIAN CANCER
: FILE REFERENCE: 210121.463
: CURRENT APPLICATION NUMBER: US/09/215,681A
: CURRENT FILING DATE: 1998-12-17
: NUMBER OF SEQ ID NOS: 310
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 74
:
: LENGTH: 1567
:
: TYPE: DNA
:
: ORGANISM: Homo sapien
:
: US-09-215-681-74

```

Query Match	59.6%	Score 1543;	DB 4;	Length 1567;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1565; Conservative	0;	Mismatches 0;	Indels 2;	Gaps 2

QY	1022	ATATCTTAAGAGCTCTGGAGTGAGCAACAAGAGCAGAGAAACAAAAGAGCCAAAGCAGA	108
Db	1	ATATCTTAAGAGCTCTGGAGTGAGCAACAAGAGCAGAGAAACAAAAGAGCCAAAGCAGA	60
QY	1082	AGGCTCCAATGTGAACAAGATTAATCTATCTTCAAGAGCATTTAGAAAGTTGGAGAAATA	114
Db	61	AGGCTCCAATGTGAACAAGATTAATCTATCTTCAAGAGCATTTAGAAAGTTGGAGAAATA	120
QY	1142	ATTCACTGGAAGCTTAACAAGAGTGCTGTTAAGAGGATTAAGTAAAAATGACAGTGAGCAAGT	120
Db	121	ATTCACTGGAAGCTTAACAAGAGTGCTGTTAAGAGGATTAAGTAAAAATGACAGTGAGCAAGT	180
QY	1202	GCATCCCCAGATCTTCAGGAGCTCCCTCCCTGCTGTACCTGGGAGTGAGAGACAGAT	1261

Db	131	GCATCCCAAGATCTCAGGAGACTCCCCCTGCTGTCACTCGGAGGTAGAGACAGAT	240
Qy	1262	AGTGCATGTTCTTTGTCTCTGAAATTTTAAATTAATGCTGTAAATGTTGCTCTGAGAA	1322
Db	241	AGTGCATGTTGTTTGTCTGTGAATTTTAAATTAATGCTGTAAATGTTGCTCTGAGAA	300
Qy	1322	GCCCTGGAAAGTCTATCCCAACATCTCAACATCTTAAATTCACAAATTAAGCTGTAGT	1388
Db	301	GCCCTGGAAAGTCTATCCCAACATCTCAACATCTTAAATTCACAAATTAAGCTGTAGT	360
Qy	1362	ATGTACCCCTAAGAGCGCTGTAAATGACCTTGCCACCTCGCAACCTGAGGGCGGCTGCATTTT	1441
Db	361	ATGTACCCCTAAGAGCGCTGTAAATGACCTTGCCACCTCGCAACCTGAGGGCGGCTGCATTTT	420
Qy	1442	AGTAATGGGTCAAAATGATTCACCTTTTAAATGATGCTTCCAAAGTGCTCTTGCTTCTTC	1501
Db	421	AGTAATGGGTCAAAATGATTCACCTTTTAAATGATGCTTCCAAAGTGCTCTTGCTTCTTC	480
Qy	1502	CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATATTTTACATPAAACAGACAGT	1561
Db	481	CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATATTTTACATPAAACAGACAGT	540
Qy	1562	CGGCGACACCAATTTTAAATPAAACATGAGACCTTCTTTTAAACAAATGCGAGT	1622
Db	541	CGGCGACACCAATTTTAAATPAAACATGAGACCTTCTTTTAAACAAATGCGAGT	600
Qy	1622	TTATTTCTCAGATGATGTTCAATCCGTGAATGGTCCAGGGAAGACCTTTCACCTTGACTA	1683
Db	601	TTATTTCTCAGATGATGTTCAATCCGTGAATGGTCCAGGGAAGACCTTTCACCTTGACTA	660
Qy	1682	TATGSCATTAATGTCATCAACAGCTCTGAGGCTTCTCTTTCCATCTCGCTGGACACTA	1744
Db	661	TATGSCATTAATGTCATCAACAGCTCTGAGGCTTCTCTTTCCATCTCGCTGGACACTA	720
Qy	1742	AGACCTCAGTTTTCATATAGCATCTTAGACAGTGGGACCTCAGCTGGGGTGATTTGGCCCC	1804
Db	721	AGACCTCAGTTTTCATATAGCATCTTAGACAGTGGGACCTCAGCTGGGGTGATTTGGCCCC	780
Qy	1802	CATCTCCCGGGGAAATGTCAGAAACAATTTTGTTAAGCTCAATGAGGAGTGAAGAGAA	1861
Db	781	CATCTCCCGGGGAAATGTCAGAAACAATTTTGTTAAGCTCAATGAGGAGTGAAGAGAA	839
Qy	1862	TACAGTGTACTACCAACTAGTGATTAAGGCGCAGGAGTGTCTCAACTCTCTCAATG	1922
Db	840	TACAGTGTACTACCAACTAGTGATTAAGGCGCAGGAGTGTCTCAACTCTCTCAATG	899
Qy	1922	TACAGGAAGTCTCCCACTTAACAATACCCATCCGAATGTCACTGTGTACAGACTAAG	1981
Db	900	TACAGGAAGTCTCCCACTTAACAATACCCATCCGAATGTCACTGTGTACAGACTAAG	959
Qy	1982	AAACCTGTTTTAGTAGTAAAAAGGGGCTGGAAAGAGGGAGCCAAACAATCTGTCTCT	2041
Db	960	AAACCTGTTTTAGTAGTAAAAAGGGGCTGGAAAGAGGGAGCCAAACAATCTGTCTCT	10115
Qy	2042	TCTCACATTAGTCAATGGCAAAATAGCAATCTGTCTTTTGACTGTGCTCAGACAG	2100
Db	1020	TCTCACATTAGTCAATGGCAAAATAGCAATCTGTCTTTTGACTGTGCTCAGACAG	1072
Qy	2101	AGAGCCAGAACTATTCGGGCAACAGATTAATCTCTCAGTGAACAGATTGACAAAGC	2166
Db	1080	AGAGCCAGAACTATTCGGGCAACAGATTAATCTCTCAGTGAACAGATTGACAAAGC	1133
Qy	2161	CTATGGGAAATGCGTAGGGATTAATCTTCAGCTTGTAAGCTTCTAAGTTCTTTCCCT	2222
Db	1140	CTATGGGAAATGCGTAGGGATTAATCTTCAGCTTGTAAGCTTCTTAAAGTTCTTTCCCT	1199
Qy	2221	TCATTCTACCTGCAAGCCAAATCTGTGAAGAAATCCTGAGTTCTAGCTCAGTTTTT	2280
Db	1200	TCATTCTACCTGCAAGCCAAATCTGTGAAGAAATCCTGAGTTCTAGCTCAGTTTTT	1255
Qy	2281	CTTACTCTGAATTTAGATCTCCAGACCTTCTTGCCCAATTCAAATTAAGCAACAA	2346

Db 1260 CTTACTGTGATTTAGATCTCCAGACCCCTTCCTGGCCACATTCATTAAGCAACAA 1319
Qy 2341 CATATACCTCCATGAGACACACACATTTTGAAGCAAGCAATGACTGTTAAAT 2400
Db 1320 CATATACCTCCATGAGACACACACATTTTGAAGCAAGCAATGACTGTTAAAT 1379
Qy 2401 TGAGGCTTGAAGATGAGATTTGAAGAAAGAAATGATTTGTTCCAGCCCTTCCC 2460
Db 1380 TGAGGCTTGAAGATGAGATTTGAAGAAAGAAATGATTTGTTCCAGCCCTTCCC 1439
Qy 2461 ACACTCTTCATGTGTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATAC 2520
Db 1440 ACACTCTTCATGTGTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATAC 1499
Qy 2521 ATGTGTATAGAAATGATTTTGAAGTTGATCTGATCTTCAAGGAATGATTAATATAC 2580
Db 1500 ATGTGTATAGAAATGATTTTGAAGTTGATCTGATCTTCAAGGAATGATTAATATAC 1559
Qy 2581 ATTTCT 2587
Db 1560 ATTTCT 1566

RESULT 6
US-09-216-003A-74
Sequence 74, Application US/09216003A
Patent No. 6670463
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Prudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
FILE REFERENCE: 210121.462
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patencin Ver. 2.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapiens
US-09-216-003A-74

Query Match 59.6%; Score 1543; DB 4; Length 1567;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1022 ATATCTAGAGTCTGAGTGAAGCAACAAAGCAAGAAACAAAAGCCAAAGCAGA 1081
Db 1 ATATCTAGAGTCTGAGTGAAGCAACAAAGCAAGAAACAAAAGCCAAAGCAGA 60
Qy 1082 AGGCTCCATATGAAACAAGATTAATCTATCTCAAGACATATTGAAGTTGGAAAAATA 1141
Db 61 AGGCTCCATATGAAACAAGATTAATCTATCTCAAGACATATTGAAGTTGGAAAAATA 120
Qy 1142 ATTCATGTGAACCTGAGCAATGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1201
Db 121 ATTCATGTGAACCTGAGCAATGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 180
Qy 1202 GCATCCCAAGATCTCAGGAGCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1261
Db 181 GCATCCCAAGATCTCAGGAGCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 1262 AGTGCAATGTTCTGTCTGAAATTTTGAATGATGTGCTGATGTTGCTCTGAGAA 1321
Db 241 AGTGCAATGTTCTGTCTGAAATTTTGAATGATGTGCTGATGTTGCTCTGAGAA 300
Qy 1322 GCGGCTGGAAGATCTATCCCAATATCCCAATATATATATATATATATATATATATAT 1381
Db 301 GCGGCTGGAAGATCTATCCCAATATCCCAATATATATATATATATATATATATATAT 360
Qy 1382 ATGTACCTTGAAGAGCTGTATATGACTGCACTTGCACACTCAGGGGCGGCTGCAATTT 1441
Db ATGTACCTTGAAGAGCTGTATATGACTGCACTTGCACACTCAGGGGCGGCTGCAATTT 1441

Db 361 ATGTACCTTGAAGAGCTGTATATGACTGCACTTGCACACTCAGGGGCGGCTGCAATTT 420
Qy 1442 AGTAATGGGTCAAAATGATTCATCTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTC 1501
Db 421 AGTAATGGGTCAAAATGATTCATCTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTC 480
Qy 1502 CCAACTGACAAATGCAAAAGTTGAGAAAAATGATTCATATTTTATGATTAACAGACAGT 1561
Db 481 CCAACTGACAAATGCAAAAGTTGAGAAAAATGATTCATATTTTATGATTAACAGACAGT 540
Qy 1562 CCGGCAACCGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1621
Db 541 CCGGCAACCGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Qy 1622 TTATTTCTCAGATGATGTTTATTCCTGATATGTTTCCAGGGAAGGACCTTTTCACTT 1681
Db 601 TTATTTCTCAGATGATGTTTATTCCTGATATGTTTCCAGGGAAGGACCTTTTCACTT 660
Qy 1682 TATGCAATATGTCATCAACAGCTGAGGCTTCTCTTCCATCTCTGCGTGAAGCTTA 1741
Db 661 TATGCAATATGTCATCAACAGCTTGAAGCTTCTCTTCCATCTCTGCGTGAAGCTTA 720
Qy 1742 AGACTCAGTTTCAATATGATCTAGAGCAAGTGAAGCTGAGTGGGTGATTTGCCCCC 1801
Db 721 AGACTCAGTTTCAATATGATCTAGAGCAAGTGAAGCTGAGTGGGTGATTTGCCCCC 780
Qy 1802 CATCTCCGGGGGAATGTCGAAGACAAATTTGTTTCTCTCATATGAGGAGTGAAGAGGA 1861
Db 781 CATCTCCGGGGGAATGTCGAAGACAAATTTT- GTTACTCATATGAGGAGTGAAGAGGA 839
Qy 1862 TACAGTCTACTACCAACTAGTGAATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1921
Db 840 TACAGTCTACTACCAACTAGTGAATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 899
Qy 1922 TACAGGAGCTCTCCCATTAACAATCCCAATCCGAAGTGTCAATCTGTGACAGACTAAG 1981
Db 900 TACAGGAGCTCTCCCATTAACAATCCCAATCCGAAGTGTCAATCTGTGACAGACTAAG 959
Qy 1982 AAACTCTGTTTGAATGAGAAAGGCTGGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAG 2041
Db 960 AAACTCTGTTTGAATGAGAAAGGCTGGAAGAAAGGAGGAGGAGGAGGAGGAGGAGG 1019
Qy 2042 T-CTCATTAGCATTTGCAATTAAGCATTTGCTCTTGGCTGCTGCTGCTGCTGCTGCTG 2100
Db 1020 TCTTCATATGATCTGAGCAATTAAGCATTTGCTCTTGGCTGCTGCTGCTGCTGCTGCTG 1079
Qy 2101 AGAGCCAGAACTCTATCGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGC 2160
Db 1080 AGAGCCAGAACTCTATCGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGC 1139
Qy 2161 CTATGGGAATGCTGATGAGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTTCCT 2220
Db 1140 CTATGGGAATGCTGATGAGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTTCCT 1199
Qy 2221 TCATTTCACTGCAAGGCAAGTCTGTAAGAAATGCTGATCTGATCTGATCTGATCTG 2280
Db 1200 TCATTTCACTGCAAGGCAAGTCTGTAAGAAATGCTGATCTGATCTGATCTGATCTG 1259
Qy 2281 CTTACTCTGAATTTGATCTCCAGACCTTCTGCGCAATTCATTAATTAAGCAACAA 2340
Db 1260 CTTACTCTGAATTTGATCTCCAGACCTTCTGCGCAATTCATTAATTAAGCAACAA 1319
Qy 2341 CATATACCTTCAATGAGACACACAGATTTTGAAGCAAGCAATGACTGTTGAAT 2400
Db 1320 CATATACCTTCAATGAGACACACAGATTTTGAAGCAAGCAATGACTGTTGAAT 1379
Qy 2401 TGAGGCTTGAAGATGAGATTTGAAGAAAGAAATGATTTGTTCCAGCCCTTCCC 2460
Db 1380 TGAGGCTTGAAGATGAGATTTGAAGAAAGAAATGATTTGTTCCAGCCCTTCCC 1439
Qy 2461 ACACTCTTCATGTGTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATATAC 2520
Db 1440 ACACTCTTCATGTGTAAACCACTGCTTCTGACCTTGAAGCCAGGTGATGTATATAC 1499

```
RESULT 7
US-09-667-857-74
; Sequence 74, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retzer, Marc W.
; APPLICANT: Ranger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.46205
; CURRENT APPLICATION NUMBER: US/09/667,857
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FaalSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-667-857-74

Query Match      59.6%; Score 1543; DB 4; Length 1567;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY      1022 ATATCTAGAGTCTGAGTGTGAGCAACAGAGCAAGAAACAAAGAGCCAAAGACCA 1081
DB      1 ATATCTAGAGTCTGAGTGTGAGCAACAGAGCAAGAAACAAAGAGCCAAAGACCA 60
QY      1082 AGGCTCCAAATATGAAACAATAATCTATCTCAAGACATATTAAGATGGGAAATA 1141
DB      61 AGGCTCCAAATATGAAACAATAATCTATCTCAAGACATATTAAGATGGGAAATA 120
QY      1142 ATTCATGTGAAGTGAAGTGTGTAAGATGATTAAGTAAATGACATGAGACAAAGT 1201
DB      121 ATTCATGTGAAGTGAAGTGTGTAAGATGATTAAGTAAATGACATGAGACAAAGT 180
QY      1202 GCATCCCAAGATCTCAGGAGACCTCCCGCTGCTGTCACCTGAGAGTGAAGAGACAGAT 1261
DB      181 GCATCCCAAGATCTCAGGAGACCTCCCGCTGCTGTCACCTGAGAGTGAAGAGACAGAT 240
QY      1262 AATGATATGTTTGTGCTGTGAATTTTAAATGATTAATGATGCTGAAGAA 1321
DB      241 AATGATATGTTTGTGCTGTGAATTTTAAATGATTAATGATGCTGAAGAA 300
QY      1322 GCCCTGGAAGATCTATCCCAATATCCCAATCTTAATTCACAAATTAAGCTGTAGT 1381
DB      301 GCCCTGGAAGATCTATCCCAATATCCCAATCTTAATTCACAAATTAAGCTGTAGT 360
QY      1382 ATGTACCTTAAGACGCTGTGAATTAAGCTGCACTTGCAAGTCAAGGAGGCGCTGACATTT 1441
DB      361 ATGTACCTTAAGACGCTGTGAATTAAGCTGCACTTGCAAGTCAAGGAGGCGCTGACATTT 420
QY      1442 AGTAATGGGTCAAAATGATTCATTTTAAATGATGCTTCCAAAGGTGCTTGGCTTCTCTTC 1501
DB      421 AGTAATGGGTCAAAATGATTCATTTTAAATGATGCTTCCAAAGGTGCTTGGCTTCTCTTC 480
```

```
QY      1502 CCMACTGACAAATGCAAAAGTTGAGAAAATGATCATTAATTTTATGACATTAACAGAGACGT 1561
DB      481 CCAACTGACAAATGCAAAAGTTGAGAAAATGATCATTAATTTTATGACATTAACAGAGACGT 540
QY      1562 CGGCGACACCGATTTTAAATTAATTAACCTGAGACCTCTTTTAAACAAATGCGGGT 1621
DB      541 CGGCGACACCGATTTTAAATTAATTAACCTGAGACCTCTTTTAAACAAATGCGGGT 600
QY      1622 TTATTTCTCAGATGATGTTCAATCCGTGAATGATGTCAGAGGAAAGACCTTTCACTTGACAT 1681
DB      601 TTATTTCTCAGATGATGTTCAATCCGTGAATGATGTCAGAGGAAAGACCTTTCACTTGACAT 660
QY      1682 TATGCAATTAATGATCAACAGCTCTGAGGCTTCTCTTCATCTGCGTGAACAGCTA 1741
DB      661 TATGCAATTAATGATCAACAGCTCTGAGGCTTCTCTTCATCTGCGTGAACAGCTA 720
QY      1742 AGACTCAGTTTTCATATGACATCTAGACAGTGGGACCTGAGTGGGATTTGGCCCC 1801
DB      721 AGACTCAGTTTTCATATGACATCTAGACAGTGGGACCTGAGTGGGATTTGGCCCC 780
QY      1802 CATCTCCGGGGGAATGTCGAAGACAAATTTTGGTTACCTCAATGAGGAGTGAAGAGAA 1861
DB      781 CATCTCCGGGGGAATGTCGAAGACAAATTTTGGTTACCTCAATGAGGAGTGAAGAGAA 839
QY      1862 TACAGTGTACTACCACTAGATGAATAAGGCGAGAGTGTCTCAACCTTCAACATG 1921
DB      840 TACAGTGTACTACCACTAGATGAATAAGGCGAGAGTGTCTCAACCTTCAACATG 899
QY      1922 TACAGAGTGTCTCCCATTAACATCACTACCAATCCGAAATGTCACCTGTGACAGCTAAG 1981
DB      900 TACAGAGTGTCTCCCATTAACATCACTACCAATCCGAAATGTCACCTGTGACAGCTAAG 959
QY      1982 AAACCTGATTTTGTAGTGAAGAAAGGCGCTGGAAGAGGAGGCCAAATCTGTCTGCT 2041
DB      960 AAACCTGATTTTGTAGTGAAGAAAGGCGCTGGAAGAGGAGGCCAAATCTGTCTGCT 1019
QY      2042 T-CTCACAATTAATGATGAGCAAAATTAAGCATTTCTGTCTTGTGCTGCTCAGACAG 2100
DB      1020 TCCTCACAATTAATGATGAGCAAAATTAAGCATTTCTGTCTTGTGCTGCTCAGACAG 1079
QY      2101 AGAGCACAAGCTCTATCGGGCACCGAGTAACATCTCTCACTGAAACAAAGTTGACAAAGC 2160
DB      1080 AGAGCACAAGCTCTATCGGGCACCGAGTAACATCTCTCACTGAAACAAAGTTGACAAAGC 1139
QY      2161 CTATGGGAAATGCGCTGATGGGATTTCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCT 2220
DB      1140 CTATGGGAAATGCGCTGATGGGATTTCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCT 1199
QY      2221 TCATTTCTACCTGCAAGCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTT 2280
DB      1200 TCATTTCTACCTGCAAGCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTT 1259
QY      2281 CTTACTCTGAATTTAGATCTCAGACCTCTTCTGCGCCAAATTCAAATTAAGGCAACAA 2340
DB      1260 CTTACTCTGAATTTAGATCTCAGACCTCTTCTGCGCCAAATTCAAATTAAGGCAACAA 1319
QY      2341 CATATACCTTCATGAGACACACAGACTTTTGAACAAAGAACATGACTGCTTGAAT 2400
DB      1320 CATATACCTTCATGAGACACACAGACTTTTGAACAAAGAACATGACTGCTTGAAT 1379
QY      2401 TGAGGCTTTGAGAAATGAAGCTTTGAAAGAAAGATACTTTGTTCCAGGCCCTTCC 2460
DB      1380 TGAGGCTTTGAGAAATGAAGCTTTGAAAGAAAGATACTTTGTTCCAGGCCCTTCC 1439
QY      2461 ACACCTTCAATGTTTAAACCACTGCTTCTGAGACCTTGAAGCCAGGCTGATCTATAC 2520
DB      1440 ACACCTTCAATGTTTAAACCACTGCTTCTGAGACCTTGAAGCCAGGCTGATCTATAC 1499
QY      2521 ATGTTGATTAAGAAACGATTTTGAAGTTCGATCGTTCAAGAGAAATGATTAATATAC 2580
DB      1500 ATGTTGATTAAGAAACGATTTTGAAGTTCGATCGTTCAAGAGAAATGATTAATATAC 1559
QY      2581 ATTTCT 2587
```



```
Db      ||| 1151 AACTAGACAAAGTGTGTAAGAGTGAATTAATAATGACAGAGCAAGTGCATCCCA 1210
        ||| 121 AACTAGACAAAGTGTGTAAGAGTGAATTAATAATGACAGAGCAAGTGCATCCCA 180
Qy      ||| 1211 GATCTCAGGAGACTCCCTGCTGCTGACCTGGGAGTGAAGAGCAGATAGTGCATGT 1270
        ||| 181 GATCTCAGGAGACTCCCTGCTGCTGACCTGGGAGTGAAGAGCAGATAGTGCATGT 240
Qy      ||| 1271 TCTTTGCTCTGAATTTTAAATTGATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 1330
        ||| 241 TCTTTGCTCTGAATTTTAAATTGATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 300
Qy      ||| 1331 AAGTATCCCAACATATCCATCTTAATTCACAAATTAAGCTGTATGTAACCT 1390
        ||| 301 AAGTATCCCAACATATCCATCTTAATTCACAAATTAAGCTGTATGTAACCT 360
Qy      ||| 1391 AAGAGCTGCTAATTAAGTGCACCTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 1450
        ||| 361 AAGAGCTGCTAATTAAGTGCACCTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 420
Qy      ||| 1451 TCAATATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTCTCTCCCACTGAC 1510
        ||| 421 TCAATATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTCTCTCCCACTGAC 480
Qy      ||| 1511 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGACATTAACAGAGCAGTGGGAGAC 1570
        ||| 481 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGACATTAACAGAGCAGTGGGAGAC 540
Qy      ||| 1571 C 1571
        ||| 541 C 541
Db      ||| 541 C 541
```

```
RESULT 10
US-09-338-933-28
; Sequence 28, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-338-933-28
```

```
Query Match      20.6%; Score 532.2; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 2.6e-150;
Matches 534; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      ||| 1031 AACTGAGTGAAGCAAAAGAGCAAGAAACAAAAGCCAAAAGCAAGAGCTCCAA 1090
        ||| 1 AACTGAGTGAAGCAAAAGAGCAAGAAACAAARRAGAGCCAAAAGCAGAGCTCCAA 60
Db      ||| 1091 TATGAACAAGATTAATCTATCTTCAAAAGCATTTTGAAGTTGGGAAAAATTAATCATGTG 1150
        ||| 61 TATGAACAAGATTAATCTATCTTCAAAAGCATTTTGAAGTTGGGAAAAATTAATCATGTG 120
Qy      ||| 1151 AACTAGACAAGTGTGTTAAGAGTGAATGAATGAATGACAGTGGAGACAAGTGCATCCCA 1210
        ||| 121 AACTAGACAAGTGTGTTAAGAGTGAATGAATGAATGACAGTGGAGACAAGTGCATCCCA 180
Qy      ||| 1211 GATCTCAGGAGACTCCCTGCTGCTGACCTGGGAGTGAAGAGCAGATAGTGCATGT 1270
```

```
Db      ||| 181 GATCTCAGGAGACTCCCTGCTGCTGACCTGGGAGTGAAGAGCAGATAGTGCATGT 240
Qy      ||| 1271 TCTTTGCTCTGAATTTTAAATTGATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 1330
        ||| 241 TCTTTGCTCTGAATTTTAAATTGATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 300
Qy      ||| 1331 AAGTATCCCAACATATCCATCTTAATTCACAAATTAAGCTGTATGTAACCT 1390
        ||| 301 AAGTATCCCAACATATCCATCTTAATTCACAAATTAAGCTGTATGTAACCT 360
Qy      ||| 1391 AAGAGCTGCTAATTAAGTGCACCTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 1450
        ||| 361 AAGAGCTGCTAATTAAGTGCACCTTCGCACTCAGGGGCGGCTGCATTTTATGTAATGG 420
Qy      ||| 1451 TCAATATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTCTCTCCCACTGAC 1510
        ||| 421 TCAATATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTCTCTCCCACTGAC 480
Qy      ||| 1511 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGACATTAACAGAGCAGTGGGAGAC 1570
        ||| 481 AATGCGCAAGTTGAGAAAAATGATCATATTTTATGACATTAACAGAGCAGTGGGAGAC 540
Qy      ||| 1571 C 1571
        ||| 541 C 541
Db      ||| 541 C 541
```

```
RESULT 11
US-09-215-681-28
; Sequence 28, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Brudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-28
```

```
Query Match      20.6%; Score 532.2; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 2.6e-150;
Matches 534; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      ||| 1031 AACTGAGTGAAGCAAAAGAGCAAGAAACAAAAGCCAAAAGCAAGAGCTCCAA 1090
        ||| 1 AACTGAGTGAAGCAAAAGAGCAAGAAACAAARRAGAGCCAAAAGCAGAGCTCCAA 60
Db      ||| 1091 TATGAACAAGATTAATCTATCTTCAAAAGCATTTTGAAGTTGGGAAAAATTAATCATGTG 1150
        ||| 61 TATGAACAAGATTAATCTATCTTCAAAAGCATTTTGAAGTTGGGAAAAATTAATCATGTG 120
Qy      ||| 1151 AACTAGACAAGTGTGTTAAGAGTGAATGAATGAATGACAGTGGAGACAAGTGCATCCCA 1210
        ||| 121 AACTAGACAAGTGTGTTAAGAGTGAATGAATGAATGACAGTGGAGACAAGTGCATCCCA 180
Qy      ||| 1211 GATCTCAGGAGACTCCCTGCTGCTGACCTGGGAGTGAAGAGCAGATAGTGCATGT 1270
        ||| 181 GATCTCAGGAGACTCCCTGCTGCTGACCTGGGAGTGAAGAGCAGATAGTGCATGT 240
Qy      ||| 1271 TCTTTGCTCTGAATTTTAAATTGATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 1330
        ||| 241 TCTTTGCTCTGAATTTTAAATTGATGCTGTAATGTTGCTCTGAGGAAGCCCTGGA 300
```

QY 1331 AAGTATCCCAATATCCACATCTTATATTCACAATTAAGCTAGTATGACCT 1390
|
|
|
Db 301 AAGTATCCCAATATCCACATCTTATATTCACAATTAAGCTAGTATGACCT 360
|
|
|
QY 1391 AAGACGCTGTAATGAGCTGCCACTTGCACACTGAGGGGCGGTGCAATTTAGTAATGGG 1450
|
|
|
Db 361 AAGACGCTGTAATGAGCTGCCACTTGCACACTGAGGGGCGGTGCAATTTAGTAATGGG 420
|
|
|
QY 1451 TCAATGATTCACCTTTTATGATGCTCCAAAGGTGCTGCTCTCTCCCAACTGAC 1510
|
|
|
Db 421 TCAATGATTCACCTTTTATGATGCTCCAAAGGTGCTGCTCTCTCCCAACTGAC 480
|
|
|
QY 1511 AAATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAAGAGAGACAGTCCGCGACAC 1570
|
|
|
Db 481 AAATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAAGAGAGACAGTCCGCGACCC 540
|
|
|
QY 1571 C 1571
|
|
|
Db 541 C 541

RESULT 12

US-09-216-003A-28
; Sequence 28, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216.003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-216-003A-28

Query Match 20.6%; Score 532.2; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 2.6e-150;
Matches 534; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1031 AGTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAAGCAGAGGCTCCAA 1090
|
|
|
Db 1 AGTCTGAGTGAAGCAAAAGAGCAAGAAACAAARAGAACCAAAAGCAGAGGCTCCAA 60
|
|
|
QY 1091 TATGAACAAGATTAATCTATCTTCAAGACATTTAGAAAGTTGGAAAAATTCATGTG 1150
|
|
|
Db 61 TATGAACAAGATTAATCTATCTTCAAGACATTTAGAAAGTTGGAAAAATTCATGTG 120
|
|
|
QY 1151 AACTAGACAAGTGTGTTAAGATGATTAAGTAAGTAAGTGAAGTGAAGCAAGTGCATCCCA 1210
|
|
|
Db 121 AACTAGACAAGTGTGTTAAGATGATTAAGTAAGTAAGTGAAGTGAAGCAAGTGCATCCCA 180
|
|
|
QY 1211 GATCTCAGGAGCTCCCTGCTGCTGCACTGGGAGTGAAGAGACAGATAGTGCATGT 1270
|
|
|
Db 181 GATCTCAGGAGCTCCCTGCTGCTGCACTGGGAGTGAAGAGACAGATAGTGCATGT 240
|
|
|
QY 1271 TCTTTGCTCTGAATTTTATGATATGCTGTATGTTGCTCTGAGAAAGCCCTCGA 1330
|
|
|
Db 241 TCTTTGCTCTGAATTTTATGATATGCTGTATGTTGCTCTGAGAAAGCCCTCGA 300
|
|
|
QY 1331 AAGTATCCCAATATCCACATCTTATATTCACAATTAAGCTAGTATGACCT 1390
|
|
|
Db 301 AAGTATCCCAATATCCACATCTTATATTCACAATTAAGCTAGTATGACCT 360
|
|
|
QY 1391 AAGACGCTGTAATGAGCTGCCACTTGCACACTGAGGGGCGGTGCAATTTAGTAATGGG 1450
|
|
|
Db 361 AAGACGCTGTAATGAGCTGCCACTTGCACACTGAGGGGCGGTGCAATTTAGTAATGGG 420
|
|
|

QY 1451 TCAATGATTCACCTTTTATGATGCTCCAAAGGTGCTGCTCTCTCCCAACTGAC 1510
|
|
|
Db 421 TCAATGATTCACCTTTTATGATGCTCCAAAGGTGCTGCTCTCTCCCAACTGAC 480
|
|
|
QY 1511 AAATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAAGAGAGACAGTCCGCGACAC 1570
|
|
|
Db 481 AAATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAAGAGAGACAGTCCGCGACCC 540
|
|
|
QY 1571 C 1571
|
|
|
Db 541 C 541

RESULT 13

US-09-667-857-28
; Sequence 28, Application US/09667857
; Patent No. 669664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Rling, Steven P.
; APPLICANT: Reller, Marc W.
; APPLICANT: Ranger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667.857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-667-857-28

Query Match 20.6%; Score 532.2; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 2.6e-150;
Matches 534; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1031 AGTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAAGCAGAGGCTCCAA 1090
|
|
|
Db 1 AGTCTGAGTGAAGCAAAAGAGCAAGAAACAAARAGAACCAAAAGCAGAGGCTCCAA 60
|
|
|
QY 1091 TATGAACAAGATTAATCTATCTTCAAGACATTTAGAAAGTTGGAAAAATTCATGTG 1150
|
|
|
Db 61 TATGAACAAGATTAATCTATCTTCAAGACATTTAGAAAGTTGGAAAAATTCATGTG 120
|
|
|
QY 1151 AACTAGACAAGTGTGTTAAGATGATTAAGTAAGTAAGTGAAGTGAAGCAAGTGCATCCCA 1210
|
|
|
Db 121 AACTAGACAAGTGTGTTAAGATGATTAAGTAAGTAAGTGAAGTGAAGCAAGTGCATCCCA 180
|
|
|
QY 1211 GATCTCAGGAGCTCCCTGCTGCTGCACTGGGAGTGAAGAGACAGATAGTGCATGT 1270
|
|
|
Db 181 GATCTCAGGAGCTCCCTGCTGCTGCACTGGGAGTGAAGAGACAGATAGTGCATGT 240
|
|
|
QY 1271 TCTTTGCTCTGAATTTTATGATATGCTGTATGTTGCTCTGAGAAAGCCCTCGA 1330
|
|
|
Db 241 TCTTTGCTCTGAATTTTATGATATGCTGTATGTTGCTCTGAGAAAGCCCTCGA 300
|
|
|
QY 1331 AAGTATCCCAATATCCACATCTTATATTCACAATTAAGCTAGTATGACCT 1390
|
|
|
Db 301 AAGTATCCCAATATCCACATCTTATATTCACAATTAAGCTAGTATGACCT 360
|
|
|
QY 1391 AAGACGCTGTAATGAGCTGCCACTTGCACACTGAGGGGCGGTGCAATTTAGTAATGGG 1450
|
|
|
Db 361 AAGACGCTGTAATGAGCTGCCACTTGCACACTGAGGGGCGGTGCAATTTAGTAATGGG 420
|
|
|
QY 1451 TCAATGATTCACCTTTTATGATGCTCCAAAGGTGCTGCTCTCTCCCAACTGAC 1510
|
|
|

```
Db 421 TCAATGATCTCTTTTATGATGCTCCCAAGGCTTGGCTTCTCTCCCAACTGAC 480
Qy 1511 AATGCCAAGTTGAGAAAAATGATCATATTTTACATTAACAGACAGTGGGACAC 1570
Db 481 AATGCCAAGTTGAGAAAAATGATCATATTTTACATTAACAGACAGTGGGACAC 540
Qy 1571 C 1571
Db 541 C 541

RESULT 14
US-09-404-879A-27/c
; Sequence 27, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-27

Query Match 17.3%; Score 448.2; DB 3; Length 461;
Best Local Similarity 99.1%; Pred. No. 6.2e-125;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 2124 CAGGATTAACATCTCTCACTGTAACAGAGTTGACAAAGGCTTATGGAAATCCTGATGGAT 2183
Db 461 CAGGATTAACATCTCTCACTGTAACAGAGTTG-CAAGGCTTATGGAAATCCTGATGGAT 403
Qy 2184 TATCTTCAGCTTGTGAGCTTCTAAATTTCTTCCCTTATTTCACTGCAAGCCAACT 2243
Db 402 TATCTTCAGCTTGTGAGCTTCTAAATTTCTTCCCTTATTTCACTGCAAGCCAACT 343
Qy 2244 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 2303
Db 342 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
Qy 2304 GACCTTCCTGGCCACAATTCATAATTAGGCAACAAACATATACCTTCATGAGACAC 2363
Db 282 GACCTTCCTGGCCACAATTCATAATTAGGCAACAAACATATACCTTCATGAGACAC 223
Qy 2364 ACAGACTTTTGAAGAGCAAGACATGCTGCTGAATTTGAGGCTTGAAGATGAAGCTT 2423
Db 222 ACAGACTTTTGAAGAGCAAGACATGCTGCTGAATTTGAGGCTTGAAGATGAAGCTT 163
Qy 2424 TGAAGGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTTAAACACT 2483
Db 162 TGAAGGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTTAAACACT 103
Qy 2484 GCCTTCCTGAGACCTTGAAGCAAGTGAATGATTAATGATGTTTGAAGAAATGATTT 2543
Db 102 GCCTTCCTGAGACCTTGAAGCAAGTGAATGATTAATGATGTTTGAAGAAATGATTT 43
Qy 2544 TAGAGTTCTGATGTTCAAGAGAAATGATTAATATACATTTT 2585
Db 42 YAGAGTTCTGATGTTCAAGAGAAATGATTAATATATACATTTT 1
```

```
RESULT 15
US-09-338-933-27/c
; Sequence 27, Application US/09338933
; Patent No. 648931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-338-933-27

Query Match 17.3%; Score 448.2; DB 4; Length 461;
Best Local Similarity 99.1%; Pred. No. 6.2e-125;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 2124 CAGGATTAACATCTCTCACTGTAACAGAGTTGACAAAGGCTTATGGAAATCCTGATGGAT 2183
Db 461 CAGGATTAACATCTCTCACTGTAACAGAGTTG-CAAGGCTTATGGAAATCCTGATGGAT 403
Qy 2184 TATCTTCAGCTTGTGAGCTTCTAAATTTCTTCCCTTATTTCACTGCAAGCCAACT 2243
Db 402 TATCTTCAGCTTGTGAGCTTCTAAATTTCTTCCCTTATTTCACTGCAAGCCAACT 343
Qy 2244 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 2303
Db 342 TCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
Qy 2304 GACCTTCCTGGCCACAATTCATAATTAGGCAACAAACATATACCTTCATGAGACAC 2363
Db 282 GACCTTCCTGGCCACAATTCATAATTAGGCAACAAACATATACCTTCATGAGACAC 223
Qy 2364 ACAGACTTTTGAAGAGCAAGACATGCTGCTGAATTTGAGGCTTGAAGATGAAGCTT 2423
Db 222 ACAGACTTTTGAAGAGCAAGACATGCTGCTGAATTTGAGGCTTGAAGATGAAGCTT 163
Qy 2424 TGAAGGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTTAAACACT 2483
Db 162 TGAAGGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTTAAACACT 103
Qy 2484 GCCTTCCTGAGACCTTGAAGCAAGTGAATGATTAATGATGTTTGAAGAAATGATTT 2543
Db 102 GCCTTCCTGAGACCTTGAAGCAAGTGAATGATTAATGATGTTTGAAGAAATGATTT 43
Qy 2544 TAGAGTTCTGATGTTCAAGAGAAATGATTAATATACATTTT 2585
Db 42 YAGAGTTCTGATGTTCAAGAGAAATGATTAATATATACATTTT 1

Search completed: May 31, 2005, 00:28:50
Job time : 485.47 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 07:16:54 ; Search time 11935.1 Seconds
(without alignments)
10502.938 Million cell updates/sec

Title: US-09-763-978B-1

Perfect score: 2587
Sequence: 1 ggaagagcagcgagcgagctcc.....tgatatacatattcct 2587

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmb1:*
1: gb ba:*
2: gb_ptg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2587	100.0	2587	6	BD235830 A novel m
2	2565	99.1	2627	6	BD265002 Compositi
3	2565	99.1	2627	6	AR238405 Sequence
4	2565	99.1	2627	6	AR478744 Sequence
5	2565	99.1	2627	6	AX156350 Sequence
6	2565	99.1	2627	6	AX366624 Sequence
7	2563	99.1	2603	6	AX403048 Sequence
8	2527.2	97.7	2626	6	AX375860 Sequence
9	2472.4	95.6	2671	9	HSM808167 Sequence
10	2154	83.3	94664	9	HSU1025A1 Human DNA
11	1921.4	74.3	1965	6	AL080312 Human DNA
12	1617.6	62.5	171595	9	AL391476 Human DNA
13	1599.8	61.8	1658	6	CO875680 Sequence
14	1599.8	61.8	1658	6	AR252569 Sequence
15	1599.8	61.8	1658	6	AX092328 Sequence
16	1599.8	61.8	1658	6	AX376150 Sequence
17	1599.8	61.8	1658	6	AX395215 Sequence
18	1599.8	61.8	1658	6	AX403403 Sequence
19	1599.8	61.8	1658	6	AX468680 Sequence

20	1599.8	61.8	1658	9	AY358352 Homo sapi
21	1543	59.6	1567	6	BD264689 Compositi
22	1543	59.6	1567	6	AR238092 Sequence
23	1543	59.6	1567	6	AR257633 Sequence
24	1543	59.6	1567	6	AR283679 Sequence
25	1543	59.6	1567	6	AR443353 Sequence
26	1543	59.6	1567	6	AR478431 Sequence
27	1543	59.6	1567	6	AX366307 Sequence
28	1142.8	44.2	1811	9	AK026071 Homo sapi
29	1042.2	40.3	1070	9	AY346100 Homo sapi
30	1032	39.9	1065	6	AX375858 Sequence
31	956.6	37.0	1190	9	BC065717 Homo sapi
32	916	35.4	890	9	BC074729 Homo sapi
33	866	32.5	890	9	BD235840 A novel m
34	849	32.8	849	9	AY280972 Homo sapi
35	806	31.2	846	6	CQ414375 Sequence
36	803.4	31.1	836	6	AX067308 Sequence
37	718.6	27.8	1343	10	BC032925 Mus muscu
38	709	27.4	1382	10	AY346099 Mus muscu
39	628	24.3	852	10	AY322147 Mus muscu
40	626	24.2	643	6	CQ405961 Sequence
41	624.8	24.2	852	10	AY280973 Mus muscu
42	601.4	23.2	71909	2	AC105192 Homo sapi
43	581.4	22.5	595	6	CQ393186 Sequence
44	581.4	22.5	595	6	CQ39576 Sequence
45	576	22.3	576	6	BD235839 A novel m

ALIGNMENTS

RESULT 1
BD235830
LOCUS
DEFINITION
A novel method of diagnosing, monitoring, staging, imaging and
treating various cancers.
ACCESSION
BD235830.1 GI:33045600
VERSION
JP 2002523760-A/1.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 2587)
Salceda,S., Sun,Y., Recipon,H. and Cafferykey,R.
AUTHORS
A novel method of diagnosing, monitoring, staging, imaging and
treating various cancers
TITLE
Patent: JP 2002523760-A 1 30-JUL-2002;
JOURNAL
DIADEXUS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002523760-A/1
PD 30-JUL-2002
PF 01-SEP-1999 JP 2000567741
PR 02-SEP-1998 US 60/098880
PI SUGANA SALCEDA YONGWING SUN, HERVE RECIPON, ROBERT CAFFERKEY PC
GON133/574, A61K39/395, A61K39/395, A61K39/395, A61K49/02 CC
A61K49/00, A61K49/00,
PC A61K51/00, C07K16/32, C12N15/09, C12Q1/68, C12N15/00, A61K49/02 CC
A novel method of diagnosing, monitoring,
staging, imaging and
treating
CC various cancers
CQ Key
FH source
FT source

FEATURES

source
1..2587
Location/Qualifiers
/organism="Homo sapiens (human)"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match

100.0%; Score 2587; DB 6; Length 2587;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGAAGGACGGGAGAGCTCCACTCAGCCGATACCCAGATACGCTGGGAACTTTCCCGACG 60
Db 1 GGAAGGACGGGAGAGCTCCACTCAGCCGATACCCAGATACGCTGGGAACTTTCCCGACG 60
QY 61 CATTGCTTCCCTGGGGCAGATCCTCTTCTGGAGCAATATTTAGCATCATATTTCTGGC 120
Db 61 CATTGCTTCCCTGGGGCAGATCCTCTTCTGGAGCAATATTTAGCATCATATTTCTGGC 120
QY 121 TGGAGCAATTTGCACTCATATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAGACTAC 180
Db 121 TGGAGCAATTTGCACTCATATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAGACTAC 180
QY 181 TACTGTCCCTCAGCTGGGAGACATTTGGGAGATGGAATCTGAGCTGCATTTTGAAC 240
Db 181 TACTGTCCCTCAGCTGGGAGACATTTGGGAGATGGAATCTGAGCTGCATTTTGAAC 240
QY 241 TGAACATCAAACTTTCTGATATGTGTATGATAGGCTGAAGGAAGTGTGTTAGGCTTGT 300
Db 241 TGAACATCAAACTTTCTGATATGTGTATGATAGGCTGAAGGAAGTGTGTTAGGCTTGT 300
QY 301 CCATGAGTTCAAGAAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTCAAGAGCCG 360
Db 301 CCATGAGTTCAAGAAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTCAAGAGCCG 360
QY 361 GACAGAGTGTGTTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAACGT 420
Db 361 GACAGAGTGTGTTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAACGT 420
QY 421 GCAACCTCAGAGATGCTGGACCTCAAAATGTTATATCATCACTTCAAGGCAAGGGAA 480
Db 421 GCAACCTCAGAGATGCTGGACCTCAAAATGTTATATCATCACTTCAAGGCAAGGGAA 480
QY 481 TGTAACTCTTGAATATTAACCTGAGACCTTCAGCATGCCGGAAGTGAATGTGACTATA 540
Db 481 TGTAACTCTTGAATATTAACCTGAGACCTTCAGCATGCCGGAAGTGAATGTGACTATA 540
QY 541 TGGCACTCAGAGACCTTGGCGGTGTAGAGCTCCCGCATGTTCCCGACCCCAAGTGT 600
Db 541 TGGCACTCAGAGACCTTGGCGGTGTAGAGCTCCCGCATGTTCCCGACCCCAAGTGT 600
QY 601 CTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATACAGCTTTGA 660
Db 601 CTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATACAGCTTTGA 660
QY 661 GCTGAACCTGTGAAGATGTGACCAAGAAAGTGTGTGTGCTCTCAATGTTACATCAA 720
Db 661 GCTGAACCTGTGAAGATGTGACCAAGAAAGTGTGTGTGCTCTCAATGTTACATCAA 720
QY 721 CAACACATCTCTGTATATGTAATAATGACATTTGCCAAGCAAGAGGAGATATCAAA 780
Db 721 CAACACATCTCTGTATATGTAATAATGACATTTGCCAAGCAAGAGGAGATATCAAA 780
QY 781 GACAGAAATGAGATCAAAAAGGCGAGTCACTCAGCTGCTAACTCAAAAGGCTTCTCT 840
Db 781 GACAGAAATGAGATCAAAAAGGCGAGTCACTCAGCTGCTAACTCAAAAGGCTTCTCT 840
QY 841 GTGTGTCTCTTCTTCTTTGCCATCAGCTGGGCACTTCTGCTCAGCCCTTACCTGAT 900
Db 841 GTGTGTCTCTTCTTCTTTGCCATCAGCTGGGCACTTCTGCTCAGCCCTTACCTGAT 900
QY 901 GCTAAATAATATGTGCTTGGCCCAAAAAGCATGCAATGTTTCAACAGGAGATC 960
Db 901 GCTAAATAATATGTGCTTGGCCCAAAAAGCATGCAATGTTTCAACAGGAGATC 960
QY 961 TACAGAACTATTTCACCAAGATATGACTAGTTTATATTTCTGGAGGAAATGAAT 1020
Db 961 TACAGAACTATTTCACCAAGATATGACTAGTTTATATTTCTGGAGGAAATGAAT 1020
QY 1021 CATATCTAGAACTGTGAGTGAACAACAAGCAAGAAACAAGAAAGCAAAAGCAG 1080
Db 1021 CATATCTAGAACTGTGAGTGAACAACAAGCAAGAAACAAGAAAGCAAAAGCAG 1080
```

```
Db 1021 CATATCTAGAACTGTGAGTGAACAACAAGCAAGAAACAAGAAAGCAAAAGCAG 1080
QY 1081 AAGGCTCCAAATATGAAACAAGATTAATCTATGTTCAAGACATATTAGAAAGTTGGAAAT 1140
Db 1081 AAGGCTCCAAATATGAAACAAGATTAATCTATGTTCAAGACATATTAGAAAGTTGGAAAT 1140
QY 1141 AATTCATGTGAACCTGACAAAGTGTGTTAAGATGAATGAATGAACGCTGGAGACAAG 1200
Db 1141 AATTCATGTGAACCTGACAAAGTGTGTTAAGATGAATGAATGAACGCTGGAGACAAG 1200
QY 1201 TGCATCCCAAGATCTCAGGAGACCTCCCGCTGCTGTACCTGGGAGATGAAGAGACAGA 1260
Db 1201 TGCATCCCAAGATCTCAGGAGACCTCCCGCTGCTGTACCTGGGAGATGAAGAGACAGA 1260
QY 1261 TAGTGCAATGTTCTTGTCTGAAATTTTATGATATGCTGATATGCTGCTGAGGA 1320
Db 1261 TAGTGCAATGTTCTTGTCTGAAATTTTATGATATGCTGATATGCTGCTGAGGA 1320
QY 1321 AGCCCTGGAAAAGTCTATCCCAACATATCAATCTATATTCACAAATTAAGCTGTAG 1380
Db 1321 AGCCCTGGAAAAGTCTATCCCAACATATCCCAACATCTTATATTCACAAATTAAGCTGTAG 1380
QY 1381 TATGTACCTTAAGACGCTGTCTAATTGACTGCCACTTCCCACTCAGGGGCGGCTGCATTT 1440
Db 1381 TATGTACCTTAAGACGCTGTCTAATTGACTGCCACTTCCCACTCAGGGGCGGCTGCATTT 1440
QY 1441 TAGTAATGGGTCAAAATGATTCATCTTTATGATGCTTCAAGAGTGCCTTGCTCTCTT 1500
Db 1441 TAGTAATGGGTCAAAATGATTCATCTTTATGATGCTTCAAAAGTGCCTTGCTCTCTT 1500
QY 1501 CCCAATGACAAATGCCAAAGTGAAGAAAATGATCATATTTTATGATTAACAGAGCAG 1560
Db 1501 CCCAATGACAAATGCCAAAGTGAAGAAAATGATCATATTTTATGATTAACAGAGCAG 1560
QY 1561 TGGGCAACCGGATTTTAAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGG 1620
Db 1561 TGGGCAACCGGATTTTAAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGG 1620
QY 1621 TTTATTTCTCAGATGATGTTCAATCCGTGAATGATGATGATGATGATGATGATGAT 1680
Db 1621 TTTATTTCTCAGATGATGTTCAATCCGTGAATGATGATGATGATGATGATGATGAT 1680
QY 1681 ATATGCAATTAATGATCATCAAGCTCTGAGGCTTCTCTTTCATCTGCGGTGACAGCT 1740
Db 1681 ATATGCAATTAATGATCATCAAGCTCTGAGGCTTCTCTTTCATCTGCGGTGACAGCT 1740
QY 1741 AAGACCTCAGTTTCAATTAAGATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCC 1800
Db 1741 AAGACCTCAGTTTCAATTAAGATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCC 1800
QY 1801 CCATCTCGGGGGGAATGTCTGAAGCAATTTTGTGTTACTCAATGAGGAGTGGAGAGG 1860
Db 1801 CCATCTCGGGGGGAATGTCTGAAGCAATTTTGTGTTACTCAATGAGGAGTGGAGAGG 1860
QY 1861 ATACAGTCTACTCAACCTAGTGTATTAAGGCCAGGAGTGTCTCAACCTCTTACCAT 1920
Db 1861 ATACAGTCTACTCAACCTAGTGTATTAAGGCCAGGAGTGTCTCAACCTCTTACCAT 1920
QY 1921 GTACAGAGCTGTCCCACTTACAACTTACCAATCCGAAGTGTCAACTGTGTGACAGACTTA 1980
Db 1921 GTACAGAGCTGTCCCACTTACAACTTACCAATCCGAAGTGTCAACTGTGTGACAGACTTA 1980
QY 1981 GAAACCTGCTTTTGTAGTGAAGAAAGGGCTGGAAGAGGGGAGCCCAAAATCTGTCTGC 2040
Db 1981 GAAACCTGCTTTTGTAGTGAAGAAAGGGCTGGAAGAGGGGAGCCCAAAATCTGTCTGC 2040
QY 2041 TTCTCACAATTAGTCAATTTGGCAAAATTAAGCAATCTGTCTTTGGCTGCTCTCAGACAG 2100
Db 2041 TTCTCACAATTAGTCAATTTGGCAAAATTAAGCAATCTGTCTTTGGCTGCTCTCAGACAG 2100
QY 2101 AGAGCCAGAACTCTATCGGGGACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGC 2160
Db 2101 AGAGCCAGAACTCTATCGGGGACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGC 2160
```

QY 2161 CTATGGGAATGCGTGAATGGGATTAATCTCAGCTTGTGAGCTTTCTAAGTTTCCTTCCCT 2220
DB 2161 CTATGGGAATGCGTGAATGGGATTAATCTCAGCTTGTGAGCTTTCTAAGTTTCCTTCCCT 2220
QY 2221 TCATTTCACTCCGCAAGCCAAAGTTCTGTAAAGAAATGCGTGAAGTTCTAGCTCAGGTTT 2280
DB 2221 TCATTTCACTCCGCAAGCCAAAGTTCTGTAAAGAAATGCGTGAAGTTCTAGCTCAGGTTT 2280
QY 2281 CTTACTCTGAATTTAGATCTTCAGACCTTCTGCGCAATTCATTAAGGCAACAA 2340
DB 2281 CTTACTCTGAATTTAGATCTTCAGACCTTCTGCGCAATTCATTAAGGCAACAA 2340
QY 2341 CATATACCTTCATGAAGACACACACAGCTTTTGAAGAACAAATGAATGATGATGAT 2400
DB 2341 CATATACCTTCATGAAGACACACACAGCTTTTGAAGAACAAATGAATGATGATGAT 2400
QY 2401 TGAAGCCTTGAAGAAATGAAGCTTTGAAGAAAGAAATGATGATGATGATGATGAT 2460
DB 2401 TGAAGCCTTGAAGAAATGAAGCTTTGAAGAAAGAAATGATGATGATGATGATGAT 2460
QY 2461 ACACTCTTCAATGTTTACCACTGCTTCTGCACTTGAAGCCAGTGAATGAT 2520
DB 2461 ACACTCTTCAATGTTTACCACTGCTTCTGCACTTGAAGCCAGTGAATGATGAT 2520
QY 2521 ATGTTGTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
DB 2521 ATGTTGTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
QY 2581 ATTTTCCT 2587
DB 2581 ATTTTCCT 2587

RESULT 2
LOCUS BD265002 2627 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for the therapy and diagnosis of ovarian cancer.
ACCESSION BD265002
VERSION BD265002.1 GI:33074770
KEYWORDS JP 2002532093-A/387.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A. and Frudakis,T.N.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer.
JOURNAL Patient: JP 2002532093-A 387 02-OCT-2002;
CORIXA CORP
OS Homo sapiens (human)
PN JP 2002532093-A/387
PD 02-OCT-2002
PR 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681,17-DEC-1998 US 09/216003 PR
23-JUN-1999 US 09/338933,24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM,GORDON E KING,PAUL A ALGATE,TONY N FRUDAKIS PC
C12N1/09,A61K31/7115,A61K35/14,A61K35/76,A61K39/00,A61K39/395, PC
A61K39/395,
PC A61K48/00,A61P35/00,A61P37/04,C07K14/82,C07K19/00,C12N1/15, PC
C12N1/19,
PC
C12N1/21,C12N5/06,C12N5/10,C12Q1/68,G01N33/53,G01N33/53,G01N33/53,
566,
PC G01N33/574,G01N33/577,C12N15/00,C12N5/00,C12N5/00 CC
Compositions and methods for the therapy and diagnosis of CC
ovarian cancer
FH Key Location/Qualifiers
FT source 1..2627 /organism='Homo sapiens (human)'.
FEATURES
source 1..2627

ORIGIN
Query Match 99.1%; Score 2565; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

QY 12 GGCAGCTCCATCAGCAGCAGTACCCAGATACGCTGGGAACCTTCCAGCCATGCTTCCC 71
DB 33 GGCAGCTCCATCAGCAGCAGTACCCAGATACGCTGGGAACCTTCCAGCCATGCTTCCC 92
QY 72 TGGGGAGATCCCTCTGAGAGATTAATAGCATCATATTTCTGGGTGAGCAATTG 131
DB 93 TGGGGAGATCCCTCTGAGAGATTAATAGCATCATATTTCTGGGTGAGCAATTG 152
QY 132 CACTCATATTTGGCTTTGGTATTTTCAGGAGACACTCATCATCACTACTGTGCGCT 191
DB 153 CACTCATATTTGGCTTTGGTATTTTCAGGAGACACTCATCATCACTACTGTGCGCT 212
QY 192 CAGCTGGGAACATTGGGGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 251
DB 213 CAGCTGGGAACATTGGGGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 272
QY 252 TTTCTGATATTCGTGATACAAATGGCTGGAAGAAAGTGTGTTAGGCTGTCCATGAGTTCA 311
DB 273 TTTCTGATATTCGTGATACAAATGGCTGGAAGAAAGTGTGTTAGGCTGTCCATGAGTTCA 332
QY 312 AAGAAAGCAAGATGAGCTGCGAGCAGATGAAATGTTCAAGAGCCGAGACAGAGTGT 371
DB 333 AAGAAAGCAAGATGAGCTGCGAGCAGATGAAATGTTCAAGAGCCGAGACAGAGTGT 392
QY 372 TTGCTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
DB 393 TTGCTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 452
QY 432 ATGCTGGGACCTTCAAAATGTTATATCATCATCTTCAAAAGGCAAGGGAATGCTAACCTTG 491
DB 453 ATGCTGGGACCTTCAAAATGTTATATCATCATCTTCAAAAGGCAAGGGAATGCTAACCTTG 512
QY 492 AGTATTAATGAGAGCTTCAAGATGCTCGAGAGTGAATGATGATGATGATGATGATGAT 551
DB 513 AGTATTAATGAGAGCTTCAAGATGCTCGAGAGTGAATGATGATGATGATGATGATGAT 572
QY 552 AGACCTTGGGTGAGGCTCCCGATGTTCCCGACGCCACAGTGTCTGGGCAATCCC 611
DB 573 AGACCTTGGGTGAGGCTCCCGATGTTCCCGACGCCACAGTGTCTGGGCAATCCC 632
QY 612 AAGTTGACCAAGGAGGCACTTCTGGAAGTCTCCAAATGCAAGCTTTGAGCTGGAATCTTG 671
DB 633 AAGTTGACCAAGGAGGCACTTCTGGAAGTCTCCAAATGCAAGCTTTGAGCTGGAATCTTG 692
QY 672 AGAATGACCAATGAAGT 731
DB 693 AGAATGACCAATGAAGT 752
QY 732 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 791
DB 753 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 812
QY 792 AGATCAAAAGGAGGAGCTCACTCAAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTTT 851
DB 813 AGATCAAAAGGAGGAGCTCACTCAAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTTT 872
QY 852 CTTTCTTTGCTCAAGCTGGGCACTTCTGCTCAAGCTTCAAGCTGCTTCAAGCTGCTTCA 911
DB 873 CTTTCTTTGCTCAAGCTGGGCACTTCTGCTCAAGCTTCAAGCTGCTTCAAGCTGCTTCA 932
QY 912 GTTCTTGGGCACAAAAAGATGCAATGATGATGATGATGATGATGATGATGATGATGAT 971
DB 933 GTTCTTGGGCACAAAAAGATGCAATGATGATGATGATGATGATGATGATGATGATGAT 992

QY 972 TTCACCAAGATATGACCTAGTTTATATTTCTGGAGGAATGAATCATATCTAGAA 1031
 |||||
 Db 993 TTCACCAAGATATGACCTAGTTTATATTTCTGGAGGAATGAATCATATCTAGAA 1052
 |||||
 QY 1032 GTCTGAGTGAACAACAAGACCAAGAACAAAAAAGACCAGAGAGAGGCTTCCAT 1091
 |||||
 Db 1053 GTCTGAGTGAACAACAAGACCAAGAACAAAAAAGACCAGAGAGAGGCTTCCAT 1112
 |||||
 QY 1092 ATGAACAGATATATCTATCTTCAAGAGATATTTGAAGTGGGAAAAATATCTATGTA 1151
 |||||
 Db 1113 ATGAACAGATATATCTATCTTCAAGAGATATTTGAAGTGGGAAAAATATCTATGTA 1172
 |||||
 QY 1152 ACTAGACAGTGTGTATAGATGATATATTAATGACAGTGGAGCAATGTCATCCGAG 1211
 |||||
 Db 1173 ACTAGACAGTGTGTATAGATGATATTAATGACAGTGGAGCAATGTCATCCGAG 1232
 |||||
 QY 1212 ATCTCAGGAGCTCCCTGCTGTCACCTGGGAGTGAAGAGACAGATATGATGTT 1271
 |||||
 Db 1233 ATCTCAGGAGCTCCCTGCTGTCACCTGGGAGTGAAGAGACAGATATGATGTT 1292
 |||||
 QY 1272 CTTTGTCTGTAAATTTTATATATATGCTGTAAATGTTGCTGTAGAGAGCCCTGAA 1331
 |||||
 Db 1293 CTTTGTCTGTAAATTTTATATATGCTGTAAATGTTGCTGTAGAGAGCCCTGAA 1352
 |||||
 QY 1332 AGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTATGTACCTTA 1391
 |||||
 Db 1353 AGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTATGTACCTTA 1412
 |||||
 QY 1392 AGACGCTGTAAATGACCTGCACTTCCGAACTCAGGGGCGCTGCATTTTATGTAATGGT 1451
 |||||
 Db 1413 AGACGCTGTAAATGACCTGCACTTCCGAACTCAGGGGCGCTGCATTTTATGTAATGGT 1472
 |||||
 QY 1452 CAAATGATTCACCTTTTATATGCTTCCAAAGTGTCTGGCTGCTCCCACTGACA 1511
 |||||
 Db 1473 CAAATGATTCACCTTTTATATGCTTCCAAAGTGTCTGGCTGCTCCCACTGACA 1532
 |||||
 QY 1512 AATGCCAAAGTTAGAAAAATATCATATTTTATAGATTAACAGACATCGGCGACAC 1571
 |||||
 Db 1533 AATGCCAAAGTTAGAAAAATATCATATTTTATAGATTAACAGACATCGGCGACAC 1592
 |||||
 QY 1572 GATTTTATATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGTTTATTTCTCA 1631
 |||||
 Db 1593 GATTTTATATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGTTTATTTCTCA 1652
 |||||
 QY 1632 GATGATGTCATCCGGAATGTCACGAGGAGAGACCTTACCTGACATATATGACATTA 1691
 |||||
 Db 1653 GATGATGTCATCCGGAATGTCACGAGGAGAGACCTTACCTGACATATATGACATTA 1712
 |||||
 QY 1692 TGTATCATCAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGACAGTAAAGCCTCAGT 1751
 |||||
 Db 1713 TGTATCATCAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGACAGTAAAGCCTCAGT 1772
 |||||
 QY 1752 TTTCAATAGCATCTAGAGCACTGAGGACTCAGCTGGGCTGATTTCCGCCCCCATCTCGGG 1811
 |||||
 Db 1773 TTTCAATAGCATCTAGAGCACTGAGGACTCAGCTGGGCTGATTTCCGCCCCCATCTCGGG 1832
 |||||
 QY 1812 GGAATGTCGAAGACAAATTTGTTTACCTCAATAGAGGAGTGGAGGATACAGTGCTA 1871
 |||||
 Db 1833 GGAATGTCGAAGACAAATTTGTTTACCTCAATAGAGGAGTGGAGGATACAGTGCTA 1892
 |||||
 QY 1872 CTACCAACTAGTGAATTAAGGCGCAGGAGTGTGCTCAACCTCTCAATCATATGACAGACGT 1931
 |||||
 Db 1893 CTACCAACTAGTGAATTAAGGCGCAGGAGTGTGCTCAACCTCTCAATCATATGACAGACGT 1952
 |||||
 QY 1932 CTCCTCATTAACAATAACCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTTGCT 1991
 |||||
 Db 1953 CTCCTCATTAACAATAACCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTTGCT 2012
 |||||
 QY 1992 TTTTGAATTAAGAAAGGCGCTGGAAGAGGAGGAGCAAAATGCTGTGCTTCTCAAT 2050
 |||||
 Db 2013 TTTTGAATTAAGAAAGGCGCTGGAAGAGGAGGAGCAAAATGCTGTGCTTCTCAAT 2072
 |||||
 QY 2051 AGTCATTTGCAAAATATAGCATTTCTGTCTCTTGTGCTGTGCTCAGACAGAGAGCCAGAA 2110
 |||||

Db 2073 AGTCATTTGCAAAATTAAGCATTTCTGTCTTTGGGCTGTGCTCAGACAGAGAGCCAGAA 2132
 |||||
 QY 2111 CTCTATCGGAGCACAGATTAACATCTCTCACTGAAACAGATGTAACAAGGCTATGGGAAA 2170
 |||||
 Db 2133 CTCTATCGGAGCACAGATTAACATCTCTCACTGAAACAGATGTAACAAGGCTATGGGAAA 2192
 |||||
 QY 2171 TGCCTGATGGGATTAATCTTCACTGTGTGAGCTTCTAAGTTCTTCCCTTCATTTAC 2230
 |||||
 Db 2193 TGCCTGATGGGATTAATCTTCACTGTGTGAGCTTCTAAGTTCTTCCCTTCATTTAC 2252
 |||||
 QY 2231 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
 |||||
 Db 2253 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
 |||||
 QY 2291 ATTTAGATCTCAGACCTTCTGCGCCCAATTCAATTAAGGCAACAATATATACCTT 2350
 |||||
 Db 2313 ATTTAGATCTCAGACCTTCTGCGCCCAATTCAATTAAGGCAACAATATATACCTT 2372
 |||||
 QY 2351 CCATGAAGCACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGA 2410
 |||||
 Db 2373 CCATGAAGCACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGA 2432
 |||||
 QY 2411 AGGAATGAAGCTTTGAAGAAAAGAAATCTTGTTCAGCCCTTCCACACTCTTCA 2470
 |||||
 Db 2433 AGGAATGAAGCTTTGAAGAAAAGAAATCTTGTTCAGCCCTTCCACACTCTTCA 2492
 |||||
 QY 2471 TGTGTTAACACTGCTCTTCTGAGACCTTGAAGCCAGGTAAGTATTAAGTTGTTAT 2530
 |||||
 Db 2493 TGTGTTAACACTGCTCTTCTGAGACCTTGAAGCCAGGTAAGTATTAAGTTGTTAT 2552
 |||||
 QY 2531 AGAAACTGATTTTATGATCTGATCTGATCAAGAGATGATTAATATATATTTCT 2587
 |||||
 Db 2553 AGAAACTGATTTTATGATCTGATCTGATCAAGAGATGATTAATATATATTTCT 2609
 |||||

RESULT 3
 AR238405 2627 bp DNA linear PAT 20-DEC-2002
 LOCUS AR238405
 DEFINITION Sequence 391 from patent US 6468546.
 ACCESSION AR238405
 VERSION AR238405.1 GI:27283369
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unclassified.
 REFERENCE
 1 (bases 1 to 2627)
 Mitchem,J.L., King,G.E. and Algate,P.A.
 Authors
 Title
 Compositions and methods for therapy and diagnosis of ovarian
 cancer
 JOURNAL
 Patent: US 6468546-A 391 22-OCT-2002;
 FEATURES
 Location/Qualifiers
 source
 1..2627
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN

Query Match 99.1%; Score 2565; DB 6; Length 2627;
 Best Local Similarity 100.0%; Pred.No. 0; Indels 1; Gaps 1;
 Matches 25/6; Conservative 0; Mismatches 0
 QY 12 GGCAGCTCACTCAGCAGTACCCAGATACGCTGGAACTTCCAGCAGTGGCTTCC 71
 |||||
 Db 33 GGCAGCTCACTCAGCAGTACCCAGATACGCTGGAACTTCCAGCAGTGGCTTCC 92
 |||||
 QY 72 TGGGCAAGTCTCTTCTGAGCATATTAATGATATATTTTGTGCTGAGCAATTTG 131
 |||||
 Db 93 TGGGCAAGTCTCTTCTGAGCATATTAATGATATATTTTGTGCTGAGCAATTTG 152
 |||||
 QY 132 CACTCATATTTGGCTTGTGATTTTCAGGAGACATCCATACAGTCACTACTGTGCT 191
 |||||
 Db 153 CACTCATATTTGGCTTGTGATTTTCAGGAGACATCCATACAGTCACTACTGTGCT 212
 |||||

QY 192 CAGCTGGGAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAC 251
| | | | |
Db 213 CAGCTGGGAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAC 272
| | | | |
QY 252 TTTTCTGATATGCTGATACAAATGCTGAAGAGAGGTTTAAAGCTTGGTCCATGAGTTCA 311
| | | | |
Db 273 TTTTCTGATATGCTGATACAAATGCTGAAGAGAGGTTTAAAGCTTGGTCCATGAGTTCA 332
| | | | |
QY 312 AAGAAGCAAGATGAGCTGTCGGAGAGAGATGAAAATGTTCAAGAGCCGGAACAGCAAGTGT 371
| | | | |
Db 333 AAGAAGCAAGATGAGCTGTCGGAGAGAGATGAAAATGTTCAAGAGCCGGAACAGCAAGTGT 392
| | | | |
QY 372 TTGCTGATCAAGTATGATGAGCAATGCTCTTTGCGGCTGAAGAAAAGTCAACTCAG 431
| | | | |
Db 393 TTGCTGATCAAGTATGATGAGCAATGCTCTTTGCGGCTGAAGAAAAGTCAACTCAG 452
| | | | |
QY 432 ATGCTGGACCTTACAAATGTTATATCATCTTTAAAGGCAAGGGGAATGCTAACCTTG 491
| | | | |
Db 453 ATGCTGGACCTTACAAATGTTATATCATCTTTAAAGGCAAGGGGAATGCTAACCTTG 512
| | | | |
QY 492 AGTATAAAGCTGAGCTTCAAGCATGCGGGAAGTGAATGTTGACTATATATGCCAGCTCAG 551
| | | | |
Db 513 AGTATAAAGCTGAGCTTCAAGCATGCGGGAAGTGAATGTTGACTATATATGCCAGCTCAG 572
| | | | |
QY 552 AGACCTTGCGGTGAGAGCTCCCGATGATGTTCCCGACCCAGCAGTGTCTGGGCACTCC 611
| | | | |
Db 573 AGACCTTGCGGTGAGAGCTCCCGATGATGTTCCCGACCCAGCAGTGTCTGGGCACTCC 632
| | | | |
QY 612 AAGTTGACGAGGAGCCAACTTCTCGGAAGTCTTCAATACAGCTTTGAGCTGAACCTTG 671
| | | | |
Db 633 AAGTTGACGAGGAGCCAACTTCTCGGAAGTCTTCAATACAGCTTTGAGCTGAACCTTG 692
| | | | |
QY 672 AGATGAGACCAAGAGGTTGTGTCTGTCTGCTTCAATATTTAGATTCATAACAACATCTACT 731
| | | | |
Db 693 AGATGAGACCAAGAGGTTGTGTCTGTCTGCTTCAATATTTAGATTCATAACAACATCTACT 752
| | | | |
QY 732 CCTGTATGATTGAAAATGATCATTTGCCAAAGCAACAGGGGATATCAAAAGTACAGAACTCG 791
| | | | |
Db 753 CCTGTATGATTGAAAATGATCATTTGCCAAAGCAACAGGGGATATCAAAAGTACAGAACTCG 812
| | | | |
QY 792 AGATCAAAAGGCGAGTCACTTCAAGTGTCTTCAAAAGGCTTCTGTGTGTCTCTT 851
| | | | |
Db 813 AGATCAAAAGGCGAGTCACTTCAAGTGTCTTCAAAAGGCTTCTGTGTGTCTCTT 872
| | | | |
QY 852 CTTTCTTTGGCATCAGTGGGCACTTCTGCTCTCAGCCCTTACCTGATCTGATTAATAT 911
| | | | |
Db 873 CTTTCTTTGGCATCAGTGGGCACTTCTGCTCTCAGCCCTTACCTGATCTGATTAATAT 932
| | | | |
QY 912 GTGCTTGGGCAAAAAAAGCATGCAAAAGTCAATGTTTACAACAGGGATCTACAGAACTAT 971
| | | | |
Db 933 GTGCTTGGGCAAAAAAAGCATGCAAAAGTCAATGTTTACAACAGGGATCTACAGAACTAT 992
| | | | |
QY 972 TTGACCAACAGATATGACCTAGTTTTATTTTCTGGAGGAAATGAATTCATATCTAGAA 1031
| | | | |
Db 993 TTGACCAACAGATATGACCTAGTTTTATTTCTGGAGGAAATGAATTCATATCTAGAA 1052
| | | | |
QY 1032 GTCTGAGTGAAGCAACAGCAAGCAAAACAAAGAACCAAGCAAGAGGCTCCAT 1091
| | | | |
Db 1053 GTCTGAGTGAAGCAACAGCAAGCAAAACAAAGAACCAAGCAAGAGGCTCCAT 1112
| | | | |
QY 1092 ATGAACAAGATTAATCTATCTTCAAGAATATTTAGAAAGTTGGGAAAATTAATTCATGTA 1151
| | | | |
Db 1113 ATGAACAAGATTAATCTATCTTCAAGAATATTTAGAAAGTTGGGAAAATTAATTCATGTA 1172
| | | | |
QY 1152 ACTAGAACAAGTGTTAAGAAGTAAATGAATGCACTGAGAGCAAGTGCATCCAG 1211
| | | | |
Db 1173 ACTAGAACAAGTGTTAAGAAGTAAATGAATGCACTGAGAGCAAGTGCATCCAG 1232
| | | | |
QY 1212 ATCTCAGGAGCTTCCCTGCTGTCACTGCGGAGTGAAGAGCAAGATATGTCATGTT 1271
| | | | |
Db 1233 ATCTCAGGAGCTTCCCTGCTGTCACTGCGGAGTGAAGAGCAAGATATGTCATGTT 1292
| | | | |
QY 1272 CTTTGTCTGAAATTTTATGTTATATGTGTCTGTAACTGCTGAGAGAGCCCTGGA 1331
| | | | |

Db 1293 CTTTGTCTGAAATTTTATGTTATATGTGCTGAATGTTGCTGAGGAAGCCCTGGA 1352
| | | | |
QY 1332 AGTCTATCCCAATATCCACATCTTATATTTCCAAATTAAGCTAGTATGCTTACCTTA 1391
| | | | |
Db 1353 AGTCTATCCCAATATCCACATCTTATATTTCCAAATTAAGCTAGTATGCTTACCTTA 1412
| | | | |
QY 1392 AGAGCTGCTAATGATGCTGCACTTGGCAACTCAGGGGGGGCTGCAATTTAGTAAGGGT 1451
| | | | |
Db 1413 AGAGCTGCTAATGATGCTGCACTTGGCAACTCAGGGGGGGCTGCAATTTAGTAAGGGT 1472
| | | | |
QY 1452 CAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCTTGGCTCTCTTCCCAACTGACA 1511
| | | | |
Db 1473 CAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCTTGGCTCTCTTCCCAACTGACA 1532
| | | | |
QY 1512 AATGCCAAAGTTGAGAAAATGATCATTAATTTAGATTAACAGACAGTGGCGACACC 1571
| | | | |
Db 1533 AATGCCAAAGTTGAGAAAATGATCATTAATTTAGATTAACAGACAGTGGCGACACC 1592
| | | | |
QY 1572 GATTTATTAATTAATGAGACCTTCTTTTAAACAAATGCGGGTTATTTCTCA 1631
| | | | |
Db 1593 GATTTATTAATTAATGAGACCTTCTTTTAAACAAATGCGGGTTATTTCTCA 1652
| | | | |
QY 1632 GATGATGTTCAATCCGTGAATGTCAGAGGAAGACCTTTCACCTTGACTATATGCACTTA 1691
| | | | |
Db 1653 GATGATGTTCAATCCGTGAATGTCAGAGGAAGACCTTTCACCTTGACTATATGCACTTA 1712
| | | | |
QY 1692 TGTCAATCAAGCTCTGAGGCTTCTCTTCCATCTGCTGTGAGCAGCTAAGCCTCAGT 1751
| | | | |
Db 1713 TGTCAATCAAGCTCTGAGGCTTCTCTTCCATCTGCTGTGAGCAGCTAAGCCTCAGT 1772
| | | | |
QY 1752 TTTTCAATGATCTAAGAGAGTGGGACAGCTGCGGGTGAATTTGCGCCCATCTCGGG 1811
| | | | |
Db 1773 TTTTCAATGATCTAAGAGAGTGGGACAGCTGCGGGTGAATTTGCGCCCATCTCGGG 1832
| | | | |
QY 1812 GGAATGTCGAAGACAAATTTTGGTTACTCAATGAGGAGTGAAGAGGATACAGTGTCTTA 1871
| | | | |
Db 1833 GGAATGTCGAAGACAAATTTTGGTTACTCAATGAGGAGTGAAGAGGATACAGTGTCTTA 1892
| | | | |
QY 1872 CTACCAATGATGATTAAGAGCCAGGGATGCTGTCTCAACTCTTACATGATACAGACGT 1931
| | | | |
Db 1893 CTACCAATGATGATTAAGAGCCAGGGATGCTGTCTCAACTCTTACATGATACAGACGT 1952
| | | | |
QY 1932 CTCCCATTAACAATCCCAATCCGAAGTGTCAACGTGTCTCAAGTAAGAAACCTGTGT 1991
| | | | |
Db 1953 CTCCCATTAACAATCCCAATCCGAAGTGTCAACGTGTCTCAAGTAAGAAACCTGTGT 2012
| | | | |
QY 1992 TTTGAGTAAAAAGGCGCTGGAAGAGGGAGCCAAATCTGTCTGCTT-CTCACATTT 2050
| | | | |
Db 2013 TTTGAGTAAAAAGGCGCTGGAAGAGGGAGCCAAATCTGTCTGCTTCTCTCACATTT 2072
| | | | |
QY 2051 AGTATGGAACAATAAGCAATCTGTCTCTTTGGCTGTCTCTCTCAGACAGAGCCAGAA 2110
| | | | |
Db 2073 AGTATGGAACAATAAGCAATCTGTCTCTTTGGCTGTCTCTCTCAGACAGAGCCAGAA 2132
| | | | |
QY 2111 CTCTATCGGGCACAGGATTAATCATCTGTGAAGAACAGAGTTGAAGAGCCCTATGGGAA 2170
| | | | |
Db 2133 CTCTATCGGGCACAGGATTAATCATCTGTGAAGAACAGAGTTGAAGAGCCCTATGGGAA 2192
| | | | |
QY 2171 TGCCTGATGGATTTATCTTCACTTGTGAGCTTCAATTTCTTTCCCTTCAATTTAC 2230
| | | | |
Db 2193 TGCCTGATGGATTTATCTTCACTTGTGAGCTTCAATTTCTTTCCCTTCAATTTAC 2252
| | | | |
QY 2231 CTGCAAGCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
| | | | |
Db 2253 CTGCAAGCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
| | | | |
QY 2291 ATTATGATCTCAGAGCCCTTCTGCGCAATTTCAATTAAGGCAACAAATATATACCTT 2350
| | | | |
Db 2313 ATTATGATCTCAGAGCCCTTCTGCGCAATTTCAATTAAGGCAACAAATATATACCTT 2372
| | | | |
QY 2351 CCAATGAGCACACAGACTTTTGAAGCAAGACATGATGCTTGAATGAGGCTTGG 2410
| | | | |

Db 2373 CCATGAGACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTGAGCCCTTG 2432
QY 2411 AGGAATGAGCTTTGAAGAAAGAAATATTGTTTCCAGCCCCCTTCCACACTCTCA 2470
Db 2433 AGGAATGAGCTTTGAAGAAAGAAATATTGTTTCCAGCCCCCTTCCACACTCTCA 2492
QY 2471 TGTGTTAACACACTGCTTCTCTGAGCTTGGAGCCACGCTGATTAACATGTTGTTAT 2530
Db 2493 TGTGTTAACACACTGCTTCTCTGAGCTTGGAGCCACGCTGATTAACATGTTGTTAT 2552
QY 2531 AGAAAACTGATTTTGAAGTTCGATCTTCAAGAGATGATTAATATACATTTCT 2587
Db 2553 AGAAAACTGATTTTGAAGTTCGATCTTCAAGAGATGATTAATATACATTTCT 2609

RESULT 4
AR478744 2627 bp DNA linear PAT 14-MAY-2004
LOCUS AR478744
DEFINITION Sequence 391 from patent US 6699664.
ACCESSION AR478744
VERSION AR478744.1 GI:47237396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W.,
Ranger,G.R., Reed,S.G., Vedicak,T.S. and Carter,D.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: US 6699664-A 391 02-MAR-2004;
FEATURES
source Location/Qualifiers
1..2627
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 99.1%; Score 2565; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 25/6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 12 GGCAGCTCAGTCAGCCAGTACCCAGATACGCTGGAGACCTTCCCGACGATGGCTTCCC 71
Db 33 GGCAGCTCAGTCAGCCAGTACCCAGATACGCTGGAGACCTTCCCGACGATGGCTTCCC 92
QY 72 TGGGGAGATCTCTTCTGAGCAATTAATGACATCATCTATATCTGCTGGAGCAATTG 131
Db 93 TGGGGAGATCTCTTCTGAGCAATTAATGACATCATCTATATCTGCTGGAGCAATTG 152
QY 132 CACTCATCTGAGCTTGGTATTTTCAGGGAGACACTCCATCAAGTCACTGTCGCT 191
Db 153 CACTCATCTGAGCTTGGTATTTTCAGGGAGACACTCCATCAAGTCACTGTCGCT 212
QY 192 CAGCTGGAGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGAGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAC 272
QY 252 TTTTCTGATATCTGATATCAATGAGCTGGAAGAGCTTTTAACTTGGTCTCATGATTTCA 311
Db 273 TTTTCTGATATCTGATATCAATGAGCTGGAAGAGCTTTTAACTTGGTCTCATGATTTCA 332
QY 312 AAGAGAGCAAAAGATGAGCTGTCGAGCAGAGATGAATGTTCAAGGCGGAGACAGAGTGT 371
Db 333 AAGAGAGCAAAAGATGAGCTGTCGAGCAGAGATGAATGTTCAAGGCGGAGACAGAGTGT 392
QY 372 TTGCTGATCAAGTATAGTTGGCAATGCTCTTTTGCGGCTGAAGAAAGTGAACCTCACAG 431
Db 393 TTGCTGATCAAGTATAGTTGGCAATGCTCTTTTGCGGCTGAAGAAAGTGAACCTCACAG 452
QY 432 ATGCTGGACCTTACAAATGTTATATCATCTTCTTAAAGGCAAGGGAATGCTAACCTTG 491
Db 453 ATGCTGGACCTTACAAATGTTATATCATCTTCTTAAAGGCAAGGGAATGCTAACCTTG 512

QY 492 AGATATAAAACTGAGCCCTTTCAGATGCCGGAAGTGAATGTGAGATATATATCCAGCTCAG 551
Db 513 AGTATAAAACTGAGCCCTTTCAGATGCCGGAAGTGAATGTGAGATATATATCCAGCTCAG 572
QY 552 AGACCTTCGGGTGAGAGCTCTCCGATGCTTCCCGAGCTCCAGCCCAAGTGTCTGGGCAATCCC 611
Db 573 AGACCTTCGGGTGAGAGCTCTCCGATGCTTCCCGAGCTCCAGCCCAAGTGTCTGGGCAATCCC 632
QY 612 AAGTTGACCAAGGAGCCCAACTCTTCGAAAGTCTCCAAATACAGCTTTGAGCTGAACCTCG 671
Db 633 AAGTTGACCAAGGAGCCCAACTCTTCGAAAGTCTCCAAATACAGCTTTGAGCTGAACCTCG 692
QY 672 AGAATGTACCATGAAGGTTGTCTGTCTCTCAATGTTATGATCAACAACATCACT 731
Db 693 AGAATGTACCATGAAGGTTGTCTGTCTCTCAATGTTATGATCAACAACATCACT 752
QY 732 CCTGTATATTTGAAATATGATTTGCAAGCAACAGGGGATATCAAAAGTGAACAAGTGG 791
Db 753 CCTGTATATTTGAAATATGATTTGCAAGCAACAGGGGATATCAAAAGTGAACAAGTGG 812
QY 792 AGATCAAAAAGGCGAGTCACTCAAGCTGCTAAACTCAAAAGGCTTCTGTGTCTCTT 851
Db 813 AGATCAAAAAGGCGAGTCACTCAAGCTGCTAAACTCAAAAGGCTTCTGTGTCTCTT 872
QY 852 CTCTTCTTTCATCAGCTGAGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 911
Db 873 CTCTTCTTTCATCAGCTGAGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 932
QY 912 GTGCTTTGGCCCAAAAAGCAATGCAAGTATTTTCAACAGGAGTCTTCAAGAACTAT 971
Db 933 GTGCTTTGGCCCAAAAAGCAATGCAAGTATTTTCAACAGGAGTCTTCAAGAACTAT 992
QY 972 TTCAACCAACAGATATGACCTATGTTTATATTTCTGGGAGAAATGATTCATCTAGAA 1031
Db 993 TTCAACCAACAGATATGACCTATGTTTATATTTCTGGGAGAAATGATTCATCTAGAA 1052
QY 1032 GTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGGCAAGAGGCTCCAT 1091
Db 1053 GTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGGCAAGAGGCTCCAT 1112
QY 1092 ATGAACAAGATTAATCTATCTTCAAGACATTAATGAAGTGGGAAATTAATTCATGTA 1151
Db 1113 ATGAACAAGATTAATCTATCTTCAAGACATTAATGAAGTGGGAAATTAATTCATGTA 1172
QY 1152 ACTAGACAAGTGTGTTAAGATGATTAAGTAAATGCAAGTGGAGACAAGTCCATCCCAG 1211
Db 1173 ACTAGACAAGTGTGTTAAGATGATTAAGTAAATGCAAGTGGAGACAAGTCCATCCCAG 1232
QY 1212 ATCTCAGGAGCTTCCCTGCTGCTGCTGCTGCTGAGGAGTGAAGACAGATATGTCATGTT 1271
Db 1233 ATCTCAGGAGCTTCCCTGCTGCTGCTGCTGAGGAGTGAAGACAGATATGTCATGTT 1292
QY 1272 CTCTTGTCTCTGAATTTTATGTTATATGTCGTATATGTTGCTCTGAGGAAAGCCCTGGAA 1331
Db 1293 CTCTTGTCTCTGAATTTTATGTTATATGTCGTATATGTTGCTCTGAGGAAAGCCCTGGAA 1352
QY 1332 AGTATATCCCAATATCCATCTTATATTCCAAAATTAAGCTGATGATGATACCTTA 1391
Db 1353 AGTATATCCCAATATCCATCTTATATTCCAAAATTAAGCTGATGATGATACCTTA 1412
QY 1392 AGACGCTGTAATGACTGCACTTTCGCACTCAGAGGCGGCTGATTTAGTATGAGGT 1451
Db 1413 AGACGCTGTAATGACTGCACTTTCGCACTCAGAGGCGGCTGATTTAGTATGAGGT 1472
QY 1452 CAATGATTTCACTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGCA 1511
Db 1473 CAATGATTTCACTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGCA 1532
QY 1512 AATGCCAAAGTTGAAGAAATGATCATATATTTTGAATTAACAAGAGCTGCGGACACCC 1571
Db 1533 AATGCCAAAGTTGAAGAAATGATCATATATTTTGAATTAACAAGAGCTGCGGACACCC 1592
QY 1572 GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1631

Db 1593 GATTTAAATAAAGAGAGACCTTCTTTTAAACAAAGAAAGCGGGTTTATTTCTCA 1652
Qy 1632 GATGATTTTCATCCGTGAATGCTCCAGGAAAGACCTTTCACTTGAATATGACATTA 1691
Db 1653 GATGATTTTCATCCGTGAATGCTCCAGGAAAGACCTTTCACTTGAATATGACATTA 1712
Qy 1692 TGTGATCAAGAGCTGAGAGCTTCTCTTCCATCCGCGGAGACCTAAGACCTAGT 1751
Db 1713 TGTGATCAAGAGCTGAGAGCTTCTCTTCCATCCGCGGAGACCTAAGACCTAGT 1772
Qy 1752 TTTCAATAGCATCTAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1811
Db 1773 TTTCAATAGCATCTAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1832
Qy 1812 GGAATGCTGAGAGCAATTTTGGTTACCTCAATAGAGAGAGAGAGATACAGTCTTA 1871
Db 1833 GGAATGCTGAGAGCAATTTTGGTTACCTCAATAGAGAGAGAGAGATACAGTCTTA 1892
Qy 1872 CTACCACTAGTGAATAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1931
Db 1893 CTACCACTAGTGAATAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1952
Qy 1932 CTCCTCATTAACAATCAATCCCAATCCGAAGTCACTGTCAGAGACTTAAGAAACCTG 1991
Db 1953 CTCCTCATTAACAATCAATCCCAATCCGAAGTCACTGTCAGAGACTTAAGAAACCTG 2012
Qy 1992 TTTGAGTGAAGAAAGGCGCTGGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2050
Db 2013 TTTGAGTGAAGAAAGGCGCTGGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2072
Qy 2051 AGCATATGGCAAAATTAACATTTCTGCTCTTGGTGTGCTGCTGAGAGAGAGAGAGAG 2110
Db 2073 AGCATATGGCAAAATTAACATTTCTGCTCTTGGTGTGCTGCTGAGAGAGAGAGAG 2132
Qy 2111 CTCTATGGGAGACAGAGATTAACATCTCTAGTGAAGAGAGAGAGAGAGAGAGAGAG 2170
Db 2133 CTCTATGGGAGACAGAGATTAACATCTCTAGTGAAGAGAGAGAGAGAGAGAGAGAG 2192
Qy 2171 TGCTGATGGGATTAATCTTCACTTGTGAGCTTCTAAGTTCTTCTCTTCACTTAC 2230
Db 2193 TGCTGATGGGATTAATCTTCACTTGTGAGCTTCTAAGTTCTTCTCTTCACTTAC 2252
Qy 2231 CTGCAACCAAGTCTCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2290
Db 2253 CTGCAACCAAGTCTCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2312
Qy 2291 ATTATGATCTCAAGACCTTCTGAGCAATTAATTAAGAGAGAGAGAGAGAGAGAGAG 2350
Db 2313 ATTATGATCTCAAGACCTTCTGAGCAATTAATTAAGAGAGAGAGAGAGAGAGAGAG 2372
Qy 2351 CCATGAAGACACAGACCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2410
Db 2373 CCATGAAGACACAGACCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2432
Qy 2411 AGGAATGAAGCTTTGAAG 2470
Db 2433 AGGAATGAAGCTTTGAAG 2492
Qy 2471 TGTGTTAACAAGCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2530
Db 2493 TGTGTTAACAAGCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2552
Qy 2531 AGAAACTGATTTAGAGTCTGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2587
Db 2553 AGAAACTGATTTAGAGTCTGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2609

RESULT 5
LOCUS AX156350 2627 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 207 from Patent WO0140269.
ACCESSION AX156350

VERSION AX156350.1 GI:14537350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dillon, D.C., Day, C.H., Jiang, Y., Houghton, R.L., Mitcham, J.L. and Wang, A.
TITLE Compositions and methods for therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0140269-A 207 07-JUN-2001;
FEATURES CORIXA CORPORATION (US)
source location/Qualifiers
1. 2627
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 99.1%; Score 2565; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 12 GCGAGCTCACTGAGCAGTACCAAGTACGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 71
Db 33 GCGAGCTCACTGAGCAGTACCAAGTACGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 92
Qy 72 TGGGAGAGATCTCTTCTGAGAGATTAATGATCATCATTAATTTCTGCTGAGAGCAATTG 131
Db 93 TGGGAGAGATCTCTTCTGAGAGATTAATGATCATCATTAATTTCTGCTGAGAGCAATTG 152
Qy 132 CACTCATCATTTGCTTTGATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
Db 153 CACTCATCATTTGCTTTGATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
Qy 192 CAGCTGGAGAGATTTGGGAG 251
Db 213 CAGCTGGAGAGATTTGGGAG 272
Qy 252 TTTCTGATATGATGATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
Db 273 TTTCTGATATGATGATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 332
Qy 312 AAGAAGCAAGATGAG 371
Db 333 AAGAAGCAAGATGAG 392
Qy 372 TTGCTGATCAAGATAGTTGGAGATGCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
Db 393 TTGCTGATCAAGATAGTTGGAGATGCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 452
Qy 432 ATGCTGGACCTTCAATGATTAATATCATCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAG 491
Db 453 ATGCTGGACCTTCAATGATTAATATCATCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAG 512
Qy 492 AGATTAAG 551
Db 513 AGATTAAG 572
Qy 552 AGACCTTGGAG 611
Db 573 AGACCTTGGAG 632
Qy 612 AAGTTGACAGGAG 671
Db 633 AAGTTGACAGGAG 692
Qy 672 AGAATGAG 731
Db 693 AGAATGAG 752
Qy 732 CTTGATGATTTGAAGATGATGAG 791

Db 753 CCTGTATGATTTGAAAATGAATTGCTCCAAAGCAACAGGGGATATCAAAAGTGAAGAAATCCG 812
QY 792 AGATCAAAAAGGCGAGTCACTTACAGCTGCTAAACTCAAGGCTTCTGTGTGTTCTTT 851
Db 813 AGATCAAAAAGGCGAGTCACTTACAGCTGCTAAACTCAAGGCTTCTGTGTGTTCTTT 872
QY 852 CTTTCTTTTCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTAACCTGATGCTAAATAT 911
Db 873 CTTTCTTTTCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTAACCTGATGCTAAATAT 932
QY 912 GTGCTTGGCCCAAAAAAGCATGCAAAAGTCAATGTTTACAACAGGATCTTACAGAACTAT 971
Db 933 GTGCTTGGCCCAAAAAAGCATGCAAAAGTCAATGTTTACAACAGGATCTTACAGAACTAT 992
QY 972 TTCCACCACAGATATGACCTAGTTTATATTTCTGGAGGAAATGAATCATATCTAGAA 1031
Db 993 TTCCACCACAGATATGACCTAGTTTATATTTCTGGAGGAAATGAATCATATCTAGAA 1052
QY 1032 GTCTGGAGTGAGCAAAACAAGCAAGAAACAAAAGAGCCAAAGCAGAGGCTTCAAT 1091
Db 1053 GTCTGGAGTGAGCAAAACAAGCAAGAAACAAAAGAGCCAAAGCAGAGGCTTCAAT 1112
QY 1092 ATGAACAATAATATCTATCTTCAAGACATATTAAGTTGGGAAATATATTCATGTA 1151
Db 1113 ATGAACAATAATATCTATCTTCAAGACATATTAAGTTGGGAAATATATTCATGTA 1172
QY 1152 ACTAGACAAGTGTATTAAGATGATTAAGTAAATGCAAGTGGAGCAATGCAATCCCAAG 1211
Db 1173 ACTAGACAAGTGTATTAAGATGATTAAGTAAATGCAAGTGGAGCAATGCAATCCCAAG 1232
QY 1212 ATCTCAGGAGCTCCCTGCTGCTCACTGGGAGTGAAGAGACAGATAGTCAATGTT 1271
Db 1233 ATCTCAGGAGCTCCCTGCTGCTCACTGGGAGTGAAGAGACAGATAGTCAATGTT 1292
QY 1272 CTTTGTCTCTGAATTTTGTATTAATGCTGTAATGTTGCTCTGAGGAGCCCTTGGA 1331
Db 1293 CTTTGTCTCTGAATTTTGTATTAATGCTGTAATGTTGCTCTGAGGAGCCCTTGGA 1352
QY 1332 AGTCTATCCCAACATATCCATCTTATATTCACAATTAAGCTGTATGATGATCCCTTA 1391
Db 1353 AGTCTATCCCAACATATCCATCTTATATTCACAATTAAGCTGTATGATGATCCCTTA 1412
QY 1392 AAGCGCTGTAAATGATGCTCCACTTGCACCTCAGGCGCGCTGCATTTTAAATAGGT 1451
Db 1413 AAGCGCTGTAAATGATGCTCCACTTGCACCTCAGGCGCGCTGCATTTTAAATAGGT 1472
QY 1452 CAAATGATCAGCTTTTATGATGCTTCCAAAGTGTGCTGCTCTCCCAACTGACA 1511
Db 1473 CAAATGATCAGCTTTTATGATGCTTCCAAAGTGTGCTGCTCTCCCAACTGACA 1532
QY 1512 AATGCCAAAGTTGAGAAAATGATCATATTTTAAAGATTAAGACAGACATCGCGCACCC 1571
Db 1533 AATGCCAAAGTTGAGAAAATGATCATATTTTAAAGATTAAGACAGACATCGCGCACCC 1592
QY 1572 GATTTTATAATAAATGATGACCTTCTTTTAAACAACAAATGCGGGTTATTTCTCA 1631
Db 1593 GATTTTATAATAAATGATGACCTTCTTTTAAACAACAAATGCGGGTTATTTCTCA 1652
QY 1632 GATGATGTTCAATCCGGAATGCTCCAGGAGAGGACCTTCACTTGAATATATGATGATTA 1691
Db 1653 GATGATGTTCAATCCGGAATGCTCCAGGAGAGGACCTTCACTTGAATATATGATGATTA 1712
QY 1692 TGTCTATCAGACGCTGAGGCTTCTCTTTCATCTGCGTGACAGCTAAGACCTCAAT 1751
Db 1713 TGTCTATCAGACGCTGAGGCTTCTCTTTCATCTGCGTGACAGCTAAGACCTCAAT 1772
QY 1752 TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGGTATTTCCGCCCATCTCCGG 1811
Db 1773 TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGGTATTTCCGCCCATCTCCGG 1832
QY 1812 GGAATGCTCTGAAGACAAATTTTGTATCCCTCAATGAGGAGTGAAGAGATACAGTGCTA 1871
Db 1833 GGAATGCTCTGAAGACAAATTTTGTATCCCTCAATGAGGAGTGAAGAGATACAGTGCTA 1892

QY 1872 CTACCAACTAGTGATTAAGGCCAGAGATGCTGCTCAACTTCTTCAATGATACAGAGCT 1931
Db 1893 CTACCAACTAGTGATTAAGGCCAGAGATGCTGCTCAACTTCTTCAATGATACAGAGCT 1952
QY 1932 CTCCTCATTAACAATCCCAATCCGAAGTGTCACTGTGTCAAGGACTTAAGAAACCTTGT 1991
Db 1953 CTCCTCATTAACAATCCCAATCCGAAGTGTCACTGTGTCAAGGACTTAAGAAACCTTGT 2012
QY 1992 TTTGATGAAAAGGCGCTGAAAAGAGGGGAGCCAAATATGCTGCTT-CTCACAT 2050
Db 2013 TTTGATGAAAAGGCGCTGAAAAGAGGGAGCCAAATATGCTGCTT-CTCACAT 2072
QY 2051 AGTCAATGGCAATTAAGCAATCTGTCTTTGCTGCTGCTCAGCAGAGAGGCTCAGA 2110
Db 2073 AGTCAATGGCAATTAAGCAATCTGTCTTTGCTGCTGCTCAGCAGAGAGGCTCAGA 2132
QY 2111 CTCTATCGGAGCCAGATTAATCTCTCAGTGAACAAGTTGACAAAGGCTTAAGGAAA 2170
Db 2133 CTCTATCGGAGCCAGATTAATCTCTCAGTGAACAAGTTGACAAAGGCTTAAGGAAA 2192
QY 2171 TGCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTCTTCCCTTCAATCTACC 2230
Db 2193 TGCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTCTTCCCTTCAATCTACC 2252
QY 2231 CTGCAAGCCAAATCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAATCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
QY 2291 ATTTGATCTCCAGACCTTCTGCGCAATTCAAATTAAGCAACAAATATACCTT 2350
Db 2313 ATTTGATCTCCAGACCTTCTGCGCAATTCAAATTAAGCAACAAATATACCTT 2372
QY 2351 CCATGAGACACACAGACTTTTGAAGCAAGACATGACTGTGAATGAGGCTTGG 2410
Db 2373 CCATGAGACACACAGACTTTTGAAGCAAGACATGACTGTGAATGAGGCTTGG 2432
QY 2411 AGGAATGAAGCTTTGAAGAAAAGATATCTTTGTTCCAGCCCTTCCCACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAAAAGATATCTTTGTTCCAGCCCTTCCCACTCTTCA 2492
QY 2471 TGTGTTAACCACTGCTTCTGAGACCTTGGAGCCAGGTGACTGATATACATGTTGAT 2530
Db 2493 TGTGTTAACCACTGCTTCTGAGACCTTGGAGCCAGGTGACTGATATACATGTTGAT 2552
QY 2531 AGAAATGATTTTGAAGTCTGATCGTTCAAGAAATGATTAATATACATTTCT 2587
Db 2553 AGAAATGATTTTGAAGTCTGATCGTTCAAGAAATGATTAATATACATTTCT 2609

RESULT 6
AX366624 2627 bp DNA linear PAT 15-FEB-2002
LOCUS AX366624
DEFINITION Sequence 391 from Patent W00206317.
ACCESSION AX366624
VERSION AX366624.1 GI:18698046
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Mitsumori, J.L., King, G.E., Algate, P.A., Fling, S.P., Retter, M.W.,
Fanger, G.R., Reed, S.G., Vedvik, T.S., Carter, D., Hill, P. and
Albone, E.
Compositions and methods for the therapy and diagnosis of ovarian
cancer
Patent: WO 0206317-A 391 24-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source
1..2627
/organism="Homo sapiens"
/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:9606"

Query Match 99.1%; Score 2565; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	12	GGGAGCTCCACTGACGACGATACCGATAGCGCTGGGAACTTCCCGGCAATGGCTTCCC	71
Db	33	GGGAGCTCCACTGACGACGATACCGATAGCGCTGGGAACTTCCCGGCAATGGCTTCCC	92
Qy	72	TGGGGAGATCTCTTCTGAGCATTAATTAGCATCATCATTAATTCTGGTGGAGCAATTTG	131
Db	93	TGGGGAGATCTCTTCTGAGCATTAATTAGCATCATCATTAATTCTGGTGGAGCAATTTG	152
Qy	132	CACCTCATATTGGCTTTGGTATTTCAGAGAGACATCCATCACTACATCTATCTGCGCT	191
Db	153	CACCTCATATTGGCTTTGGTATTTCAGAGAGACATCCATCACTACATCTATCTGCGCT	212
Qy	192	CAGCTGGGAACATTTGGGGAGATGGAAATCCAGACTGCATTTTGAACCTGACATCAAC	251
Db	213	CAGCTGGGAACATTTGGGGAGATGGAAATCCAGACTGCATTTTGAACCTGACATCAAC	272
Qy	252	TTTCTGATATCGTATCAATAGCTGAAGAGGTGTTTAGGCTTGGTCCATGATTTCA	311
Db	273	TTTCTGATATCGTATCAATAGCTGAAGAGGTGTTTAGGCTTGGTCCATGATTTCA	332
Qy	312	AAGAGGCAAAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGGAACAGAGTGT	371
Db	333	AAGAGGCAAAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGGAACAGAGTGT	392
Qy	372	TTTGTGATCAAGTAGTAGTTGGGCAATGCTCTTGGCGCTGAAAAGCTGAATCTCAG	431
Db	393	TTTGTGATCAAGTAGTAGTTGGGCAATGCTCTTGGCGCTGAAAAGCTGAATCTCAG	452
Qy	432	ATGCTGCACTCAAAATGTTATATCATCACTTCTAAGGCAAGGGGATGCTAACTTG	491
Db	453	ATGCTGCACTCAAAATGTTATATCATCACTTCTAAGGCAAGGGGATGCTAACTTG	512
Qy	492	AGATTAATACTGAGCTTCAAGATGCGGGAAGTGAATGTTGACTAATATGCCAGTCTAG	551
Db	513	AGATTAATACTGAGCTTCAAGATGCGGGAAGTGAATGTTGACTAATATGCCAGTCTAG	572
Qy	552	AGACCTTGGCGGTGAGAGCTTCCCGAGTTCCTCCCGGACCCCAAGTGTCTGGGCACTCC	611
Db	573	AGACCTTGGCGGTGAGAGCTTCCCGAGTTCCTCCCGGACCCCAAGTGTCTGGGCACTCC	632
Qy	612	AAGTTGACAGGAGCACTTCTCGGAAGCTCTCAATACAGGCTTGAAGCTGAATCTTG	671
Db	633	AAGTTGACAGGAGCACTTCTCGGAAGCTCTCAATACAGGCTTGAAGCTGAATCTTG	692
Qy	672	AGAAATGATCATGAAGGTGTGTCTGTGCTTCAAAATGTTACGATCAACAACATCACT	731
Db	693	AGAAATGATCATGAAGGTGTGTGTGTGCTGTCAATATGTTACGATCAACAACATCACT	752
Qy	732	CCCTGATGATTTGAATAAGATTTGCGCAAGCAAGGGGATATCAAGTGCAGAAATCCG	791
Db	753	CCCTGATGATTTGAATAAGATTTGCGCAAGCAAGGGGATATCAAGTGCAGAAATCCG	812
Qy	792	AGATCAAAAGGCGAGTCACTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTT	851
Db	813	AGATCAAAAGGCGAGTCACTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTT	872
Qy	852	CTTTCTTGGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATAT	911
Db	873	CTTTCTTGGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATAT	932
Qy	912	GTCCTTGGGCAAAAGATGCAAGTCAATGTTTACAAAGGGATCTACAGAAATAT	971
Db	933	GTCCTTGGGCAAAAGATGCAAGTCAATGTTTACAAAGGGATCTACAGAAATAT	992
Qy	972	TTTACCAACAGATATGACTAGTTTATTTATTTCTGGAGGAAATGAATTCATATCTGAA	1031

Db	993	TTACCAACAGATATGACTAGTTTATTTATTTCTGGAGGAAATGAATTCATATCTGAA	1052
Qy	1032	GTCCTGAGTGAAGCAACAGAGCAAGAAACAAAAGAGCCAAACAGAGAGCTCCAT	1091
Db	1053	GTCCTGAGTGAAGCAACAGAGCAAGAAACAAAAGAGCCAAACAGAGAGCTCCAT	1112
Qy	1092	ATGAAACAGATATATCTATCTTCAAGACATATTTAGAGTTGGGAAAATTAATCATGTGA	1151
Db	1113	ATGAAACAGATATATCTATCTTCAAGACATATTTAGAGTTGGGAAAATTAATCATGTGA	1172
Qy	1152	ACTAGCAAGTGTATTAAGATGATTAAGTAAATGCAAGTGAAGCAAGTGCATCCGAG	1211
Db	1173	ACTAGCAAGTGTATTAAGATGATTAAGTAAATGCAAGTGAAGCAAGTGCATCCGAG	1232
Qy	1212	ATCTCAGGAGCTTCCCTGCTGCTCACTGGGAGTGAAGAGCAGATATGTCATGTT	1271
Db	1233	ATCTCAGGAGCTTCCCTGCTGCTCACTGGGAGTGAAGAGCAGATATGTCATGTT	1292
Qy	1272	CTTTGCTCTGAATTTTATGATATGCTGATATGTTGCTCTGAGGAAAGCCCTGGA	1331
Db	1293	CTTTGCTCTGAATTTTATGATATGCTGATATGTTGCTCTGAGGAAAGCCCTGGA	1352
Qy	1332	AGTCTATCCCAACATATCCACATCTTATATTTCCAAATTAAGCTGATATGCTCA	1391
Db	1353	AGTCTATCCCAACATATCCACATCTTATATTTCCAAATTAAGCTGATATGCTCA	1412
Qy	1392	AGACGCTGCTAATTTGACTGCTGCACTTGGCACTAGGGGCGGCTGCAATTTAGTAATGGT	1451
Db	1413	AGACGCTGCTAATTTGACTGCTGCACTTGGCACTAGGGGCGGCTGCAATTTAGTAATGGT	1472
Qy	1452	CAATGATGATCACTTTTATGATGCTTCCAAAGGCTGCTGCTTCCCAACTGACA	1511
Db	1473	CAATGATGATCACTTTTATGATGCTTCCAAAGGCTGCTGCTTCCCAACTGACA	1532
Qy	1512	AATGCCAAGTTGAGAAAAATGATCAATATTTTGAATAAACAGAGCAGTGGCGACCC	1571
Db	1533	AATGCCAAGTTGAGAAAAATGATCAATATTTTGAATAAACAGAGCAGTGGCGACCC	1592
Qy	1572	GATTTTATTAATTAATCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA	1631
Db	1593	GATTTTATTAATTAATCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA	1652
Qy	1632	GATGATGTTGATCCGGAATATGTCAGGGAAGGACCTTTCACCTGACTATATGGCACTTA	1691
Db	1653	GATGATGTTGATCCGGAATATGTCAGGGAAGGACCTTTCACCTGACTATATGGCACTTA	1712
Qy	1692	TGTATCATCAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGCAGCTAAGACTTCAGT	1751
Db	1713	TGTATCATCAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGCAGCTAAGACTTCAGT	1772
Qy	1752	TTTCAATAGCATTTAAGAGCTGGAAGTCAAGCTGGGGTGAATTTGCGCCCATCTCGGG	1811
Db	1773	TTTCAATAGCATTTAAGAGCTGGAAGTCAAGCTGGGGTGAATTTGCGCCCATCTCGGG	1832
Qy	1812	GGAATGTCGAAGCAATTTTGGTTACTTCAAGAGGAGTGAAGAGGATACAGTCTTA	1871
Db	1833	GGAATGTCGAAGCAATTTTGGTTACTTCAAGAGGAGTGAAGAGGATACAGTCTTA	1892
Qy	1872	CTACCAACTAGTGAATTAAGGCGAGGAGTCTGCTCAACCTCTCACTACATGACAGAGCT	1931
Db	1893	CTACCAACTAGTGAATTAAGGCGAGGAGTCTGCTCAACCTCTCACTACATGACAGAGCT	1952
Qy	1932	CTTCCCATTTAACAATCCCAATCGGAAGTCACTGCTGCTGAGAGCTAAGAAACCTGGT	1991
Db	1953	CTTCCCATTTAACAATCCCAATCGGAAGTCACTGCTGCTGAGAGCTAAGAAACCTGGT	2012
Qy	1992	TTTGAATGAAGGAGCTGGAAGAGGAGGAGCAAAATCTGTCTGCTT -CTCACTT	2050
Db	2013	TTTGAATGAAGGAGCTGGAAGAGGAGGAGCAAAATCTGTCTGCTTCTCTCACTT	2072
Qy	2051	AGTCATTTGCAAAATTAAGCATTTCTGCTCTTTGGCTGCTGCTGACAGACAGAGCCAGAA	2110
Db	2073	AGTCATTTGCAAAATTAAGCATTTCTGCTCTTTGGCTGCTGCTGACAGACAGAGCCAGAA	2132

QY 2111 CTCATCGGACACAGATTAACATCTCTCAGTGAACAGAGTGAACAAGCCTATGGGAAA 2170
|
|
|
Db 2133 CTCATCGGACACAGATTAACATCTCTCAGTGAACAGAGTGAACAAGCCTATGGGAAA 2192
|
|
|
QY 2171 TGCCTGATGGATTAATCTTCAAGCTTGTAGCTTCAAGTTTCTTCCCTCACTTACC 2230
|
|
|
Db 2193 TGCCTGATGGATTAATCTTCAAGCTTGTAGCTTCAAGTTTCTTCCCTCACTTACC 2252
|
|
|
QY 2231 CTGCAAGCCAAAGTTCGTGAAGAAATGCTGAGTTCAGTCAAGTTTCTTACCTGA 2290
|
|
|
Db 2253 CTGCAAGCCAAAGTTCGTGAAGAAATGCTGAGTTCAGTCAAGTTTCTTACCTGA 2312
|
|
|
QY 2291 ATTATGATCTCCAGACCTTCCCTGCGCAATTCATTAAGCAACAATATACCTT 2350
|
|
|
Db 2313 ATTATGATCTCCAGACCTTCCCTGCGCAATTCATTAAGCAACAATATACCTT 2372
|
|
|
QY 2351 CCATGAAGACACACAGACTTTTGAAGAAGCAATGATGCTTGAATTGAGGCTTG 2410
|
|
|
Db 2373 CCATGAAGACACACAGACTTTTGAAGAAGCAATGATGCTTGAATTGAGGCTTG 2432
|
|
|
QY 2411 AGGAATGAAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCACTCTTA 2470
|
|
|
Db 2433 AGGAATGAAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCCACTCTTA 2492
|
|
|
QY 2471 TGTGTTAACCACTGCTTCTGAGCCTTGGAGCCAGGTGATGATATCATGTTGTTAT 2530
|
|
|
Db 2493 TGTGTTAACCACTGCTTCTGAGCCTTGGAGCCAGGTGATGATATCATGTTGTTAT 2552
|
|
|
QY 2531 AGAAAATGATTTTGAAGTTCTGATGCTTCAAGAGAATGATTAATATACATTTCT 2587
|
|
|
Db 2553 AGAAAATGATTTTGAAGTTCTGATGCTTCAAGAGAATGATTAATATACATTTCT 2609
|
|
|

RESULT 7
AX403048 2603 bp DNA 1linear PART 07-JUN-2002
LOCUS Sequence 1 from Patent WO0202624.
DEFINITION AX403048
ACCESSION AX403048
VERSION AX403048.1 GI:21388028
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Fox, G., Sullivan, J.K. and Fang, M.
TITLE B7-like molecules and uses thereof
JOURNAL Patent: WO 0202624-A 1 10-JAN-2002;
Amgen, Inc. (US)
FEATURES
source Location/Qualifiers
1..2603
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
53..901
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD33698.1"
/db_xref="GI:21388028"
/translation="MASHGQILFWIISIIIIILAGAILIIGRISGRHSITVTVAS
AGNIGEDGILCTFEPDIKLSIDVLIOMLEGVGLVHREKGEDELSDENFRGRTA
VFADQVIVGNASIRLKNVOLTDAGTYKCTIISKGGANLAEKIGAFMPENVADYN
ASSETIRCARPRFPPTPYVMASQVNOGANSFBSVTSFELNSENVTVVSLVAVNT
INNTSMTIENDIARATGDIKVTESIRKSRSHQLINLSRSLCVSSFPALSWALLPLS
PYLMLK"

ORIGIN

Query Match 99.1%; Score 2563; DB 6; Length 2603;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2574; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 12 GGAGCTCCACTAGCCAGTACCAAGATAGCTGGAGACCTTCCCGAGCATGGCTTCCC 71

Db 3 GGAGCTCCACTAGCCAGTACCAAGATAGCTGGAGACCTTCCCGAGCATGGCTTCCC 62
|
|
|
QY 72 TGGGGCAGATCCTCTTCGAGACATTAATTAGATCATATTTCTGCTGAGCAATTG 131
|
|
|
Db 63 TGGGGCAGATCCTCTTCGAGACATTAATTAGATCATATTTCTGCTGAGCAATTG 122
|
|
|
QY 132 CACTCATATTTGGCTTTTGGTATTTTCAGGAGACATCTCATCACTCATCTGTGCT 191
|
|
|
Db 123 CACTCATATTTGGCTTTTGGTATTTTCAGGAGACATCTCATCACTCATCTGTGCT 182
|
|
|
QY 192 CAGCTGGGAAACATTGGGAGAGATGGAATCTGAGCTGCACTTTTGAACCTGACATCAAC 251
|
|
|
Db 183 CAGCTGGGAAACATTGGGAGAGATGGAATCTGAGCTGCACTTTTGAACCTGACATCAAC 242
|
|
|
QY 252 TTTCTGATATGCTGATACATAGGCTGGAAGGAAGGTTTATAGGCTTGGCTCATGAGTTCA 311
|
|
|
Db 243 TTTCTGATATGCTGATACATAGGCTGGAAGGAAGGTTTATAGGCTTGGCTCATGAGTTCA 302
|
|
|
QY 312 AAGAAGCAAGATGAGCTGTGAGCAGATGAATGTAATGTTCAAGAGCCGAGACAGTGT 371
|
|
|
Db 303 AAGAAGCAAGATGAGCTGTGAGCAGATGAATGTAATGTTCAAGAGCCGAGACAGTGT 362
|
|
|
QY 372 TTGCTGATCAGTATAGTTGGCAATGCTCTTTTGGCTGAAAACCTGCACTCAAG 431
|
|
|
Db 363 TTGCTGATCAGTATAGTTGGCAATGCTCTTTTGGCTGAAAACCTGCACTCAAG 422
|
|
|
QY 432 ATGCTGGACCTCAAAATGTTATATCATCACTTCAAAAGGCAAGGGGAATGTAACCTTG 491
|
|
|
Db 423 ATGCTGGACCTCAAAATGTTATATCATCACTTCAAAAGGCAAGGGGAATGTAACCTTG 482
|
|
|
QY 492 AGTATMAAATGAGACCTTTCAGCATGCGGAAGTAATGTGAGCTAATATGCGACCTGAG 551
|
|
|
Db 483 AGTATMAAATGAGACCTTTCAGCATGCGGAAGTAATGTGAGCTAATATGCGACCTGAG 542
|
|
|
QY 552 AGACCTTGGGCTGTGAGGCTCCCGATGCTTCCCGACCCACAGTGTGCTGGGATCCC 611
|
|
|
Db 543 AGACCTTGGGCTGTGAGGCTCCCGATGCTTCCCGACCCACAGTGTGCTGGGATCCC 602
|
|
|
QY 612 AGTTGACAGGGAGCCCAACTTCTGGAAGTCTCCAAATACAGCTTTGAGCTGAACCTG 671
|
|
|
Db 603 AGTTGACAGGGAGCCCAACTTCTGGAAGTCTCCAAATACAGCTTTGAGCTGAACCTG 662
|
|
|
QY 672 AGAATGTGACATGAAGGTTGTGCTGTGCTCTCAATGTTACGATCAACAACACATACT 731
|
|
|
Db 663 AGAATGTGACATGAAGGTTGTGCTGTGCTCTCAATGTTACGATCAACAACACATACT 722
|
|
|
QY 722 CCTGTATGATGAATAATGACATTTGCCAAGCAAGGGGATRTCAAAGTGACAGAAATGG 791
|
|
|
Db 723 CCTGTATGATGAATAATGACATTTGCCAAGCAAGGGGATRTCAAAGTGACAGAAATGG 782
|
|
|
QY 792 AGATCAAAAGGCGGAGTCACTAGCTGCTTAACTCAAAAGGCTTCTGTGTGCTCTT 851
|
|
|
Db 783 AGATCAAAAGGCGGAGTCACTAGCTGCTTAACTCAAAAGGCTTCTGTGTGCTCTT 842
|
|
|
QY 852 CTTCCTTTGGCATCAGCTGGGACCTTGTGCTCTGAGCCCTTACCTGATGCTAAATAT 911
|
|
|
Db 843 CTTCCTTTGGCATCAGCTGGGACCTTGTGCTCTGAGCCCTTACCTGATGCTAAATAT 902
|
|
|
QY 912 GTTGCCTTGGCCCAAAAAAGCATGCAAAATGCTATTTTACACAGGGAATCTACAGAACTAT 971
|
|
|
Db 903 GTTGCCTTGGCCCAAAAAAGCATGCAAAATGCTATTTTACACAGGGAATCTACAGAACTAT 962
|
|
|
QY 972 TTCACACACAGATAGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA 1031
|
|
|
Db 963 TTCACACACAGATAGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA 1022
|
|
|
QY 1032 GTCTGAGTGAACAACAAGCAAGCAAGAAACAAAGGAGCAAGAGCTCCAT 1091
|
|
|
Db 1023 GTCTGAGTGAACAACAAGCAAGCAAGAAACAAAGGAGCAAGAGCTCCAT 1082
|
|
|
QY 1092 ATGAACAAAGTAAATCTATCTTCAAGACATTTTGAAGTTGGAAATTAATTCATGCA 1151
|
|
|

Db 1083 ATGACAAAGATTAATCTATCTTCAAGACATATTAGAAGTTGGGAAATAATTCATGTGA 1142
 Qy 1152 ACTAGCAAGTGTTAAGAGTGTATAGTAAATGACGTGAGACAAAGTCAATCCCCAG 1211
 Db 1143 ACTAGCAAGTGTTAAGAGTGTATAGTAAATGACGTGAGACAAAGTCAATCCCCAG 1202
 Qy 1212 ATCTCAGGAGACCTCCCTCCTCCTGCTCACTGAGGAGTGAAGAGACAGATATGTCATGT 1271
 Db 1203 ATCTCAGGAGACCTCCCTCCTCCTGCTCACTGAGGAGTGAAGAGACAGATATGTCATGT 1262
 Qy 1272 CTCTTCTCTGAATTTTAAAGTATATGCTGTATATGCTGTCTGAGGAAAGCCCTGGAA 1331
 Db 1263 CTCTTCTCTGAATTTTAAAGTATATGCTGTATATGCTGTCTGAGGAAAGCCCTGGAA 1322
 Qy 1332 AGCTATCCCAACATATCCACATCTTATATCCCAATTAAGCTGTATATGATACCTTA 1391
 Db 1323 AGCTATCCCAACATATCCACATCTTATATCCCAATTAAGCTGTATATGATACCTTA 1382
 Qy 1392 AGAGCTGTATATGACCTGCACTTCCCACTCAGGAGGAGCTGCAATTTATAGTATGGGT 1451
 Db 1383 AGAGCTGTATATGACCTGCACTTCCCACTCAGGAGGAGCTGCAATTTATAGTATGGGT 1442
 Qy 1452 CAATATGATCACTTTTATATGATGCTTCCAAAGTGCCTTGGCTTCTCTCCCACTGACA 1511
 Db 1443 CAATATGATCACTTTTATATGATGCTTCCAAAGTGCCTTGGCTTCTCTCCCACTGACA 1502
 Qy 1512 AATGCCAAAGTTGAGAAATATGATCAATATTTAGTAAACAGAGAGTCCGAGACACC 1571
 Db 1503 AATGCCAAAGTTGAGAAATATGATCAATATTTAGTAAACAGAGAGTCCGAGACACC 1562
 Qy 1572 GATTTTATATATTAATCACTGACACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1631
 Db 1563 GATTTTATATATTAATCACTGACACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1622
 Qy 1632 GATGATGTTTCATCCGTGATATGTCAGAGGAAAGACCTTTCACTGATATATGACATTA 1691
 Db 1623 GATGATGTTTCATCCGTGATATGTCAGAGGAAAGACCTTTCACTGATATATGACATTA 1682
 Qy 1692 TGTCATCAACAAGCTCTGAGGCTTCTCTTCCATCCCTGCTGACAGCTAAGACCTTCAGT 1751
 Db 1683 TGTCATCAACAAGCTCTGAGGCTTCTCTTCCATCCCTGCTGACAGCTAAGACCTTCAGT 1742
 Qy 1752 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGG 1811
 Db 1743 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGG 1802
 Qy 1812 GGAATGTCTGAAGACAAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTGTCTA 1871
 Db 1803 GGAATGTCTGAAGACAAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTGTCTA 1862
 Qy 1872 CTACCAACTAGTGTGAATTAAGGCCAGGAGTGTCTCACTCTCAATGATACAGAGCT 1931
 Db 1863 CTACCAACTAGTGTGAATTAAGGCCAGGAGTGTCTCACTCTCAATGATACAGAGCT 1922
 Qy 1932 CTCCCCATTAACAATAACCAATCCGAAGTGTCACTGTCTCAGGACTTAAGAAACCCCTGCT 1991
 Db 1923 CTCCCCATTAACAATAACCAATCCGAAGTGTCACTGTCTCAGGACTTAAGAAACCCCTGCT 1982
 Qy 1992 TTTGAGTAGAAAAGGGCTGGAAAAGAGGGAGCCCAACAAATCTGTCTGCTT-CTCACTT 2050
 Db 1983 TTTGAGTAGAAAAGGGCTGGAAAAGAGGGAGCCCAACAAATCTGTCTGCTTCACTT 2042
 Qy 2051 AGTCATTTGGCAATTAAGCATTTCTGTCTCTTTGGCTGTCTGCTCAGCAACAAGGCCAGAA 2110
 Db 2043 AGTCATTTGGCAATTAAGCATTTCTGTCTCTTTGGCTGTCTGCTCAGCAACAAGGCCAGAA 2102
 Qy 2111 CTCTATCGGGACCAAGATTAACATCTCTCAGTGAACAGATTTGAAGGCCCTAATGGGAAA 2170
 Db 2103 CTCTATCGGGACCAAGATTAACATCTCTCAGTGAACAGATTTGAAGGCCCTAATGGGAAA 2162
 Qy 2171 TGCCTGATGGGATTAATCTTCACTTGTGTGAGCTTTCTAAGTTTCTTTCCCTTCAATTCACC 2230
 Db 2163 TGCCTGATGGGATTAATCTTCACTTGTGTGAGCTTTCTAAGTTTCTTTCCCTTCAATTCACC 2222

Qy 2231 CTGCAAGCCCAAGTTCTGTAAAGAAATGCCGTGAGTTCTAGCTGAGTTTCTTACTCTGA 2290
 Db 2223 CTGCAAGCCCAAGTTCTGTAAAGAAATGCCGTGAGTTCTTACTGAGTTTCTTACTCTGA 2282
 Qy 2291 ATTTAGATCTCCAGACCTTCTCTGCGCACAAATTCATTAAGGCAACAAATATACCTT 2350
 Db 2283 ATTTAGATCTCCAGACCTTCTCTGCGCACAAATTCATTAAGGCAACAAATATACCTT 2342
 Qy 2351 CCATGAAGCACACACAGACTTTTGAAGCAAGACATATGACTGCTTGAATGAGGCTTG 2410
 Db 2343 CCATGAAGCACACACAGACTTTTGAAGCAAGACATATGACTGCTTGAATGAGGCTTG 2402
 Qy 2411 AGGAATGAGCTTTGAAGGAAAGAAATPACTTGTCTCCAGCCCTCCACACTCTCTCA 2470
 Db 2403 AGGAATGAGCTTTGAAGGAAAGAAATPACTTGTCTCCAGCCCTCCACACTCTCTCA 2462
 Qy 2471 TGTGTTAACCACTGCTTCTCTGACCTTGGAGCCAGGAGTACTGTATTAATATGTTTAT 2530
 Db 2463 TGTGTTAACCACTGCTTCTCTGACCTTGGAGCCAGGAGTACTGTATTAATATGTTTAT 2522
 Qy 2531 AGAAACTGATTTTGAAGTCTGTATGCTTCAAGAGAAATGATTAATATATACATTTCT 2587
 Db 2523 AGAAACTGATTTTGAAGTCTGTATGCTTCAAGAGAAATGATTAATATATACATTTCT 2579
 RESULT 8
 AX375860 2626 bp DNA linear PAT 01-MAR-2002
 LOCUS AX375860
 DEFINITION Sequence 7 from Patent WO0194641.
 ACCESSION AX375860
 VERSION AX375860.1 GI:19170332
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 Ople, E., McLachlan, K. and Heard, C.
 Gene targets and ligands that bind thereto for treatment and
 diagnosis of ovarian carcinomas
 Patent: WO 0194641-A 7 13-DEC-2001;
 JOURNAL Idec Pharmaceuticals Corporation (US)
 FEATURES
 source location/Qualifiers
 1..2626
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 97.7%; Score 2527.2; DB 6; Length 2626;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2565; Conservative 0; Mismatches 10; Indels 3; Gaps 3;
 Qy 12 GGCAGCTCCACATGAGCCAGTACCCAGATAGGCTGGGAGACCTTCCAGCCATGAGCTTCCC 71
 Db 11 GGCAGCTCCACATGAGCCAGTACCCAGATAGGCTGGGAGACCTTCCAGCCATGAGCTTCCC 70
 Qy 72 TGGGGAGATCTCTCTGAGCATTAATGACATCATTAATTTGCTGAGCAATG 131
 Db 71 TGGGGAGATCTCTCTGAGCATTAATGACATCATTAATTTGCTGAGCAATG 130
 Qy 132 CATCATCATTTGGCTTTGGTATTTTCAAGGAGACATCTCATACATGATCTGTGGCT 191
 Db 131 CATCATCATTTGGCTTTGGTATTTTCAAGGAGACATCTCATACATGATCTGTGGCT 190
 Qy 192 CAGCTGGGAACTTTGGGAGATGATCTGAGCTGCACTTTTGAACCTGACATCAAA 251
 Db 191 CAGCTGGGAACTTTGGGAGATGATCTGAGCTGCACTTTTGAACCTGACATCAAA 250
 Qy 252 TTTCTGATATGCTGATACAAATGGCTGAAGAAAGTGTATTAAGCTTGTTCATGACTCA 311
 Db 251 TTTCTGATATGCTGATACAAATGGCTGAAGAAAGTGTATTAAGCTTGTTCATGACTCA 310

312 AAGAAAGCAAGATGAGCTGTGGAGCAGGATGAATGTTCAAGAGCGGAGCAGAGTGT 371
311 AAGAAAGCAAGATGAGCTGTGGAGCAGGATGAATGTTCAAGAGCGGAGCAGAGTGT 370
372 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGAGCTGAAAAAGTCAACTCAG 431
371 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGAGCTGAAAAAGTCAACTCAG 430
432 ATGCTGGCACTTCAAAATGTTATATCATCTTAAAGCAAGGGGAATGCTAACCTTG 491
431 ATGCTGGCACTTCAAAATGTTATATCATCTTAAAGCAAGGGGAATGCTAACCTTG 490
492 AGATTAATACTGGAGCTTCAGATGCGGAAAGTGAATGAGCTAATATGCACTCAG 551
491 AGATTAATACTGGAGCTTCAGATGCGGAAAGTGAATGAGCTAATATGCACTCAG 550
552 AGACCTTGGAGTGTGAGGCTCCCGATGGTTCCCGAGCCCAAGTGTCTGGGCAATCC 611
551 AGACCTTGGAGTGTGAGGCTCCCGATGGTTCCCGAGCCCAAGTGTCTGGGCAATCC 610
612 AAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTTCAATACAGCTTTGAGCTGAATCTG 671
611 AAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTTCAATACAGCTTTGAGCTGAATCTG 670
672 AGAATGTGACATGAAGTGTGTCTGTGCTCTAACAATGTTACGATCAACAACATATCT 731
671 AGAATGTGACATGAAGTGTGTGTCTGTGCTCTAACAATGTTACGATCAACAACATATCT 730
732 CCTGTATGATTTGAAAAATGACATTTGCCAAAGCAAGGGGATATCAAAAGTGAAGAAATCG 791
731 CCTGTATGATTTGAAAAATGACATTTGCCAAAGCAAGGGGATATCAAAAGTGAAGAAATCG 790
792 AGATCAAAAGGCGGAGTCACTTACAGCTGTAAATCTCAAAAGGTTTCTGTGTGTCTT 851
791 AGATCAAAAGGCGGAGTCACTTACAGCTGTAAATCTCAAAAGGTTTCTGTGTGTCTT 850
852 CTTTCTTTGGCAATCAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGTAAATAT 911
851 CTTTCTTTGGCAATCAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGTAAATAT 910
912 GTGCTTTGGCCAC-AAAAAGCATGCAAGTCAATTTTCAACAGGGAATCTACAGAACTA 970
911 GTGCTTTGGCCACAAAAAGCATGCAAGTCAATTTTCAACAGGGAATCTACAGAACTA 970
971 TTTTCAACCAAGATATGAGCTTATTTTCTGTGAGGAAATGAATTCATATCTTAA 1030
971 TTTTCAACCAAGATATGAGCTTATTTTCTGTGAGGAAATGAATTCATATCTTAA 1030
971 TTTTCAACCAAGATATGAGCTTATTTTCTGTGAGGAAATGAATTCATATCTTAA 1030
1031 AGTCTGAGTGAACAAGCAAGCAAGAAACAAAGAAAGCCAAAGCAAGAGGCTCCAA 1090
1031 AGTCTGAGTGAACAAGCAAGCAAGAAACAAAGAAAGCCAAAGCAAGAGGCTCCAA 1090
1091 TATGAACAAGATTAATCTATCTTCAAGACATATTAAGATTGGAAAAATTAATTCATGTG 1150
1091 TATGAACAAGATTAATCTATCTTCAAGACATATTAAGATTGGAAAAATTAATTCATGTG 1150
1151 AACTAACAAGTGTGTTAAGATGATTAAGTAAATGACGTGAGCAAGTGTGATCCCA 1210
1151 AACTAACAAGTGTGTTAAGATGATTAAGTAAATGACGTGAGCAAGTGTGATCCCA 1210
1151 AACTAACAAGTGTGTTAAGATGATTAAGTAAATGACGTGAGCAAGTGTGATCCCA 1209
1211 GATCTGAGGAGCTCCCGCTGCTGCACTGGGAGTGAAGAGCAAGATATGATGTAT 1270
1210 GATCTGAGGAGCTCCCGCTGCTGCTGCACTGGGAGTGAAGAGCAAGATATGATGTAT 1269
1271 TCTTTGTCTGTAATTTTATATATATGCTGTAAATGTTGCTCTGAGGAAGCCCTGGA 1330
1270 TCTTTGTCTGTAATTTTATATATATGCTGTAAATGTTGCTCTGAGGAAGCCCTGGA 1329
1331 AAGTCTATCCCAATATCACAATCTTATATTTTCAAAATTAAGCTGTATATGATCCCT 1390
1330 AAGTCTATCCCAATATCACAATCTTATATTTTCAAAATTAAGCTGTATATGATCCCT 1389

1391 AAGACGTGCTAATTTGACTGCACTTCCGAATCTCAGGGGCGGCTGCAATTTATGATGGG 1450
1390 AAGACGTGCTAATTTGACTGCACTTCCGAATCTCAGGGGCGGCTGCAATTTATGATGGG 1449
1451 TCAATGATTCACCTTTTATGATGCTTCCAAAGGTCCTTGGCTTCTTCCCACTGAC 1510
1450 TCAATGATTCACCTTTTATGATGCTTCCAAAGGTCCTTGGCTTCTTCCCACTGAC 1509
1511 AAATGCCAAAGTGAAGAAAAATGATCATATTTTATGATTAACAGAGAGTGGGAGAC 1570
1510 AAATGCCAAAGTGAAGAAAAATGATCATATTTTATGATTAACAGAGAGTGGGAGAC 1569
1571 CGATTTTATTAATAACTGAGCACTTCTTTTAAACAAACAATGCGGTTTATTTCTC 1630
1570 CGATTTTATTAATAACTGAGCACTTCTTTTAAACAAACAATGCGGTTTATTTCTC 1629
1631 AGATGATGTTACTCGGTGAATGCTCAGGAAAGGACCTTTACCTTGACTATATGGCAAT 1690
1630 AGATGATGTTACTCGGTGAATGCTCAGGAAAGGACCTTTACCTTGACTATATGGCAAT 1689
1691 ATGTGATCAACAAGCTCTGAGGCTTCTCTTTCATCTGCGTGAACAAGTGAACCTGAG 1750
1690 ATGTGATCAACAAGCTCTGAGGCTTCTCTTTCATCTGCGTGAACAAGTGAACCTGAG 1749
1751 TTTTCAATAGCATCTAGAGCAAGTGGGACTCAGCTGGGATGATTTGCCCCCATCTCGG 1810
1750 TTTTCAATAGCATCTAGAGCAAGTGGGACTCAGCTGGGATGATTTGCCCCCATCTCGG 1809
1811 GGGAAATGCTGGAAGCAATTTTGTACTCTCAATGAGGAGTGGAGGAGATGAGTCT 1870
1810 GGGAAATGCTGGAAGCAATTTTGTACTCTCAATGAGGAGTGGAGGAGATGAGTCT 1869
1871 ACTTCAACTAGTGAATTAAGGCGCAGGAGTGTGCTCAACCTCTTACATGTAACAGAG 1930
1870 ACTTCAACTAGTGAATTAAGGCGCAGGAGTGTGCTCAACCTCTTACATGTAACAGAG 1929
1931 TCTCCCATTTACACTACCCCAATCCGAAGTGTCAACTGTGTGACAGACTAAGAAACCTCG 1990
1930 TCTCCCATTTACACTACCCCAATCCGAAGTGTCAACTGTGTGACAGACTAAGAAACCTCG 1989
1991 TTTTGAATGAAGAAAGGCGCTGGAAGAGGGGAGCAACAATCTGTGCTT-CTCACAT 2049
1990 TTTTGAATGAAGAAAGGCGCTGGAAGAGGGGAGCAACAATCTGTGCTTCTTCAAT 2049
2050 TAGTCAATTTGGCAATTAAGCAATCTGTCTTTTGGTGTGCTGCTGACACAGAGACCA 2109
2050 TAGTCAATTTGGCAATTAAGCAATCTGTCTTTTGGTGTGCTGCTGACACAGAGACCA 2109
2110 ACTTATCGGAGCAACAAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTATGGGA 2169
2110 ACTTATCGGAGCAACAAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTATGGGA 2169
2170 ATGCTGATGAGGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTCCCTCATTTTAC 2229
2170 ATGCTGATGAGGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTCCCTCATTTTAC 2229
2230 CCTGCAAGCAAGTCTGTGAAGAAATGCTGATTTCACTGACGATTTTCTTACTG 2289
2230 CCTGCAAGCAAGTCTGTGAAGAAATGCTGATTTCACTGACGATTTTCTTACTG 2289
2290 AATTTAGATCTTCAGACCTTCTCTGAGCAATTCATTAAGGCAACAACATATTAATCT 2349
2290 AATTTAGATCTTCAGACCTTCTCTGAGCAATTCATTAAGGCAACAACATATTAATCT 2349
2350 TCCATGAAGCAACAACAGCTTTTGAAGCAAGCAATGATGCTTGAATGAGGCTT 2409
2350 TCCATGAAGCAACAACAGCTTTTGAAGCAAGCAATGATGCTTGAATGAGGCTT 2409
2410 GAGGATGAAGCTTTGAAGAAAGAAATTAATTTGTTTCCAGGCCCCCTTCCACATCTTC 2469
2410 GAGGATGAAGCTTTGAAGAAAGAAATTAATTTGTTTCCAGGCCCCCTTCCACATCTTC 2469
2470 ATGTGTTAACCACTGCTTCTGACCTTGAAGCAAGGAGTGAATTAATTAATGTTGTTA 2529

|||||
Db 2470 ATGTGTTAACCACTGCTTCTCGAGCTTGAGCAACGGTACGTATTTACATGTTGTTA 2529
QY 2530 TAGAAAACGTATTTAGAGTTTCGATGCTTCAAGAGAAATGATTATATCATTTCTT 2587
Db 2530 TAGAAAACGTATTTAGAGTTTCGATGCTTCAAGAGAAATGATTATATCATTTCTT 2587
RESULT 9
HSM808167
LOCUS HSM808167 2671 bp mRNA linear PRI 30-AUG-2003
DEFINITION Homo sapiens mRNA; cDNA DKFp7981717 (from clone DKFp7981717).
ACCESSION BX648021
VERSION BX648021.1 GI:34367180
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2671)
AUTHORS Pouscka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenteucher, R.,
Mewes, H.W., Weil, B., Amid, C., Obanger, A., Fodor, G., Han, M. and
Wiemann, S.
CONSTRM The German Human cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFp7981717) is available at the RZPD in Berlin.
Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
FEATURES
source Location/Qualifiers
1..2671
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFp7981717"
/issue_type="silver"
/clone_lib="779 (synonym: hnccl). Vector pSport1_Sfi; host
DH10b; sites SfiIA + SfiIB"
/dev_stage="fetal"
2599..2604
polyA_signal
polyA_site 2616
ORIGIN
Query Match 95.6%; Score 2472.4; DB 9; Length 2671;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2499; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
QY 63 TGGCTTCCCGGGGCGATCTCTCTCGAGCATTAATTAGCATCATCATTTCTGCTG 122
Db 91 TGACTTCAAGATGAAGCGCGCTGACCTCGCGCATTAATGATCATCATTAATTCGCTG 150
QY 123 GAGCAATTGCACTCATCATTTGCTTGGTATTTCAAGGAGACATCCATCAGTCACTA 182
Db 151 GAGCAATTGCACTCATCATTTGCTTGGTATTTCAAGGAGACATCCATCAGTCACTA 210
QY 183 CTGTGCGCTCAGCTGGGAACATTTGGGAGAGATGGAATCTGAGCTGCATTTGAACTG 242
Db 211 CTGTGCGCTCAGCTGGGAACATTTGGGAGAGATGGAATCTGAGCTGCATTTGAACTG 270
QY 243 AATCAAACTTTCTGATTCGTGATCAATGCTGAAGGAAGGTTTATAGCTTGCTTC 302
Db 271 AATCAAACTTTCTGATTCGTGATCAATGCTGAAGGAAGGTTTATAGCTTGCTTC 330
QY 303 ATGAGTTCAAGGAAGCAAGATGAGCTGTGAGAGAGATGAATGTTTCAAGAGCGCGA 362
|||||

Db 331 ATGAGTTCAAGGAAGCAAGATGAGCTGTGAGAGAGATGAATGTTTCAAGAGCGCGA 390
QY 363 CAGCATGTTTGTGATCAAGTATAGTTGGCAATGCTCTTGGCGCTGAAAAGCTGC 422
Db 391 CAGCATGTTTGTGATCAAGTATAGTTGGCAATGCTCTTGGCGCTGAAAAGCTGC 450
QY 423 AACTCAGATGCTGCACTCACTCAATGTTATATCATCTTCAATGAAGCAAGGGAAATG 482
Db 451 AACTCAGATGCTGCACTCACTCAATGTTATATCATCTTCAATGAAGCAAGGGAAATG 510
QY 483 CTAACTTGATTAATAACTGAGCTTCAGCATGCGGAAGTGAATGTAATGTAATG 542
Db 511 CTAACTTGATTAATAACTGAGCTTCAGCATGCGGAAGTGAATGTAATGTAATG 570
QY 543 CCAAGCTCAGAGACCTTGGCGGTGAGAGCTCCCGAATGTTCCCGGACCCCAAGTGTCT 602
Db 571 CCAAGCTCAGAGACCTTGGCGGTGAGAGCTCCCGAATGTTCCCGGACCCCAAGTGTCT 630
QY 603 GGGCATCCCAAGTTGACAGAGGAGCAACTTCTCGAAGTCTCAATACAGCTTGAGC 662
Db 631 GGGCATCCCAAGTTGACAGAGGAGCAACTTCTCGAAGTCTCAATACAGCTTGAGC 690
QY 663 TGAACCTGAGAAATGATGACCATGAAGTTGTGTGTGCTCTAACAATGTTACGATCACA 722
Db 691 TGAACCTGAGAAATGATGACCATGAAGTTGTGTGTGCTCTAACAATGTTACGATCACA 750
QY 723 ACACATATCTCTGTATGATTTGAATAATGACATTTGCCAAGCAGGGGATTTCAAGTGA 782
Db 751 ACACATATCTCTGTATGATTTGAATAATGACATTTGCCAAGCAGGGGATTTCAAGTGA 810
QY 783 CAGAACTCGAGATCAAAAGCGGAGTCACTTCAGCTGTAACTCAAAAGGCTTCTGTG 842
Db 811 CAGAACTCGAGATCAAAAGCGGAGTCACTTCAGCTGTAACTCAAAAGGCTTCTGTG 870
QY 843 GTGTCTCTTCTTCTTGTGCAATCAGCTGGGCACTTCTGCTCAGCCCTTACCTGATGC 902
Db 871 GTGTCTCTTCTTCTTGTGCAATCAGCTGGGCACTTCTGCTCAGCCCTTACCTGATGC 930
QY 903 TAAATATATGTCCTTGGGCAAAAAAGCATGCAAGTCTTATTCACAGGATCTA 962
Db 931 TAAATATATGTCCTTGGGCAAAAAAGCATGCAAGTCTTATTCACAGGATCTA 990
QY 963 CAGAACTATTTACCAACAGATATGCTAGTTTATATTTCTGGGAGAAATGAATTC 1022
Db 991 CAGAACTATTTACCAACAGATATGCTAGTTTATATTTCTGGGAGAAATGAATTC 1050
QY 1023 TATCTAAGAGTCTGAGTGAAGCAACAGAGCAAGAAACAAAGCAAGCAAG 1082
Db 1051 TATCTAAGAGTCTGAGTGAAGCAACAGAGCAAGAAACAAAGCAAGCAAG 1110
QY 1083 GGTCTCAATATGAACAAGTAAATCTATCTTCAAAAGCATATTTAGAAAGTTGGAAATTA 1142
Db 1111 GGTCTCAATATGAACAAGTAAATCTATCTTCAAAAGCATATTTAGAAAGTTGGAAATTA 1170
QY 1143 TTCAATGTAAGTGAACAAGTGTATTAAGTGTAAATGACGCTGAGACAAGT 1202
Db 1171 TTCAATGTAAGTGAACAAGTGTATTAAGTGTAAATGACGCTGAGACAAGT 1230
QY 1203 CATCCCAAGATCTCAGGAGCTTCCCTGCTGCACTTGGGAGTGAAGGACAGAT 1262
Db 1231 CATCCCAAGATCTCAGGAGCTTCCCTGCTGCACTTGGGAGTGAAGGACAGAT 1290
QY 1263 GTGCATGTTCTTGTCTCTGAATTTTATATATGCTGTATATGTTGCTCTGAGGAAG 1322
Db 1291 GTGCATGTTCTTGTCTCTGAATTTTATATATGCTGTATATGTTGCTCTGAGGAAG 1350
QY 1323 CCCCTGGAAGTCTATCCCAATATCCACATCTTATATTTCCACAAATTAAGCTGTAGTA 1382
Db 1351 CCCCTGGAAGTCTATCCCAATATCCACATCTTATATTTCCACAAATTAAGCTGTAGTA 1410
QY 1383 TGTACCTTAAGAAGCTGCTTAATGATGCTGCACTTGCACCTGAGGGCGGCTGATTTTA 1442
Db 1411 TGTACCTTAAGAAGCTGCTTAATGATGCTGCACTTGCACCTGAGGGCGGCTGATTTTA 1470
|||||

```

QY 1443 GGAATGGGCAAAATGATTCATTTTATGATGCTTCCAAAGGAGCTGGCTCTCTCC 1502
DB 1471 GTAATGGGCAAAATGATTCATTTTATGATGCTTCCAAAGGAGCTGGCTCTCTCC 1530
QY 1503 CAATGACAAATGCAAAAGTTGAGAAAAATGATCAATTTTATGAGTAAACAGACAGTC 1562
DB 1531 CAATGACAAATGCAAAAGTTGAGAAAAATGATCAATTTTATGAGTAAACAGACAGTC 1590
QY 1563 GGGGACACCGATTTTATTAATAAATGAGACCTTCTTTTAAACAAACAAATGGGGGT 1622
DB 1591 GGGGACACCGATTTTATTAATAAATGAGACCTTCTTTTAAACAAACAAATGGGGGT 1650
QY 1623 TATTTCTGATGATGATGATCCGGAATGATCCAGGAGGAGGACCTTTCACCTTGATAT 1682
DB 1651 TATTTCTGATGATGATGATCCGGAATGATCCAGGAGGAGGACCTTTCACCTTGATAT 1710
QY 1683 ATGGCATTTATGTCATCAAGAGCTCTGAGGCTTCTCTTTCCATCTGCTGAGACAGCTAA 1742
DB 1711 ATGGCATTTATGTCATCAAGAGCTCTGAGGCTTCTCTTTCCATCTGCTGAGACAGCTAA 1770
QY 1743 GACCTCAGTTTTCATATAGCATCTAAGAGCTGAGGAGCTGAGGAGTTCGCCCCC 1802
DB 1771 GACCTCAGTTTTCATATAGCATCTAAGAGCTGAGGAGCTGAGGAGTTCGCCCCC 1830
QY 1803 ATCTCCGGGGGATGTCGTAAGACATTTTGTACCTCAATGAGGAGTGAAGAGAT 1862
DB 1831 ATCTCCGGGGGATGTCGTAAGACATTTTGTACCTCAATGAGGAGTGAAGAGAT 1890
QY 1863 ACAGTGTCTACTACCACTAGATGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1922
DB 1891 ACAGTGTCTACTACCACTAGATGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1950
QY 1923 ACAGAGCTCTCCCTCAATCACTACCACTCCGAGTCAAGTGTCAAGAGGAGGAGTAA 1982
DB 1951 ACAGAGCTCTCCCTCAATCACTACCACTCCGAGTCAAGTGTCAAGAGGAGGAGTAA 2010
QY 1983 AACCCGTGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2042
DB 2011 AACCCGTGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2070
QY 2043 -CTCATTAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2101
DB 2071 CTCATTAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2130
QY 2102 GAGCCGAACTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2161
DB 2131 GAGCCGAACTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2190
QY 2162 TATGGGAAATGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2221
DB 2191 TATGGGAAATGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2250
QY 2222 CATTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2281
DB 2251 CATTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2310
QY 2282 TTAATCTGAAATGATGATCTCCAGACCTTCCGAGGAGGAGGAGGAGGAGGAGGAGT 2341
DB 2311 TTAATCTGAAATGATGATCTCCAGACCTTCCGAGGAGGAGGAGGAGGAGGAGGAGT 2370
QY 2342 ATATACCTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2401
DB 2371 ATATACCTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2430
QY 2402 GAGGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2461
DB 2431 GAGGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2490
QY 2462 CACTCTTCAATGATTAACCACTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2521
DB 2491 CACTCTTCAATGATTAACCACTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 2550

```

```

QY 2522 TGTGTATATAGAAAACTGATTTTATGAGTCTGATGCTTCAAGAGGAGTAAATATACA 2581
DB 2551 TGTGTATATAGAAAACTGATTTTATGAGTCTGATGCTTCAAGAGGAGTAAATATACA 2610
QY 2582 TTTTCT 2587
DB 2611 TTTTCT 2616

RESULT 10
HS11025A1
LOCUS
DEFINITION
Human DNA sequence from clone RPS-1025A1 on chromosome
20p11.21-11.23 Contains part of a novel gene (similar to
acetyl-coenzyme A synthetase), part of a novel gene (similar to
paired-like homeobox protein), ESTs, STSs and CpG islands,
complete sequence.
ACCESSION
AL080312
VERSION
AL080312.14 GI:6630798
KEYWORDS
HTG; CPG Island.
SOURCE
Homo sapiens
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
Bates, K.
Direct Submission
Submitted (20-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Dec 22, 1999 this sequence version replaced gi:6541398.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
RPS-1025A1 is from the library RPL-5 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RPS-1025A1 it may be shorter because we only sequence overlapping
sections once, or longer because we arrange for a small overlap
between neighbouring submissions.
The true left end of clone RPL-738P15 is at 94565 in this sequence.
The right end of clone RPL-568C11 is at 104 in this sequence.
This sequence was generated from part of bacterial clone contigs of
human chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20.
FEATURES
source
1..94664
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
/map="p11.21-11.23"
/clone="RPS-1025A1"
/clone_id="RPL-5"
1..1008
repeat_region
/note="LIM4 repeat: matches 4043..5082 of consensus"

```

repeat_region	1009..1280 /note="AluSc repeat: matches 41..309 of consensus" repeat_region
misc_feature	1281..2012 /note="LIM4 repeat: matches 5082..5769 of consensus"
misc_feature	/note="match: GSS: Em:AQ309030" complement(1818..2452)
misc_feature	/note="match: GSS: Em:AQ424952" complement(1944..2452) 2010..2160 /note="LIMB4 repeat: matches 6001..6152 of consensus"
repeat_region	2177..2268 /note="MIR repeat: matches 152..234 of consensus"
repeat_region	2240..2275 /note="L2 repeat: matches 2688..2723 of consensus"
repeat_region	2742..2920 /note="L2 repeat: matches 2255..2460 of consensus"
gene	complement(join(3088..3287,20390..20510,23609..30431)) /gene="d1025A1.1" complement(join(<3088..3287,20390..20510,29609..30431)) /gene="d1025A1.1" Em:A024994 /note="match: ESTs: Em:AW007194 Em:AI762466 Em:AI356425 Em:AM024994 match: Proteins: Sw:Q01576 Sw:F36333 Sw:O13440 Tr:O12662 Sw:P16928" /codon_start=1 /evidence=not experimental /product="d1025A1.1 (similar to aceyl- coenzyme A synthetase)" /protein_id="CAB81884.1" /db_xref="GI:7288046" /db_xref="GOA:Q9NU28" /db_xref="GOL:Q9NU28" /db_xref="UniProt/Swiss-Prot:Q9NUB1" /translation="MAARTIGRGVRLGISRGSGAPRPGCVSAPRASGPSSG APYAAAAQGSYPALSAQAAREBAATWGLPARDTYMDPTPYTWDDBDSTRTKICW FLGGUNLSGEASGDPCRPLQLGPEGRISPPAAAVGQRSGPCPKSPSSIGTAPV LAASSGTSSSHRAPDPRAOLGPAPGTRSPLOTAPCWCSARLARIPDELRYEV HSAAGCPAGSKGLHPASPEGLSITRSYGVKTKRWMLSLRAVPQGQPDKCPINLP CLIDHOZPSFEVALIMERDEGTERTTVYVCALCEGRELLFTTCRLANLTKHGVAH RSDRAIVMPVSPLVAAMLACARGAHVTIYIPAGFSMSLAGIND" repeat_region
misc_feature	3554..4085 /note="MER41D repeat: matches 3..557 of consensus" complement(6437..6701) /gene="d1025A1.1" /note="match: STS: Em:AA759166" 6904..7199 /note="AluSg repeat: matches 1..291 of consensus" 7211..7523 /note="AluYa5 repeat: matches 1..310 of consensus" 7740..8032 /note="AluXk repeat: matches 1..295 of consensus" 9002..9311 /note="AluY repeat: matches 1..311 of consensus" 9313..9384 /note="36 copies 2 mer aa 65% conserved" 9315..9394 /note="20 copies 4 mer aaag 80% conserved" 9473..9584 /note="L2 repeat: matches 2624..2747 of consensus" 10665..10735 /note="MIR repeat: matches 117..189 of consensus" 11392..11630 /note="MIR repeat: matches 15..252 of consensus" 13308..13604 /note="AluY repeat: matches 3..299 of consensus" 14417..15158 /note="match: GSS: Em:AQ878476" 15274..15356 /note="MIR repeat: matches 64..142 of consensus" 15357..15494 /note="2 copies 69 mer 84% conserved" 16153..16256 /note="MIR repeat: matches 19..147 of consensus"

misc_feature	complement(16240. .16517) /gene="dJ1025A1.1" /note="match: STS: Em:G05103 match: STS: Em:G05103" 16675. .16971
repeat_region	/note="Aluub repeat: matches 1. .311 of consensus" 17508. .17612
repeat_region	/note="MIR repeat: matches 52. .153 of consensus" complement(18067. .18673) /gene="dJ1025A1.1"
misc_feature	/note="match: GSS: Em:A0348168" complement(18204. .18679) /gene="dJ1025A1.1"
misc_feature	/note="match: GSS: Em:A0283179" 18246. .18569
repeat_region	/note="Alusd repeat: matches 1. .307 of consensus" 19567. .19730
repeat_region	/note="L2 repeat: matches 2330. .2493 of consensus" 19772. .19815
repeat_region	/note="MLT11 repeat: matches 360. .403 of consensus" 20748. .20880
repeat_region	/note="MER5B repeat: matches 1. .178 of consensus" 21500. .21569
repeat_region	/note="J5 copies 2 mer aa 67% conserved" 22036. .22157
repeat_region	/note="MIR repeat: matches 26. .158 of consensus" 22724. .22777
repeat_region	/note="MER5A repeat: matches 47. .102 of consensus" 23801. .23946
repeat_region	/note="MER5A repeat: matches 10. .189 of consensus" 24489. .24360
repeat_region	/note="18 copies 4 mer agga 75% conserved" 24906. .24994
repeat_region	/note="12 repeat: matches 2595. .2682 of consensus" 25390. .25693
repeat_region	/note="Alusg repeat: matches 1. .301 of consensus" 26691. .26856
repeat_region	/note="MIR repeat: matches 87. .259 of consensus" 27077. .27186
repeat_region	/note="MER57-internal repeat: matches 7151. .7267 of consensus"
repeat_region	27513. .27624
repeat_region	/note="MLT1b repeat: matches 436. .547 of consensus" 27864. .28049
repeat_region	/note="MER5A repeat: matches 1. .189 of consensus" 29401. .30904
misc_feature	/note="CPG island" /evidence=not_experimental
repeat_region	31236. .31327
repeat_region	/note="MIR repeat: matches 79. .150 of consensus" 31812. .31987
repeat_region	/note="PRAM repeat: matches -1. .174 of consensus" 32054. .32138
repeat_region	/note="MIR repeat: matches 48. .134 of consensus" 32360. .32572
repeat_region	/note="MLT1f repeat: matches 125. .354 of consensus" 32664. .32743
repeat_region	/note="MLT1f repeat: matches 423. .547 of consensus" 32777. .33416
repeat_region	/note="12 repeat: matches 1497. .2249 of consensus" 33426. .33520
repeat_region	/note="MER5A repeat: matches 9. .109 of consensus" 33590. .33937
repeat_region	/note="12 repeat: matches 2283. .2657 of consensus" 34595. .34697

	Query Match	83.3%	Score 2154;	DB 9;	Length 94664;
	Best Local Similarity	92.9%;	Pred. No. 0;		
	Matches 2328;	Conservative	0;	Matches 160;	Indels 18; Gaps 6;
QY	86	TTCTGGAGCAATATTAGCATCATCATATTATCTTGCGTGGAGCAATTGCACCTCATCATTTGCG	145		
DB	71434	TTCTACAGCAATATTAGCATCATCATATTACTCTGTGGAGCAATTCATCTCATCATTTGCG	714939		

146 TTTGGATTTCAGGGAGACACTCAATCAAGTCACTACTGTGCGCTCAGCTGGAAACATT 205
| | | | |
Db 71494 TTTTGTATTTCAGGGAGACACTCAATCAAGTCACTACTGTGCGCTCAGCTGGAAACATT 71553
| | | | |
Qy 206 GGGGAGGATGGAATCTGAGCTGCATTTTGAACCTGACATCAAACTTTCTGATATCGTG 265
| | | | |
Db 71554 GGGGAGGATGGAATCTGAGCTGCATTTTGAACCTGACATCAAACTTTCTGATATCATG 71613
| | | | |
Qy 266 ATACAAATGCTGAAGGAAGGTGTTTAAAGCTTGTCATGAGTCAAAAGGCAAAAGT 325
| | | | |
Db 71614 ATACAAATGCTGAAGGAAGGTGTTAAGCTTGTCATGAGTCAAAAGGCAAAAGT 71673
| | | | |
Qy 326 GAGCTGCGAGAGAGATGAAAATGTTCAAGGCGGAGACAGAGTGTGCTGATCAAGTG 385
| | | | |
Db 71674 GAGCTGCGAGAGAGATGAAAATGTTCAAGGCGGAGACAGAGTGTGCTGATCAAGTG 71733
| | | | |
Qy 386 ATAGTTGGCAATGCTCTTTTGCGGCTGAAAACGTGCAACTCAAGATGCTGGCACTAC 445
| | | | |
Db 71734 ATAGTTGGCAATGCTCTCTGCGAGCTGAAAACATCACTCAAGATGCTGGCACTAC 71793
| | | | |
Qy 446 AAATGTTATATCATCACTTTAAAGGCAAGGGGAAGCTTAACCTTGAGTATAAACTGGA 505
| | | | |
Db 71794 AAATGTTATATCATCACTTTAAAGGCAAGGGGAAGCTTAACCTTGAGTATAAACTGGA 71853
| | | | |
Qy 506 GCCTTCAGCATGCGGGAAGTGAATGGAATAATGATCCAGCTCAGAGACCTTGCGGTTG 565
| | | | |
Db 71854 GCCTTCAGCATGCGGGAAGTGAATGGAATAATGATCCAGACCTTGCGGTTG 71913
| | | | |
Qy 566 GAGGCTCCCGAGTGTTCCTCCCAAGCCCAAGTGTCTGGGCAATCCCAAGTTGACAGGA 625
| | | | |
Db 71914 GAGGCTCCCGATGAGTGTCTCTAGGCCCAAGTGTCTGAAAGATCCCTAGTTGACAGGA 71973
| | | | |
Qy 626 GCCAATTCCTCGGAATGCTCCCAATACAGCTTTGAGCTGAATGAGATGAGCAGT 685
| | | | |
Db 71974 GCCAATTCCTCGGAATGCTCCCAATACAGCTTTGAGCTGAATGAGATGAGCAGT 72033
| | | | |
Qy 686 AAGGTGTGTGTGTCTCTCAATATGTAAGTCAACAACATCTCTGTATGATTTGA 745
| | | | |
Db 72034 AAGGTGTGTGTGTCTCTCAATATGTAAGTCAACAACATCTCTGTATGATTTGA 72093
| | | | |
Qy 746 AATGACATTTGCCAAGCAACAGGGGATTCAAAGTGAAGAATCGGAGATCAAAAGCGG 805
| | | | |
Db 72094 AATGACATTTGCCAAGCAACAGGGGATTCAAAGTGAAGAATCGGAGATCAAAAGCGG 72152
| | | | |
Qy 806 AGTCACTTCAAGTGTCTTAACTCAAGGCTTCTGTGTGTCTCTCTTTTGTGCAATC 865
| | | | |
Db 72153 AGTCACTTCAAGTGTCTTAACTCAAGGCTTCTGTGTGTCTCTCTTTTGTGCAATC 72212
| | | | |
Qy 866 AGCTGGGCACTTCTGTCTCTCAGCCCTTACCTGATCTAAAATATGTCCTTGCGACA 925
| | | | |
Db 72213 AGCTGGGCACTTCTGTCTCTCAGCCCTTACCTGATCTAAAATATGTCCTTGCGACA 72272
| | | | |
Qy 926 AAAAGCATGCAAAAGTCAATTTTGAACAAGGATCTTACAGAACTTATTCACACAGATA 985
| | | | |
Db 72273 AAAAGCATGCAAAAGTCAATTTTGAACAAGGATCTTACAGAACTTATTTGCCAGATA 72332
| | | | |
Qy 986 TGAACCTAGTTTATTTCTGCGAGGAAGTGAATTCATATCTAGAGTCTGAGGTGAGA 1045
| | | | |
Db 72333 TGAACCTAGTTTATTTCTGCGAGGAAGTGAATTCATATCTAGAGTCTGAGGTGAGA 72392
| | | | |
Qy 1046 AACCAAGACAAGAAACAAAAGAACCAAAAGCAGAAAGGCTCCATATGAAACAAGATAA 1105
| | | | |
Db 72393 AACCAAGACAAGAAACAAAAGAACCAAAAGCAGAAAGGCTCCATATGAAACAAGATAA 72452
| | | | |
Qy 1106 TCTATCTTCAAAAGACATATTTAGAGTTGGAAAAATATTCATGTGAATCAAGTGTG 1165
| | | | |
Db 72453 TCTATCTTCAAAAGACATATTTAGAGTTGGAAAAATATTCATGTGAATCAAGTGTG 72505
| | | | |
Qy 1166 TTAAAGTATAGTAAATATGACCTGAGAGACAAAGTGCATCCCAATCTCAGGGAATC 1225
| | | | |
Db 72506 --AAGGATATAGTAAATATGACGAGAGACAAAGTGCATCCCAATCTCAGGGAATC 72563
| | | | |

1226 CCCCTGCTGTCACTGGGAGGTGAGAGACAGATAGTCATGTTCTTTGTCTCTGAT 1285
| | | | |
Db 72564 CCCCTGCTGTCACTGGGAGGTGAGAGATAGTATGATGCGTGTCTTTGCTCTGAAA 72623
| | | | |
Qy 1286 TTTTATGTTATATGTCCTGTAATGTTGCTCTGAGGAAGCCCTGGAAAG--TCTATCCCA 1343
| | | | |
Db 72624 TTTTATGTTATATGTCCTGTAATGTTGCTCTGAGGAAGCCCAAGAAATCTCTATCCCA 72683
| | | | |
Qy 1344 CATATCCATCTTATATTTCCAAATTAAGCTGATGATGATACCTTAAGACGCTGTAA 1403
| | | | |
Db 72684 TATATACATCTTATATTTCCATGAAATTAAGTGTAGTATATCTTAAGATGCTGTAA 72743
| | | | |
Qy 1404 TTGACTGCACTTGGCAACTCAAGGGCGGCTGCATTTTATGATAGGTCAATGATTAAC 1463
| | | | |
Db 72744 TTGACTGCACTTGGCAACTCAAGGGCGGCTGCATTTTATGATAGGTCAATGATTAAC 72803
| | | | |
Qy 1464 TTTTATGATAGCTTCCAAAGGTCCTTGAGCTTCTCTTCCCAACTGACAAATGCCAAAGT 1523
| | | | |
Db 72804 TTTTATGATAGCTTCCAAAGGTCCTTGAGCTTCTCTTCCCAACTGACAAATGCCAAAGT 72863
| | | | |
Qy 1524 GAGAAAAATGATCATATTTTATGATTAACAGAGAGTCCGAGACCCGATTTTATAAT 1583
| | | | |
Db 72864 AAGAAAAATGATCATATTTTATGATTAACAGAGAGTCCGAGACCCGATTTTATAAGT 72923
| | | | |
Qy 1584 AAATGAGCACTTCTTTTAAACAAACAATGCGGTTTATTTCTCAATGATGTTCAAT 1643
| | | | |
Db 72924 AAATGAGCACTTCTTTTAAACAAACAATGCGGTTTATTTCTCAATGATGTTCAAT 72979
| | | | |
Qy 1644 CCGTAAATGTCACAGGAAGGACCTTTGACCTGATCTATATGAGCAATTAATGATCACAAG 1703
| | | | |
Db 72980 CCGTAAATGTCACAGGAAGGACCTTTGACCTGATCTATATGAGCAATTAATGATCACAAG 73039
| | | | |
Qy 1704 CTCTGAGCTTCTCTTTTCAATCTGCGTGAACAGCTTAAGACCTTCAATTTCAATAGCAT 1763
| | | | |
Db 73040 CTCTGAGCTTCTCTTTTCAATCTGCGTGAACAGCTTAAGACCTTCAATTTCAATAGCAT 73099
| | | | |
Qy 1764 CTAGAGCAGTGGGACTCAGCTGGGGTGAATTT--CGCCCCCATCTCGGGGGAATGTCTGA 1822
| | | | |
Db 73100 CTAGAGCAGTGGGACTCAGCTGGGGGGAATTTTTCGCCCCCATCTCGGGGGAATGTCTGA 73159
| | | | |
Qy 1822 AGACAAATTTGGTTACCTCAATAGAGGAGTGGAGGAGATACAGTCACTTACCAACTAG 1882
| | | | |
Db 73160 AGACAAATTTGGTTACCTCAATAGAGGAGTGGAGGAGATACAGTCACTTACCAACTAG 73219
| | | | |
Qy 1883 TGGATTAAGGCGCAGGGAATGCTGCTCAACCTCTCAATGATCAGAGACGTCTCCCAATAC 1942
| | | | |
Db 73220 TGGATTAAGGCGCAGGGAATGCTGCTCAACCTCTCAATGATCAGAGACGTCTCCCAATAC 73279
| | | | |
Qy 1943 AACTAACCAATCGAAGTGTCAACTGTGTCAAGGACTTAAGAAAACCTTGTTTTGAATGAA 2002
| | | | |
Db 73280 AACTAACCAATCGAAGTGTCAACTGTGTCAAGGACTTAAGAAAACCTTGTTTTGAATGAA 73339
| | | | |
Qy 2003 AAGGCGCTGGAAGAGGGGAGGCAACAATCTGTGCTGCT--CTGACATTTAGCATTTGGA 2061
| | | | |
Db 73340 AAGGCGCTGGAAGAGGGGAGGCAACAATCTGTGCTGCTGCTCTCAATTTAGCATTTGGA 73399
| | | | |
Qy 2062 AATAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATCGGCT 2121
| | | | |
Db 73400 AATAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATCGGCT 73459
| | | | |
Qy 2122 ACCAGATTAATCTCTCTCAGTGAACAAGTGTGAACAAGGCTTATGGAATATGCTATGGG 2181
| | | | |
Db 73460 ACCAGATTAATCTCTCAGTGAACAAGTGTGAACAAGGCTTATGGAATATGCTATGGG 73519
| | | | |
Qy 2182 ATTTATCTTCAAGTTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTACCTCGCAAGCCAA 2241
| | | | |
Db 73520 ATTTATCTTCAAGTTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTACCTCGCAAGCCAA 73579
| | | | |
Qy 2242 GTTCTGTAAAGAAATGCGTGAATCTAGCTCAGGTTTTTTCTTCACTGTAATTTAGATCTC 2301
| | | | |
Db 73580 GTTCTGTAAAGAGCTGCTGAGTTCTTACCTCAATGTTTTCTTCACTGTAATTTAGATCTC 73639
| | | | |
Qy 2302 CAGACCTTCTGTGCAACAATTTCAATTAAGCAACAAACATTAATCTTCCATGAAGCAC 2361
| | | | |

Db 73640 CAGACCTGCTGCGCCAGATTGAAATTAGCGCAACAAATATACCTTCCATGAAAGCAC 73699
Qy 2362 ACACAGACTTTTGAAGCAAGACATGACTGCTGTAATTGAGCCCTTGAAGAAATGAGC 2421
Db 73700 ACAGAGACTTTTGAAGCAAGACATGACTGCTGTAATTGAGCCCTTGAAGAAATGAGC 73759
Qy 2422 TTGGAAGAAATAATCTTTGTTTCCAGGCCCTTCCCACTCTTCACTGTTAAACA 2481
Db 73760 TTGGAAGAAATAATCTTTGTTTCCAGGCCCTTCCCACTCTTCACTGTTAAACA 73819
Qy 2482 CTGCTCTTCTGACACTTGGAGCAACGCTGACTGATTAACATGTTGTTAGAAACTGAT 2541
Db 73820 CTGCTCTTCTGACACTTGGAGCAACGCTGACTGATTAACATGTTGTTAGAAACTGAT 73879
Qy 2542 TTTAGACTTCTGATCGTTCAAGAGATGATTAAATATACATTTCTT 2587
Db 73880 TTTAGACTTCTGATCGTTCAAGAGATGATTAAATATATATTTCTT 73925

RESULT 11
CQ412191 1965 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 19262 from Patent WO0170979.
DEFINITION CQ412191
ACCESSION CQ412191
VERSION CQ412191.1 GI:41319972
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Lee,J. and Lillie,J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 19262 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source location/Qualifiers
1..1965
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 74.3%; Score 1921.4; DB 6; Length 1965;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1933; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 12 GGCAGCTCCACTAGCAGCAGTACCAGATGAGTACGCTGGGAACTTCCCGCAGCATGGCTTCCC 71
Db 30 GGCAGCTCCACTAGCAGCAGTACCAGATGAGTACGCTGGGAACTTCCCGCAGCATGGCTTCCC 89
Qy 72 TGGGGGAGATCTTCTGAGCATTAATTAGCATCATTAATTCTGGCTGGAGCAATTG 131
Db 90 TGGGGGAGATCTTCTGAGCATTAATTAGCATCATTAATTCTGGCTGGAGCAATTG 149
Qy 132 CACTCATATTGGCTTTGTAATTTCAAGGAGACATCTCATCAAGTACTACTGTGCGCT 191
Db 150 CACTCATATTGGCTTTGTAATTTCAAGGAGACATCTCATCAAGTACTACTGTGCGCT 209
Qy 192 CAGCTGGGAACATTGGGGAGATGGAATCTGAGCTGACATTTTGAACCTGACATCAAC 251
Db 210 CAGCTGGGAACATTGGGGAGATGGAATCTGAGCTGACATTTTGAACCTGACATCAAC 269
Qy 252 TTTCTGATATCGTATACAAATGCTGAAGAGAGTGTGTTAGGCTTGGTCCATGAGTTCA 311
Db 270 TTTCTGATATCGTATACAAATGCTGAAGAGAGTGTGTTAGGCTTGGTCCATGAGTTCA 329
Qy 312 AAGAAAGCAAAAGATGAGCTGTCCGAGAGAGATGAAATGTTCAAGAGCCGAGACAGATGT 371
Db 330 AAGAAAGCAAAAGATGAGCTGTCCGAGAGAGATGAAATGTTCAAGAGCCGAGACAGATGT 389
Qy 372 TTGCTATCAAGATGATGTTGGCAATGCTCTTTGGCGGTGAAAAAAGTGCACATCTCAG 431

Db 390 TTGCTATCAAGATGATGTTGGCAATGCTCTTTGGCGGTGAAAAAAGTGCACATCTCAG 449
Qy 432 ATGCTGAGCACTTCAAAATGTTATATATCACTTCTTAAAGCAAGGGAATGTAACCTTG 491
Db 450 ATGCTGAGCACTTCAAAATGTTATATATCACTTCTTAAAGCAAGGGAATGTAACCTTG 509
Qy 492 AGTATAAACTGAGGCTTCAAGATGCCGAATGGAATGGAATGGAATGGAATGGAATGGAAT 551
Db 510 AGTATAAACTGAGGCTTCAAGATGCCGAATGGAATGGAATGGAATGGAATGGAATGGAAT 569
Qy 552 AGACCTTGGGCTGAGAGGCTCCCGAGTGGTTCCCGCAGCCACAGTGTCTGGGCAATCCC 611
Db 570 AGACCTTGGGCTGAGAGGCTCCCGAGTGGTTCCCGCAGCCACAGTGTCTGGGCAATCCC 629
Qy 612 AAGTTGACAGGAGCAACTTCTGGAAGTCTCAATACAGCTTTGAGCTGAACCTTG 671
Db 630 AAGTTGACAGGAGCAACTTCTGGAAGTCTCAATACAGCTTTGAGCTGAACCTTG 689
Qy 672 AGAATGTGACATGAAGGCTTGTGCTGTCTGATGATGATGATGATGATGATGATGATGAT 731
Db 690 AGAATGTGACATGAAGGCTTGTGCTGTCTGATGATGATGATGATGATGATGATGATGAT 749
Qy 732 CTTGATGATTTGAATGACATTTGCCAAAGCAAGGGGATATCAAAAGTGCAGAAATCGG 791
Db 750 CTTGATGATTTGAATGACATTTGCCAAAGCAAGGGGATATCAAAAGTGCAGAAATCGG 809
Qy 792 AGATCAAAAGGCGAGTCACTACAGCTGCTAAATCTCAAAAGCTTCTGTGTCTCTT 851
Db 810 AGATCAAAAGGCGAGTCACTACAGCTGCTAAATCTCAAAAGCTTCTGTGTCTCTT 869
Qy 852 CTTTCTTGTGACATGACCTGGGCACTTCTGCTCTGAGCCCTTACCTGATGCTAAATTAAT 911
Db 870 CTTTCTTGTGACATGACCTGGGCACTTCTGCTCTGAGCCCTTACCTGATGCTAAATTAAT 929
Qy 912 GTGCTTGGGCAAAAGGATGACATGCAAGTCTTTTACCAACAGGATCTACAGAACTAT 971
Db 930 GTGCTTGGGCAAAAGGATGACATGCAAGTCTTTTACCAACAGGATCTACAGAACTAT 989
Qy 972 TTCAACAACAGATATGACCTAGTTTATATTTCTGGAGAGAAATGAATTCATATCTTGA 1031
Db 990 TTCAACAACAGATATGACCTAGTTTATATTTCTGGAGAGAAATGAATTCATATCTTGA 1049
Qy 1032 GTCTGAGTGAAGCAAAAGGATGACAAAGCAAAAGGATGACAAAGGATGACAAAGGATGAC 1091
Db 1050 GTCTGAGTGAAGCAAAAGGATGACAAAGCAAAAGGATGACAAAGGATGACAAAGGATGAC 1109
Qy 1092 ATGAACAAGATTAATCTATCTTCAAGACATATTAGAAGTGGGAAATTAATCATGTGA 1151
Db 1110 ATGAACAAGATTAATCTATCTTCAAGACATATTAGAAGTGGGAAATTAATCATGTGA 1169
Qy 1152 ACTAGAACAAGTGTGTTAAGAGTATAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1211
Db 1170 ACTAGAACAAGTGTGTTAAGAGTATAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1229
Qy 1212 ATCTCAGGAGCTTCCCGCTGCTGCACTGGGGAGTGAAGAGACAGATAGTCAATGTT 1271
Db 1230 ATCTCAGGAGCTTCCCGCTGCTGCACTGGGGAGTGAAGAGACAGATAGTCAATGTT 1289
Qy 1272 CTTTGTCTGAAATTTTATGTTATATGCTGTAATGTTGCTCTGAGAAAGCCCTGAA 1331
Db 1290 CTTTGTCTGAAATTTTATGTTATATGCTGTAATGTTGCTCTGAGAAAGCCCTGAA 1349
Qy 1332 AGTCTATCCCAATATCCACATCTTATATTTCCAAATTAAGCTGTAGATATACCTTA 1391
Db 1350 AGTCTATCCCAATATCCACATCTTATATTTCCAAATTAAGCTGTAGATATACCTTA 1409
Qy 1392 AGAGCTGCTAATTTGATGCTGCACTTGCAGAACTCAGGGGGGCTGCAATTTAGTAAGGGT 1451
Db 1410 AGAGCTGCTAATTTGATGCTGCACTTGCAGAACTCAGGGGGGCTGCAATTTAGTAAGGGT 1469
Qy 1452 CAATGATTCATTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCAACTGACA 1511

Db 1470 CAATGATTCACCTTTTATGATGCTTCCAAAGGCTGCTTGGCTCTCTTCCCACTGACA 1529
QY 1512 AATGCCAAGTGGAGAAAATATCATATTTAGATATAAGAGAGCTGGGACACC 1571
Db 1530 AATGCCAAGTGGAGAAAATATCATATTTAGATATAAGAGAGCTGGGACACC 1589
QY 1572 GATTTTATTAATAAATGAGACCTCTTTTAAACAAACAATGGGATTATTTCTCA 1631
Db 1590 GATTTTATTAATAAATGAGACCTCTTTTAAACAAACAATGGGATTATTTCTCA 1649
QY 1632 GATGATGTTTCATCCGTAATGGTCCAGGAGAGACCTTTCACCTGACTATATGCGATTA 1691
Db 1650 GATGATGTTTCATCCGTAATGGTCCAGGAGAGACCTTTCACCTGACTATATGCGATTA 1709
QY 1692 TGTTCATCAACAGCTCGAGGCTTCTCTTCATCTCTGCTGAGACAGCTAAGACCTCAGT 1751
Db 1710 TGTTCATCAACAGCTCGAGGCTTCTCTTCATCTCTGCTGAGACAGCTAAGACCTCAGT 1769
QY 1752 TTTTCATAGCATCTAGAGAGAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGG 1811
Db 1770 TTTTCATAGCATCTAGAGAGAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGG 1829
QY 1812 GGAATGCTGGAAGACAAATTTGGTTACTCAATGAGGAGATGAGAGATACAGTCTTA 1871
Db 1830 GGAATGCTGGAAGACAAATTTGGTTACTCAATGAGGAGATGAGAGATACAGTCTTA 1889
QY 1872 CTACCAACTAGTGGATTAAGGCGAGGAGATGCTGCTCCTCACTCATGTA-CAGGAGC 1930
Db 1890 CTACCAACTAGTGGATTAAGGCGAGGAGATGCTGCTCCTCACTCATGTA-CAGGAGC 1949
QY 1931 TCTCCCATTAACAC 1945
Db 1950 TCTCCCATTAACAC 1964

RESULT 12
AL391476/c 171595 bp DNA linear PRI 03-AUG-2001
LOCUS Human DNA sequence from clone RP11-229A19 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL391476
VERSION AL391476.20 GI:15131484
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171595)
AUTHORS Wallis, J.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
Requesters: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:14970375.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Bm: EMBL; SW:
SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human

FEATURES

Source

Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
RP11-229A19 is from the library RP11-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6
This sequence is the entire insert of clone RP11-229A19 The true
left end of clone RP11-287H7 is at 67254 in this sequence. The true
right end of clone RP4-570D9 is at 57439 in this sequence.

Location/Qualifiers

1..171595
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-229A19"
/clone_11b="RP11-11.1"
324..685
/note="L1MB3 repeat: matches 5769..6141 of consensus"
745..1182
/note="L1MD2 repeat: matches 5890..6341 of consensus"
1261..1466
/note="AluX repeat: matches 1..183 of consensus"
1471..1567
/note="L1 repeat: matches 5042..5132 of consensus"
1568..1880
/note="AluX repeat: matches 1..312 of consensus"
1881..2391
/note="L1 repeat: matches 4471..5042 of consensus"
2392..2668
/note="AluY repeat: matches 1..291 of consensus"
2669..2813
/note="L1 repeat: matches 4336..4471 of consensus"
3066..3198
/note="FLAM_C repeat: matches 1..133 of consensus"
3264..3367
/note="MIR repeat: matches 32..134 of consensus"
3758..4064
/note="AluX repeat: matches 1..305 of consensus"
4312..4610
/note="AluX repeat: matches 1..306 of consensus"
5330..5607
/note="L1PA5 repeat: matches 5866..6143 of consensus"
6639..6803
/note="MIR repeat: matches 27..189 of consensus"
7176..7218
/note="L2 repeat: matches 2654..2698 of consensus"
7287..7593
/note="MER7A repeat: matches 1..346 of consensus"
8914..8963
/note="MADE1 repeat: matches 31..80 of consensus"
9335..9484
/note="L1MCS repeat: matches 7699..7849 of consensus"
9485..9784
/note="AluSc repeat: matches 1..300 of consensus"
9785..9811
/note="L1MCS repeat: matches 7673..7699 of consensus"
9812..9975
/note="FAM repeat: matches 1..170 of consensus"
9976..10469
/note="L1MCS repeat: matches 7185..7673 of consensus"
11613..11858
/note="L1PA16 repeat: matches 5857..6157 of consensus"
13950..14280
/note="MER44A repeat: matches 1..333 of consensus"
14390..14493
/note="L2 repeat: matches 2601..2705 of consensus"
16020..16325
/note="AluX repeat: matches 1..308 of consensus"
16726..16892
/note="MIR repeat: matches 79..261 of consensus"
17071..17373


```
/note="AluSq repeat: matches 1. .301 of consensus"
repeat_region 17708. .18140
/note="MER68A repeat: matches 1. .435 of consensus"
repeat_region 19282. .19574
/note="Aluub repeat: matches 1. .294 of consensus"
repeat_region 19774. .19904
/note="FLAM A repeat: matches 1. .133 of consensus"
repeat_region 20023. .20325
/note="AluY repeat: matches 1. .303 of consensus"
repeat_region 20904. .21029
/note="Aluub repeat: matches 10. .136 of consensus"
repeat_region 22334. .22596
/note="AluSX repeat: matches 1. .264 of consensus"
repeat_region 23089. .23144
/note="2 copies 28 mer 98% conserved"
repeat_region 23310. .23345
/note="9 copies 4 mer tgtg 94% conserved"
repeat_region 24358. .24654
/note="AluSX repeat: matches 1. .297 of consensus"
repeat_region 25318. .25615
/note="AluY repeat: matches 1. .297 of consensus"
repeat_region 26469. .26775
/note="Aluuo repeat: matches 1. .304 of consensus"
repeat_region 31909. .32321
/note="L2 repeat: matches 2035. .2515 of consensus"
repeat_region 33438. .33739
/note="AluSq repeat: matches 1. .302 of consensus"
repeat_region 35428. .35499
/note="MIR repeat: matches 78. .145 of consensus"
repeat_region 35687. .35843
/note="MER58C repeat: matches 9. .45 of consensus"
repeat_region 36245. .36311
/note="L1MD3 repeat: matches 7674. .7739 of consensus"
repeat_region 36338. .36699
/note="L1MC4 repeat: matches 7358. .7643 of consensus"
repeat_region 36702. .36938
/note="L2 repeat: matches 1141. .1372 of consensus"
repeat_region 37430. .37621
/note="L2 repeat: matches 2088. .2281 of consensus"
repeat_region 37655. .38005
/note="L2 repeat: matches 2335. .2710 of consensus"
repeat_region 38922. .39220
/note="Aluuo repeat: matches 1. .299 of consensus"
repeat_region 39802. .39885
/note="3 copies 28 mer 96% conserved"
repeat_region 39931. .40073
/note="MLT1I repeat: matches 11. .157 of consensus"
repeat_region 40191. .40247
/note="Char1e4 repeat: matches 1906. .1961 of consensus"
repeat_region 40286. .40363
/note="MLT1I repeat: matches 288. .372 of consensus"
repeat_region 40657. .40734
/note="MIR repeat: matches 28. .99 of consensus"
repeat_region 40735. .41048
/note="AluSX repeat: matches 1. .309 of consensus"
repeat_region 41049. .41092
/note="MIR repeat: matches 99. .144 of consensus"
repeat_region 41248. .41351
/note="MIR repeat: matches 57. .167 of consensus"
repeat_region 42498. .42761
/note="AluSq repeat: matches 1. .265 of consensus"
repeat_region 43527. .43770
/note="L2 repeat: matches 2465. .2742 of consensus"
repeat_region 44795. .44944
/note="L2 repeat: matches 2620. .2749 of consensus"
repeat_region 44945. .45231
/note="Aluub repeat: matches 21. .307 of consensus"
repeat_region 45232. .45629
/note="L2 repeat: matches 2129. .2620 of consensus"
repeat_region 45828. .45864
/note="L2 repeat: matches 1162. .1409 of consensus"
repeat_region 45880. .46206
/note="MLT1B repeat: matches 43. .390 of consensus"
```

```
misc_feature 45990. .46265
/note="Sequence from overlapping clone RP4-570D9
(AL139248). Assembly confirmed by restriction digest."
repeat_region 46271. .47156
/note="L2 repeat: matches 3. .1061 of consensus"
repeat_region 47227. .47442
/note="MER20 repeat: matches 2. .218 of consensus"
repeat_region 47449. .47755
/note="AluSq repeat: matches 1. .304 of consensus"
repeat_region 48722. .49035
/note="AluSX repeat: matches 1. .307 of consensus"
repeat_region 51378. .51522
/note="PRAM repeat: matches 4. .162 of consensus"
repeat_region 53299. .53600
/note="Aluuo repeat: matches 1. .296 of consensus"
repeat_region 55969. .56042
/note="MIR repeat: matches 106. .187 of consensus"
repeat_region 56386. .56695

Query Match 62.5%; Score 1617.6; DB 9; Length 171595;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1631; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 953 CAGGATCTACAGAACTATTTCACACAGATATGACCTGTTTATTTCTGGAGGA 1012
DB 82290 CAGGATCTACAGAACTATTTCACACAGATATGACCTGTTTATTTCTGGAGGA 82231
QY 1013 AATGAATTCATATCTAGAAAGTCTGAGTGAAGCAACAGAGCAAGAAAGCAAGCC 1072
DB 82230 AATGAATTCATATCTAGAAAGTCTGAGTGAAGCAACAGAGCAAGAAAGCAAGCC 82171
QY 1073 AAAAGCAAGAGCTCCAAATATGAAAGATATATCTATCTTCAAGACATATTAAGAGTT 1132
DB 82170 AAAAGCAAGAGCTCCAAATATGAAAGATATATCTTCAAGACATATTAAGAGTT 82111
QY 1133 GGGAAATATATTCATGTGAAGTGAAGCAAGTGTCTTAAAGTGAAGTAAATGACAGTG 1192
DB 82110 GGGAAATATATTCATGTGAAGTGAAGCAAGTGTCTTAAAGTGAAGTAAATGACAGTG 82051
QY 1193 GAGACAAGTCAATCCCAAGTCTCAGAGACCTCCCTGCTGTCACTGGGAGTGAAGA 1252
DB 82050 GAGACAAGTCAATCCCAAGTCTCAGAGACCTCCCTGCTGTCACTGGGAGTGAAGA 81991
QY 1253 GGAAGATATGACAGTCTTGTCTGGAATTTTATGATATGCTGATATGTC 1312
DB 81990 GGAAGATATGACAGTCTTGTCTGGAATTTTATGATATGCTGATATGTC 81931
QY 1313 TCTGAGAAAGCCCTGAAAGTCTATCCCAATATCCACATCTTATTTCCAAATTA 1372
DB 81930 TCTGAGAAAGCCCTGAAAGTCTATCCCAATATCCACATCTTATTTCCAAATTA 81871
QY 1373 AGCTGATATGATACCTTAAGAGCGTCTAATTAAGTCTCCACTTCCCACTCAGGGCGG 1432
DB 81870 AGCTGATATGATACCTTAAGAGCGTCTAATTAAGTCTCCACTCAGGGCGG 81811
QY 1433 CTGCATTTTATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 1492
DB 81810 CTGCATTTTATGATATGATATGATATGATATGATATGATATGATATGATATG 81751
QY 1493 CTTCCTTCCCACTGCAAAATGCCAAAGTGGAGAAATATGATATTTTATGATTA 1552
DB 81750 CTTCCTTCCCACTGCAAAATGCCAAAGTGGAGAAATATGATATTTTATGATTA 81691
QY 1553 CAGAGCAGTCGGGAGACCGGATTTTAATTAATTAATTAATTAATTAATTAATTA 1612
DB 81690 CAGAGCAGTCGGGAGACCGGATTTTAATTAATTAATTAATTAATTAATTA 81631
QY 1613 AATGCGGTTTATTTTCTAGATATGATATGATATGATATGATATGATATGATATG 1672
DB 81630 AATGCGGTTTATTTTCTAGATATGATATGATATGATATGATATGATATGATATG 81571
QY 1673 CTTGACTATATGAGCATTAATGATATGATATGATATGATATGATATGATATGATATG 1732
DB 81571 CTTGACTATATGAGCATTAATGATATGATATGATATGATATGATATGATATGATATG
```

```

Db      81570 CCTGTCTATATGAGCATATATGTCATCAAGCTTGAGGCTTCTCCTTTCATCTGCGCT 81511
Qy      1733 GGAACGCTAAGACCTCAGTTTTCATATAGATCTAAGACGTGGGACTGCTAGCTGGGGTGT 1792
Db      81510 GGAACGCTAAGACCTCAGTTTTCATATAGATCTAAGACGTGGGACTGCTAGCTGGGGTGT 81451
Qy      1793 TTGCCCCCCTATCTCGGGGGAATGCTGAGAACATTTTGGTTACCTTCATATAGAGAGT 1852
Db      81450 TTGCCCCCCTATCTCGGGGGAATGCTGAGAACATTTTGGTTACCTTCATATAGAGAGT 81391
Qy      1853 GGAAGAGATACAGTGTCTACTACCACTATGAGATTAAGCCAGGAGTCTGCTCAACT 1912
Db      81390 GGAAGAGATACAGTGTCTACTACCACTATGAGATTAAGCCAGGAGTCTGCTCAACT 81331
Qy      1913 CCTACATATACAGACGCTCTCCCTTCACTACCTACCACTCCGAGTGTCACTGCTGC 1972
Db      81330 CCTACATATACAGACGCTCTCCCTTCACTACCTACCACTCCGAGTGTCACTGCTGC 81271
Qy      1973 AGGACTAAGAAACCTGTTTGAAGTAAAGAGGCTGGAAGAGGAGCCAACT 2032
Db      81270 AGGACTAAGAAACCTGTTTGAAGTAAAGAGGCTGGAAGAGGAGCCAACT 81211
Qy      2033 CTGTCTGCTT-CTCATTAGTCAATTTGCAAAATAGCAATTTCTGTCTCTTTGCTGCTGCC 2091
Db      81210 CTGTCTGCTTCTCATTAGTCAATTTGCAAAATAGCAATTTCTGTCTCTTTGCTGCTGCC 81151
Qy      2092 TGAGCACAAGAGCCGAACTCTATCGGACACAGATTAACATCTCTCGTGAACAGAT 2151
Db      81150 TGAGCACAAGAGCCGAACTCTATCGGACACAGATTAACATCTCTCGTGAACAGAT 81091
Qy      2152 TGACAAGGCTATGGAAGATGCTGATGGAATTAATCTTCAAGCTTTGAGCTTCAAGT 2211
Db      81090 TGACAAGGCTATGGAAGATGCTGATGGAATTAATCTTCAAGCTTTGAGCTTCAAGT 81031
Qy      2212 TCTTTCCTTTCATTCTACCTCTGAGCCAACTTCTGTAAGAAATGCTGAGTCTTAC 2271
Db      81030 TCTTTCCTTTCATTCTACCTCTGAGCCAACTTCTGTAAGAAATGCTGAGTCTTAC 80971
Qy      2272 TCAGGTTTCTTACTCTGTAATTAATCTTCAAGCCCTCTGGCCCAATTCATTA 2331
Db      80970 TCAGGTTTCTTACTCTGTAATTAATCTTCAAGCCCTCTGGCCCAATTCATTA 80911
Qy      2332 GGCACAAACATATACCTTTCATGAGACACACACAGACTTTTGAAGACAGACATGAC 2391
Db      80910 GGCACAAACATATACCTTTCATGAGACACACACAGACTTTTGAAGACAGACATGAC 80851
Qy      2392 TGTCTGAATTAAGGCTTGAAGATGAAGCTTTGAAGAAAGAAATACCTTTGTTCCAGC 2451
Db      80850 TGTCTGAATTAAGGCTTGAAGATGAAGCTTTGAAGAAAGAAATACCTTTGTTCCAGC 80791
Qy      2452 CCCCTTCCCACTCTTCAATGTTTAACCACTGCTTCCGAGCCTTGAAGCCAGGAGTGA 2511
Db      80790 CCCCTTCCCACTCTTCAATGTTTAACCACTGCTTCCGAGCCTTGAAGCCAGGAGTGA 80731
Qy      2512 CTGTATTAATGTTTGAAGAACTGATTTTGAAGTTCTGATCTTCAAGAGATGAT 2571
Db      80730 CTGTATTAATGTTTGAAGAACTGATTTTGAAGTTCTGATCTTCAAGAGATGAT 80671
Qy      2572 TAAATATACATTTCT 2587
Db      80670 TAAATATACATTTCT 80655

```

```

REFERENCE
1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS
Goddard, A., Godowski, P. J., Gurney, A. L., Hillan, K. J., Polakie, P.,
Smith, V., Wood, W. I., Wu, T. D., and Zhang, Z.
TITLE
Compositions and methods for the diagnosis and treatment of tumor
JOURNAL
Patent: EP 145317-A 3 11-AUG-2004;
Genentech Inc. (US)
FEATURES
source
Location/Qualifiers
1..1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 61.8%; Score 1599.8; DB 6; Length 1658;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1601; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      12 GGCAGCTCCACTCAGCCAGTACCCAGATAGCTGGAACTTCCCGACATGCTTCCC 71
Db      11 GGCAGCTCCACTCAGCCAGTACCCAGATAGCTGGAACTTCCCGACATGCTTCCC 70
Qy      72 TGGGGCAATCTCTTCTGAGACATTAATTAGCATATATTTCTGGCTGGAGCAATTG 131
Db      71 TGGGGCAATCTCTTCTGAGACATTAATTAGCATATATTTCTGGCTGGAGCAATTG 130
Qy      132 CACTCATCATTTGGCTTTGATTTTCAAGGAGACACTCCATCACTACTCTGCTGCT 191
Db      131 CACTCATCATTTGGCTTTGATTTTCAAGGAGACACTCCATCACTACTCTGCTGCT 190
Qy      192 CAGCTGGGAACTTTGGGAGAGATGGAATCTGAGCTGACATTTTGAACCTGACATCAAC 251
Db      191 CAGCTGGGAACTTTGGGAGAGATGGAATCTGAGCTGACATTTTGAACCTGACATCAAC 250
Qy      252 TTTCTGATATGCTGTAATTAATGCTGAGAGAAAGTTTGAAGCTTGGCTGCAATGCTCA 311
Db      251 TTTCTGATATGCTGTAATTAATGCTGAGAGAAAGTTTGAAGCTTGGCTGCAATGCTCA 310
Qy      312 AAGAAGCAAGATAGCTGCGAGCAGATGAATGTAATGTTGAGAGCCGAGCAGAGTGT 371
Db      311 AAGAAGCAAGATAGCTGCGAGCAGATGAATGTAATGTTGAGAGCCGAGCAGAGTGT 370
Qy      372 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGCGGCTGAAAAGCTGCACTCAAG 431
Db      371 TTGCTGATCAAGTATGTTGGCAATGCTCTTTGCGGCTGAAAAGCTGCACTCAAG 430
Qy      432 ATGCTGGCACTTCAAAATGTTATATCATCTTCAAAAGGCAAGGGGAATGTAACCTTG 491
Db      431 ATGCTGGCACTTCAAAATGTTATATCATCTTCAAAAGGCAAGGGGAATGTAACCTTG 490
Qy      492 AGTATTAACCTGGAAGCTTCAAGCATGCGGAAGTGAATGTGACTATATATGCAAGCTGAG 551
Db      491 AGTATTAACCTGGAAGCTTCAAGCATGCGGAAGTGAATGTGACTATATATGCAAGCTGAG 550
Qy      552 AGACCTTGGGTTGAGGCTCCCGATGATGTTCCCGACGCCACAGTGTCTGGGATCCC 611
Db      551 AGACCTTGGGTTGAGGCTCCCGATGATGTTCCCGACGCCACAGTGTCTGGGATCCC 610
Qy      612 AAGTTGACCAAGGAGCCAACTTCTGGAAGTCCCAATTAACAAGCTTGAAGCTGAGCTCG 671
Db      611 AAGTTGACCAAGGAGCCAACTTCTGGAAGTCCCAATTAACAAGCTTGAAGCTGAGCTCG 670
Qy      672 AGAATGTGACATGAAGGTTGTCTGTGCTCTACATATGTTACATCAACACATACT 731
Db      671 AGAATGTGACATGAAGGTTGTGTGTCTGTCTCTACATATGTTACATCAACACATACT 730
Qy      732 CCTGTATGATTAATAATGACATTTGCAAGCAAGCGGATATCAAAAGTACAGATGCG 791
Db      731 CCTGTATGATTAATAATGACATTTGCAAGCAAGCGGATATCAAAAGTACAGATGCG 790
Qy      792 AGATCAAAAAGGCGAGTCACTCAAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTCT 851
Db      791 AGATCAAAAAGGCGAGTCACTCAAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTCT 850

```

```

RESULT 13
LOCUS      CQ875680      1658 bp      DNA      linear      PAT 27-SEP-2004
DEFINITION Sequence 3 from Patent EP1445317.
ACCESSION  CQ875680
VERSION    CQ875680.1 GI:52748533
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

QY	853	CTTTCTTTGCCATCAGCTGGGACATCTTGCCCTCTCAGGCCCTTACTGATGCTMAAATAT	911
Db	851	CTTTCTTTGGCCATCGAGCTGGGACATCTTGCCCTCTCAGGCCCTTACTGATGCTMAAATAT	910
QY	912	GTGCCCTTGGCCCAAAAAAGCATGCAAGTCAATTGTTCAACAGGGATCTACAGAACTAT	971
Db	911	GTGCCCTTGGCCCAAAAAAGCATGCAAGTCAATTGTTCAACAGGGATCTACAGAACTAT	970
QY	972	TTGACCAACAGATATGACCTAGTTTATATTTCTGGAGAGAAATGAATTCATATCTAGAA	1031
Db	971	TTGACCAACAGATATGACCTAGTTTATATTTCTGGAGAGAAATGAATTCATATCTAGAA	1030
QY	1032	GCTTCGAGATGAGCAAAACAAGACCAAAACAAAAGGCCAAAAGCGAAGGCTTCAAT	1091
Db	1031	GCTTCGAGATGAGCAAAACAAGACCAAAACAAAAGGCCAAAAGCGAAGGCTTCAAT	1090
QY	1092	ATGAACAAGATAAATCTATCTCTCAAGAACAATTAGAAATTGGGAAAAATTAATTCATGGA	1151
Db	1091	ATGAACAAGATAAATCTATCTCTCAAGAACAATTAGAAATTGGGAAAAATTAATTCATGGA	1150
QY	1152	ACTAGACAAGTGTGTTAAGAGTGATPAAGTAAATSCAGCTGGAGACAAAGTCATCCAG	1211
Db	1151	ACTAGACAAGTGTGTTAAGAGTGATPAAGTAAATSCAGCTGGAGACAAAGTCATCCAG	1210
QY	1212	ATCTAGGGACCTCCCGCCCTGCTCACCCTGGGAGTGAAGAGAAAGATAGTGAAGTT	1271
Db	1211	ATCTAGGGACCTCCCGCCCTGCTCACCCTGGGAGTGAAGAGAAAGATAGTGAAGTT	1270
QY	1272	CTTTGTCTCTGAATTTTATAGTATATGTGCTGTAATGTGTGCTCTAGAGAAGCCCTGGAA	1331
Db	1271	CTTTGTCTCTGAATTTTATAGTATATGTGCTGTAATGTGTGCTCTAGAGAAGCCCTGGAA	1330
QY	1332	AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAGATGTAACCTTA	1391
Db	1331	AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAGATGTAACCTTA	1390
QY	1392	AGAGCGTGTATTTGACAGCGCACTTCGGCACTCAGGGCGGCTGATTTAGTAAATGGGT	1451
Db	1391	AGAGCGTGTATTTGACAGCGCACTTCGGCACTCAGGGCGGCTGATTTAGTAAATGGGT	1450
QY	1452	CAATATCATCTTTTATATGATGCTTCGAAAGGTCCTTGCTCTCTCCCACTGACA	1511
Db	1451	CAATATCATCTTTTATATGATGCTTCGAAAGGTCCTTGCTCTCTCCCACTGACA	1510
QY	1512	AATGCCAAAGTTGAGAAAAATGATCATTAATTTTACATPAACAGACAGTGGGACACCC	1571
Db	1511	AATGCCAAAGTTGAGAAAAATGATCATTAATTTTACATPAACAGACAGTGGGACACCC	1570
QY	1572	GATTTTATTAATTAACCTGACGACCTCTCTTTTAAACAAACAAA	1614
Db	1571	GATTTTATTAATTAACCTGACGACCTCTCTTTTAAACAAACAAA	1613
RESULT 14			
AR252569			
LOCUS			
DEFINITION Sequence 290 from patent US 6478825.			
ACCESSION AR252569			
VERSION AR252569.1			
KEYWORDS			
SOURCE			
ORGANISM			
Unknown.			
REFERENCE			
AUTHORS 1 (bases 1 to 1658)			
TITLE Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.			
JOURNAL Implant, method of making same and use of the implant for the			
FEATURES treatment of bone defects			
PATENT: US 6478825-A 290 12-NOV-2002;			
location/Qualifiers			
1..1658			
/organism="unknown"			
/mol_type="genomic DNA"			

Query Match	61.8%;	Score 1599.8;	DB 6;	Length 1658;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1601;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	12	GGCAGCTTCACTCAGCCAGTACCCAGATACGCTGGGAACTTCCCAAGCCATGCTTCCC	71	
DB	11	GGCAGCTTCACTCAGCCAGTACCCAGATACGCTGGGAACTTCCCAAGCCATGCTTCCC	70	
QY	72	TGGGGGAGATCTCTTCGAGGCAATATTCAGATCATCATATTCGCTGGAGCAATTCG	131	
DB	71	TGGGGGAGATCTCTTCGAGGCAATATTCAGATCATCATATTCGCTGGAGCAATTCG	130	
QY	132	CACATCATATGGCTTTGGTATTCACAGGAGACATCCATCATCAGTCACTACTGCGCT	191	
DB	131	CACATCATATGGCTTTGGTATTCACAGGAGACATCCATCATCAGTCACTACTGCGCT	190	
QY	192	CAGCTGGGACATTTGGGGAGGATGGAATCCTGAGCTGCATTTTGAACCTTGACATCAAC	251	
DB	191	CAGCTGGGACATTTGGGGAGGATGGAATCCTGAGCTGCATTTTGAACCTTGACATCAAC	250	
QY	252	TTTCTGATATTCGTATTCACATGCTGAAAGAGTGTATTAAGCTTGGCTTCATAGTTCA	311	
DB	251	TTTCTGATATTCGTATTCACATGCTGAAAGAGTGTATTAAGCTTGGCTTCATAGTTCA	310	
QY	312	AAGAAGCCAAAGATGAGCTGTCGAGACGAGATGAAATGTTACAGAGCCGACACAGTGT	371	
DB	311	AAGAAGCCAAAGATGAGCTGTCGAGACGAGATGAAATGTTACAGAGCCGACACAGTGT	370	
QY	372	TTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAACGTGCACTCAG	431	
DB	371	TTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAACGTGCACTCAG	430	
QY	432	ATGCTGGGACCTACAAATGTTATTCATCACTTTTAAAGGCAAGGGGATGCTAACTTGG	491	
DB	431	ATGCTGGGACCTACAAATGTTATTCATCACTTTTAAAGGCAAGGGGATGCTAACTTGG	490	
QY	492	AGTATTAACCTGAGACCTTCAGCATGTCGCGAAGTGAATGTGACCTATTAATCCAGCTCAG	551	
DB	491	AGTATTAACCTGAGACCTTCAGCATGTCGCGAAGTGAATGTGACCTATTAATCCAGCTCAG	550	
QY	552	AGACCTTGCCTGTGAGGCTCCCGATGTTCCCCAGCCCAAGTGGTCTGGGCACTCC	611	
DB	551	AGACCTTGCCTGTGAGGCTCCCGATGTTCCCCAGCCCAAGTGGTCTGGGCACTCC	610	
QY	612	AAAGTTGACGAGGAGCCAACTTCTCGGAGTCTTCCAAATACCAGCTTTGAGTGAACCTCTG	671	
DB	611	AAAGTTGACGAGGAGCCAACTTCTCGGAGTCTTCCAAATACCAGCTTTGAGTGAACCTCTG	670	
QY	672	AGAAATGAGCATAAAGGTTGTCTGTGCTCTACAAATGTTAGATCAACAACACATTA	731	
DB	671	AGAAATGAGCATAAAGGTTGTGTCTGTGCTCTACAAATGTTAGATCAACAACACATTA	730	
QY	732	CCTGTATGATTTGAAAATGACATTTGCCCAAAGCAACAGGGGATATCAAAAGTGACAGAAATCGG	791	
DB	731	CCTGTATGATTTGAAAATGACATTTGCCCAAAGCAACAGGGGATATCAAAAGTGACAGAAATCGG	790	
QY	792	AGATCAAAAAGGCGGAGTCACTTACAGCTGCTAAACTCAAAAGGCTTCTGTGTGTCTT	851	
DB	791	AGATCAAAAAGGCGGAGTCACTTACAGCTGCTAAACTCAAAAGGCTTCTGTGTGTCTT	850	
QY	852	CTTTCTTTTGCATGAGCTGGGCACTTTCGCTCTCAGCCCTTACCTGATGCTAAATTAAT	911	
DB	851	CTTTCTTTTGCATGAGCTGGGCACTTTCGCTCTCAGCCCTTACCTGATGCTAAATTAAT	910	
QY	912	GTGCTTGGCCACAAAAGAGATCAAAAGTCAATGTTTACACAGGATCTTACAGAACTAT	971	
DB	911	GTGCTTGGCCACAAAAGAGATCAAAAGTCAATGTTTACACAGGATCTTACAGAACTAT	970	
QY	972	TTTCAACACAGATATGACCTATGTTTATATTTCTGGAGGAAATGAAATTCATATCTAGAA	1031	
DB	971	TTTCAACACAGATATGACCTATGTTTATATTTCTGGAGGAAATGAAATTCATATCTAGAA	1030	

QY 1032 GTCGTGAGTGAACAACAAGACAGAAACAAAAGACCAAAAGCAGAGGCTCCAAAT 1091
|
|
|
Db 1031 GTCGTGAGTGAACAACAAGACAGAAACAAAAGACCAAAAGCAGAGGCTCCAAAT 1090
|
|
|
QY 1092 ATGAACAAGATTAATCTATCTTCAAGACATATTAGAAAGTTGGAAATTAATTCATGTGA 1151
|
|
|
Db 1091 ATGAACAAGATTAATCTATCTTCAAGACATATTAGAAAGTTGGAAATTAATTCATGTGA 1150
|
|
|
QY 1152 ACTAGACAGTGTGTAAAGATGATTAAGTAAATGACAGTGGAGACAAATGCAATCCCGAG 1211
|
|
|
Db 1151 ACTAGACAGTGTGTAAAGATGATTAAGTAAATGACAGTGGAGACAAATGCAATCCCGAG 1210
|
|
|
QY 1212 ATCTGAGGAGCTCCCGCTGCTGTCACCTGGGAGTGAAGAGACAGATAGTCAATGTT 1271
|
|
|
Db 1211 ATCTGAGGAGCTCCCGCTGCTGTCACCTGGGAGTGAAGAGACAGATAGTCAATGTT 1270
|
|
|
QY 1272 CTTTGTCTGTAAATTTTATAGTATATGTCGTGTATGTTGCTCTGAGAAAGCCCTTGAA 1331
|
|
|
Db 1271 CTTTGTCTGTAAATTTTATAGTATATGTCGTGTATGTTGCTCTGAGAAAGCCCTTGAA 1330
|
|
|
QY 1332 AGCTTATCCCAACATTCACACATCTTAATTCACAAATTAAGCTGTATGTACCTTA 1391
|
|
|
Db 1331 AGCTTATCCCAACATTCACACATCTTAATTCACAAATTAAGCTGTATGTACCTTA 1390
|
|
|
QY 1392 AGACGCTGCTAATGACCTGCACTTGCAACTCAGGGGCGGCTGCAATTTAAGTAATGGT 1451
|
|
|
Db 1391 AGACGCTGCTAATGACCTGCACTTGCAACTCAGGGGCGGCTGCAATTTAAGTAATGGT 1450
|
|
|
QY 1452 CAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGGCTTCTCTTCCCACTGACA 1511
|
|
|
Db 1451 CAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGGCTTCTCTTCCCACTGACA 1510
|
|
|
QY 1512 AATGCCAAAGTTGAAGAAATATGATCTAATTTTAAAGTAAACAGACGATCGGCGACAC 1571
|
|
|
Db 1511 AATGCCAAAGTTGAAGAAATATGATCTAATTTTAAAGTAAACAGACGATCGGCGACAC 1570
|
|
|
QY 1572 GATTTTAAATTAATTAATGAGACACCTCTTTTAAACAAACAAA 1614
|
|
|
Db 1571 GATTTTAAATTAATTAATGAGACACCTCTTTTAAACAAACAAA 1613
|
|
|

RESULT 15
AX092328 1658 bp DNA linear PAT 23-MAR-2001
LOCUS AX092328
DEFINITION Sequence 59 from Patent WO0116318.
ACCESSION AX092328
VERSION AX092328.1 GI:13444478
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1. Baton, D.L., Filvaroff, E., Gerlitsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, M.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0116318-A 59 08-MAR-2001;
JOURNAL
Genentech, Inc. (US)
FEATURES
source
1. 1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 61.8%; Score 1599.8; DB 6; Length 1658;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1601; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 GGCAGCTCCACTAGCCAGTACCGAGATACGCTGGAGACCTTCCCGACGATAGCTTCCC 71

Db 11 GGCAGCTCCACTAGCCAGTACCGAGATACGCTGGAGACCTTCCCGACGATAGCTTCCC 70
|
|
|
QY 72 TGGGGCAATCTCTTTCGAGCAATTAATGATATATATTCGTGGAGCAATTG 131
|
|
|
Db 71 TGGGGCAATCTCTTTCGAGCAATTAATGATATATATTCGTGGAGCAATTG 130
|
|
|
QY 132 CACTCATATGAGCTTTGGTATTTTCAGGAGACATCTCATGACATCTGTGGCT 191
|
|
|
Db 131 CACTCATATGAGCTTTGGTATTTTCAGGAGACATCTCATGACATCTGTGGCT 190
|
|
|
QY 192 CAGCTGGGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAAC 251
|
|
|
Db 191 CAGCTGGGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACATCAAAC 250
|
|
|
QY 252 TTTCTGATATGCTGATCAATAGGCTGGAAGAAAGGTTTGGCTTGGTCCATGAGTTCA 311
|
|
|
Db 251 TTTCTGATATGCTGATCAATAGGCTGGAAGAAAGGTTTGGCTTGGTCCATGAGTTCA 310
|
|
|
QY 312 AAGAAGCAAAAGATGAGCTGTGAGCAGATGAATGTTCAAGAGCCGAGACAGAGTGT 371
|
|
|
Db 311 AAGAAGCAAAAGATGAGCTGTGAGCAGATGAATGTTCAAGAGCCGAGACAGAGTGT 370
|
|
|
QY 372 TTGCTGATCAAGTATAGTTGSCAATGCTCTTTGCGCTGAATAAAGCTGCACTCAAG 431
|
|
|
Db 371 TTGCTGATCAAGTATAGTTGSCAATGCTCTTTGCGCTGAATAAAGCTGCACTCAAG 430
|
|
|
QY 432 ATGCTGGGACCTTACAAAGTTTATATCATCATCTTCAAAAGGCAAGGGGAATGTAACCTTG 491
|
|
|
Db 431 ATGCTGGGACCTTACAAAGTTTATATCATCATCTTCAAAAGGCAAGGGGAATGTAACCTTG 490
|
|
|
QY 492 AGTATTAACCTGAGACCTTTCAGCATGCGGAAAGTGAATGTGACTTAATGACAGCTGAG 551
|
|
|
Db 491 AGTATTAACCTGAGACCTTTCAGCATGCGGAAAGTGAATGTGACTTAATGACAGCTGAG 550
|
|
|
QY 552 AGACCTTGGGCTGAGAGCTGCCGATGCTTCCCGACGACAGTGTCTGGGCAATGCC 611
|
|
|
Db 551 AGACCTTGGGCTGAGAGCTGCCGATGCTTCCCGACGACAGTGTCTGGGCAATGCC 610
|
|
|
QY 612 AAGTTGACGAGGAGACCAACTCTTGGGAAGTCCCAATACCAAGCTTTGAGCTGAACTGCG 671
|
|
|
Db 611 AAGTTGACGAGGAGACCAACTCTTGGGAAGTCCCAATACCAAGCTTTGAGCTGAACTGCG 670
|
|
|
QY 672 AGAATGTACATGAGGTTGTGTGCTGTACATGTTACATCAACACATCACT 731
|
|
|
Db 671 AGAATGTACATGAGGTTGTGTGCTGTACATGTTACATCAACACATCACT 730
|
|
|
QY 732 CCTGTATGTTGAATAATGACATTTGCCAAAGCAAGGGGATATCAAAATGACAGAAATCGG 791
|
|
|
Db 731 CCTGTATGTTGAATAATGACATTTGCCAAAGCAAGGGGATATCAAAATGACAGAAATCGG 790
|
|
|
QY 792 AGATCAAAAGGCGAGTCACTGACCTGCTTAACTCAAAAGGCTTCTGTGTGCTCTT 851
|
|
|
Db 791 AGATCAAAAGGCGAGTCACTGACCTGCTTAACTCAAAAGGCTTCTGTGTGCTCTT 850
|
|
|
QY 852 CTTTCTTTGCCATCAGCTGGGCACTTGCCTCTGAGCCCTTACCTGATGCTAAATATAT 911
|
|
|
Db 851 CTTTCTTTGCCATCAGCTGGGCACTTGCCTCTGAGCCCTTACCTGATGCTAAATATAT 910
|
|
|
QY 912 GTGCTTGGCCCAAAAAGCATGCAAGTCAATTTGTTCAACAGGAGTCTACAGAACTAT 971
|
|
|
Db 911 GTGCTTGGCCCAAAAAGCATGCAAGTCAATTTGTTCAACAGGAGTCTACAGAACTAT 970
|
|
|
QY 972 TTCACACACAGTATGACCTATGTTTATATTTTCGGGAGAAATGATTCATATCTAGAA 1031
|
|
|
Db 971 TTCACACACAGTATGACCTATGTTTATATTTTCGGGAGAAATGATTCATATCTAGAA 1030
|
|
|
QY 1032 GTCGTGAGTGAACAACAAGACAGAAACAAAAGACCAAAAGCAGAGGCTCCAAAT 1091
|
|
|
Db 1031 GTCGTGAGTGAACAACAAGACAGAAACAAAAGACCAAAAGCAGAGGCTCCAAAT 1090
|
|
|
QY 1092 ATGAACAAGATTAATCTATCTTCAAGACATATTAGAAAGTTGGAAATTAATTCATGTGA 1151
|
|
|

```
Db      1091 ATGACAAGATAAATCTATCTTCAAGACATATTAGAAAGTTGGAAAATAATTCATGGA 1150
Qy      1152 ACTAGACAAGTGTGTAAAGTGTGAATAGTAAATGCACTGGAGACAAGTGCATCCCCAG 1211
Db      1151 ACTAGACAAGTGTGTAAAGTGTGAATAGTAAATGCACTGGAGACAAGTGCATCCCCAG 1210
Qy      1212 ATCTCAGGAGACCTCCCTGCTGCTGCACTGGGAGTGAAGACAGGATAGTGCATGTT 1271
Db      1211 ATCTCAGGAGACCTCCCTGCTGCTGCACTGGGAGTGAAGACAGGATAGTGCATGTT 1270
Qy      1272 CTTTGCTCTGGAATTTTAAATTATATATGTGCTGTAATGTGCTCTGAGGAAGCCCCTGAA 1331
Db      1271 CTTTGCTCTGGAATTTTAAATTATATATGTGCTGTAATGTGCTCTGAGGAAGCCCCTGAA 1330
Qy      1332 AGTCTATCCCAACATCCACATCTTATATTCACAATTAAGCTGATATGTACCCTA 1391
Db      1331 AGTCTATCCCAACATCCACATCTTATATTCACAATTAAGCTGATATGTACCCTA 1390
Qy      1392 AGACGCTGCTAATTGACTGCACTTGGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGT 1451
Db      1391 AGACGCTGCTAATTGACTGCACTTGGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGT 1450
Qy      1452 CAAATGATGACCTTTTATATGATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACA 1511
Db      1451 CAAATGATGACCTTTTATATGATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACA 1510
Qy      1512 AATGCCAAAGTTGGAATAATGATCATATTTTAGCATTAACAGAGCAGTGGGACACC 1571
Db      1511 AATGCCAAAGTTGGAATAATGATCATATTTTAGCATTAACAGAGCAGTGGGACACC 1570
Qy      1572 GATTTTAAATAAATGAGACCTTCTTTTAAACAACAAA 1614
Db      1571 GATTTTAAATAAATGAGACCTTCTTTTAAACAACAAA 1613
```

Search completed: May 30, 2005, 17:54:01
Job time : 1194.1 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 05:15:03 ; Search time 1586.66 Seconds

(Without alignments)
9651.969 Million cell updates/sec

Title: US-09-763-978B-1

Perfect score: 2587

Sequence: 1 ggaagcgacagggcgagctcc.....tgatataatatacatcttcc 2587

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2002as:*
6: geneseqn2002bs:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2003ds:*
11: geneseqn2003as:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2587	100.0	2587	3	AAZ90470
2	2565	99.1	2627	3	AAA70077
3	2565	99.1	2627	4	AAH5681
4	2565	99.1	2627	6	ABN72971
5	2565	99.1	2627	9	ADA08544
6	2565	99.1	2627	10	ADP08887
7	2565	99.1	2627	10	ADG46174
8	2565	99.1	2627	12	ADNA0452
9	2563	99.1	3357	6	ADD32519
10	2563	99.1	2603	6	ADD29253
11	2554	98.7	2591	6	ABL57354
12	2527	97.7	2626	6	ABL56582
13	2460	95.1	2690	12	ADP81075
14	2421	93.6	2626	4	AAF26593
15	2421	93.6	2626	6	AAI32526
16	1931	74.3	1965	5	ADL45372
17	1589	61.8	1657	3	AAZ65059
18	1589	61.8	1657	10	ADB90935
19	1589	61.8	1658	4	AA546033
20	1589	61.8	1658	4	AAI92087

21	1599.8	61.8	1658	5	AAF44205
22	1599.8	61.8	1658	6	ABK11744
23	1599.8	61.8	1658	6	AB574407
24	1599.8	61.8	1658	6	ABK11091
25	1599.8	61.8	1658	8	ACA89483
26	1599.8	61.8	1658	8	ACA73493
27	1599.8	61.8	1658	8	ACA05808
28	1599.8	61.8	1658	8	ACA66642
29	1599.8	61.8	1658	8	ACA64352
30	1599.8	61.8	1658	8	ACA91193
31	1599.8	61.8	1658	8	ACD81570
32	1599.8	61.8	1658	8	ACF20217
33	1599.8	61.8	1658	8	ACF19603
34	1599.8	61.8	1658	8	ACD12891
35	1599.8	61.8	1658	8	ACD13056
36	1599.8	61.8	1658	8	ACD25159
37	1599.8	61.8	1658	8	ACF00208
38	1599.8	61.8	1658	8	ACA60392
39	1599.8	61.8	1658	8	ACA72265
40	1599.8	61.8	1658	8	ACD04789
41	1599.8	61.8	1658	8	ACD18250
42	1599.8	61.8	1658	8	ACD08257
43	1599.8	61.8	1658	8	ACA88691
44	1599.8	61.8	1658	8	ACA70133
45	1599.8	61.8	1658	8	ACD12355

ALIGNMENTS

RESULT 1
AAZ90470
ID AAZ90470 standard; cDNA; 2587 BP.
XX
AC AAZ90470;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cancer specific gene (CSG) sequence (clone ID 16656542).
XX
KW CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KM endometrial; uterine; lung; cytotoxic; ss.
XX
OS Homo sapiens.
XX
XX W0200012758-A1.
XX
XX 09-MAR-2000.
XX
XX 01-SEP-1999; 99MO-US019655.
XX
XX 02-SEP-1998; 98US-0098880P.
XX
XX (DIAD-) DIADEXUS LLC.
XX
XX Salceda S, Sun Y, Recipon H, Cafferkey R;
XX WPI; 2000-256657/22.
XX
XX Claim 9; Page 44-45; 58pp; English.
XX
XX The invention relates to detecting, diagnosing metastasis and staging
XX cancer by measuring levels of cancer specific genes (CSG) in cells,
XX tissues or body fluids. Their remission and progression, decreases and
XX increases in CSG levels, is also monitored, by periodic sample analysis.
XX The methods are useful for detecting cancers, especially gynecologic
XX cancers which include ovarian, breast, endometrial and uterine cancer and
XX lung cancer. Antibodies against the CSBs labeled with paramagnetic ions
XX or a radioisotope is useful for imaging cancer and when conjugated with a

CC cytotoxic agent are useful for treating cancer. The present sequence
CC represents a CSG sequence (clone ID: 16656542 and gene ID: 234617)
CC
CC
CQ Sequence 2567 BP; 737 A; 588 C; 580 G; 682 T; 0 U; 0 Other;
XX

Query Match 100.0%; Score 2587; DB 3; Length 2587;

```

Best Local Similarity 100.0%; Read. NO. 0;
Matches 2587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY	1	GGAAAGGCAAGCGGGCAAGCTCCACTCAAGCCAGTACCCAGATACAGCTGGGAACCTTCCCCACG	60
Db	1	GGAAAGGCAAGCGGGCAAGCTCCACTCAAGCCAGTACCCAGATACAGCTGGGAACCTTCCCCACG	60
OY	61	CATGCGCTCCCTGGGGGAGATCCTCTTCTGGAGCATPAATTAGCATCATTAATTTCTGGC	120
Db	61	CATGCGCTCCCTGGGGGAGATCCTCTTCTGGAGCATPAATTAGCATCATTAATTTCTGGC	120
OY	121	TGGAGCAATTGCACTCATCAATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAAGTCAAC	180
Db	121	TGGAGCAATTGCACTCATCAATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAAGTCAAC	180
OY	181	TACTGTCCCTCAAGCTGGGAAACATTGGGGAGATGGAAATCTTGAAGTGCACCTTTGAACC	240
Db	181	TACTGTCCCTCAAGCTGGGAAACATTGGGGAGATGGAAATCTTGAAGTGCACCTTTGAACC	240
OY	241	TGACATCAAACTTTCTGATATGCTGATACAAATGGCTGGAAGAAAGTTTATAGCTTGGT	300
Db	241	TGACATCAAACTTTCTGATATGCTGATACAAATGGCTGGAAGAAAGTTTATAGCTTGGT	300
OY	301	CCATGAGTTCAAAAGAGGCAAAAGATGAGCTGTCCGAGCAGATGAAATGTTCAGAGGCCG	360
Db	301	CCATGAGTTCAAAAGAGGCAAAAGATGAGCTGTCCGAGCAGATGAAATGTTCAGAGGCCG	360
OY	361	GACAGCAGTGTTCGTGATCAAGTGAATAGTTGGCAATGCTCTCTTTGGCGCTGAAAAAGCT	420
Db	361	GACAGCAGTGTTCGTGATCAAGTGAATAGTTGGCAATGCTCTTTGGCGCTGAAAAAGCT	420
OY	421	GCAATCAACAGATGCTGGCACCCTCAAAATGTTATATCATCATCTTCAAAAGGCAAGGGAA	480
Db	421	GCAATCAACAGATGCTGGCACCCTCAAAATGTTATATCATCATCTTCAAAAGGCAAGGGAA	480
OY	481	TGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCGGAAATGTAATGTGACTATAA	540
Db	481	TGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCGGAAATGTAATGTGACTATAA	540
OY	541	TGCCAGCTCAGAGACTTGGCGGTGAGAGGCTCCCCGATGTTCCCCCAAGCCACAATGGT	600
Db	541	TGCCAGCTCAGAGACTTGGCGGTGAGAGGCTCCCCGATGTTCCCCCAAGCCACAATGGT	600
OY	601	CTGGGCACTCCCAAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATACCAAGCTTTGA	660
Db	601	CTGGGCACTCCCAAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATACCAAGCTTTGA	660
OY	661	GCTGAACCTTGAGAAATGTGACCATGAAAGGTTGTCTGTGCTCTCAATGTTACATCAATCA	720
Db	661	GCTGAACCTTGAGAAATGTGACCATGAAAGGTTGTGTGCTGTCTCAATGTTACATCAATCA	720
OY	721	CAACACATCTCTCTGTATATTTGAAAAATGACATTTGCCAAAGCAACAGGGGATATCAAAAT	780
Db	721	CAACACATCTCTCTGTATATTTGAAAAATGACATTTGCCAAAGCAACAGGGGATATCAAAAT	780
OY	781	GACACAATCGAGATCAAAAGGCGGAGTCACTTACAGCTGTCTAAATCTCAAAAGGCTTCTCT	840
Db	781	GACACAATCGAGATCAAAAGGCGGAGTCACTTACAGCTGTCTAAATCTCAAAAGGCTTCTCT	840
OY	841	GTTGTCTCTTCTTCTTCTTTCATCAAGCTTGGGCACTTTCGCTCTCAGCCCTTACCTGTAT	900
Db	841	GTTGTCTCTTCTTCTTCTTTCATCAAGCTTGGGCACTTTCGCTCTCAGCCCTTACCTGTAT	900
OY	901	GCTAAAAATATATGTGCTTGGCCACAAAAAAGCATGCAAAAGTCAATTTTTCACACAGGGAATC	960
Db	901	GCTAAAAATATATGTGCTTGGCCACAAAAAAGCATGCAAAAGTCAATTTTTCACACAGGGAATC	960

QY	961	TACGAACTATTTCCACCACCAAGATATGACCTAGTTTATATTTCTGGAGGAAATGAAAT	1020
Db	961	TACGAACTATTTCCACCACCAAGATATGACCTAGTTTATATTTCTGGAGGAAATGAAAT	1020
QY	1021	CATATCTTGAAGTCTGGAGTGAGCAAAACAAGACAAGAAACAAACAAAGACCAAAAGCAG	1080
Db	1021	CATATCTTGAAGTCTGGAGTGAGCAAAACAAGACAAGAAACAAACAAAGACCAAAAGCAG	1080
QY	1081	AAGGCTCCAAATATGAAACAAGATAAATCTATCTTCAAGACAATATTAGAGTTGGAAAAT	1140
Db	1081	AAGGCTCCAAATATGAAACAAGATAAATCTATCTTCAAGACAATATTAGAGTTGGAAAAT	1140
QY	1141	AATTCATGTGAACCTAGACAAAGTGTGTTAAGAGTAAATGATAAAATGCACTGTGAGACAAG	1200
Db	1141	AATTCATGTGAACCTAGACAAAGTGTGTTAAGAGTAAATGATAAAATGCACTGTGAGACAAG	1200
QY	1201	TGCATCCCCCAATCTCAGAGACCTCCCCCTGCTGTCACTGGGGAATGAGAGACAGGA	1260
Db	1201	TGCATCCCCCAATCTCAGAGACCTCCCCCTGCTGTCACTGGGGAATGAGAGACAGGA	1260
QY	1261	TAGTCATGTTCTTTGTCCTGCAATTTTATGATATATGTGCTGTATGTTGCTCTGAGA	1320
Db	1261	TAGTCATGTTCTTTGTCCTGCAATTTTATGATATATGTGCTGTATGTTGCTCTGAGA	1320
QY	1321	AGCCCTTGAAAGTCTATCCCAACATATCCACATCTTATCTTCCACAAATTAAGCTGTAG	1380
Db	1321	AGCCCTTGAAAGTCTATCCCAACATATCCACATCTTATCTTCCACAAATTAAGCTGTAG	1380
QY	1381	TATGTAACCTTAAGACGCTGCTAATTTGACTGCACTTGCGCAACTAGGGGGGGCTGCATTT	1440
Db	1381	TATGTAACCTTAAGACGCTGCTAATTTGACTGCACTTGCGCAACTAGGGGGGGCTGCATTT	1440
QY	1441	TAGTATATGGTCAATATGATTCACTTTATATGATGCTTCCAAAGGTGCTTGCTTCTCTT	1500
Db	1441	TAGTATATGGTCAATATGATTCACTTTATATGATGCTTCCAAAGGTGCTTGCTTCTCTT	1500
QY	1501	CCCAACTGACAATATGCCAAAGTTGAGAAAATGATCATTAATTTTATGATTAACAGACAG	1560
Db	1501	CCCAACTGACAATATGCCAAAGTTGAGAAAATGATCATTAATTTTATGATTAACAGACAG	1560
QY	1561	TCGGGACACCGATTTTATTAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGG	1620
Db	1561	TCGGGACACCGATTTTATTAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGG	1620
QY	1621	TTTATTTCTCAGATGATGTTGATCCGTAATGTCACGAGAAAGACCTTTCACCTTGACT	1680
Db	1621	TTTATTTCTCAGATGATGTTGATCCGTAATGTCACGAGAAAGACCTTTCACCTTGACT	1680
QY	1681	ATATGGACTTATGTATCATCAACAGCTCTGAGGCTTCTCTTCCATCTCTGCTGAGACGCT	1740
Db	1681	ATATGGACTTATGTATCATCAACAGCTCTGAGGCTTCTCTTCCATCTCTGCTGAGACGCT	1740
QY	1741	AAGACTCTAGTTTCAATAGATCTTAAGACAGTGGGACTAGCTGGGGGTATTTCCGCCCC	1800
Db	1741	AAGACTCTAGTTTCAATAGATCTTAAGACAGTGGGACTAGCTGGGGGTATTTCCGCCCC	1800
QY	1801	CCATCTCCGGGGGATGCTGTAACAACAATTTTGTATCTCAATGAGAGGAGTGGAGAGG	1860
Db	1801	CCATCTCCGGGGGATGCTGTAACAACAATTTTGTATCTCAATGAGAGGAGTGGAGAGG	1860
QY	1861	ATACAGTGTCTAATACTAGTGGATTAAGGCGCAGGAGATGCTGCTCAACCTCTTACAT	1920
Db	1861	ATACAGTGTCTAATACTAGTGGATTAAGGCGCAGGAGATGCTGCTCAACCTCTTACAT	1920
QY	1921	GTACAGAGCTCTCCCAATTACAACTAACCTGGAAGTGTCAACGTGTCTCAGAGACTAA	1980
Db	1921	GTACAGAGCTCTCCCAATTACAACTAACCTGGAAGTGTCAACGTGTCTCAGAGACTAA	1980
QY	1981	GAAACCCCTGTGTTGAGTAAAGAGGCGTGGAAAGGGGGAAGCAACATCTGTCTGC	2040
Db	1981	GAAACCCCTGTGTTGAGTAAAGAGGCGTGGAAAGGGGGAAGCAACATCTGTCTGC	2040
QY	2041	TTCTCACATTAATGATGGCAAAATTAACATCTCTCTTGTGGCTGTGCTCAGACAG	2100

```
Db 2041 TTGTCACATTAGTCATTGGCAAAATAGCATTTCTGTCCTTTGGTGTGCTGACGACAG 2100
Qy 2101 AGAGCCGAACCTCTATGTGGGACCAAGATTAACATCTTCTGCTGAACAGAGTTGACAAAGC 2160
Db 2101 AGAGCCGAACCTCTATGTGGGACCAAGATTAACATCTTCTGCTGAACAGAGTTGACAAAGC 2160
Qy 2161 CTATGGGAATGCGCTGATGGGATTAATCTTCAAGCTGTGTGGCTTCTTAAGTTCTTCCCT 2220
Db 2161 CTATGGGAATGCGCTGATGGGATTAATCTTCAAGCTGTGTGGCTTCTTAAGTTCTTCCCT 2220
Qy 2221 TCATTTACCCCTGCAACCCAAAGTTCTGTAAAGAAATGCGTAGTTCTAGCTCAGGTTTT 2280
Db 2221 TCATTTACCCCTGCAACCCAAAGTTCTGTAAAGAAATGCGTAGTTCTAGCTCAGGTTTT 2280
Qy 2281 CTATCTGTGAATTTAGATCTTCAGACCCCTTCCTGGCAACATTCAAATTAAGCAACAA 2340
Db 2281 CTATCTGTGAATTTAGATCTTCAGACCCCTTCCTGGCAACATTCAAATTAAGCAACAA 2340
Qy 2341 CATATACCTTCATGAAAGCAACACACTTTTGAAGCAAGACATGACTGTGAAT 2400
Db 2341 CATATACCTTCATGAAAGCAACACACTTTTGAAGCAAGACATGACTGTGAAT 2400
Qy 2401 TGAAGCCTTGAGGAATGAACTTTGAAAGAAAGAAATACTTTGTTCCAGCCCTTCCC 2460
Db 2401 TGAAGCCTTGAGGAATGAACTTTGAAAGAAAGAAATACTTTGTTCCAGCCCTTCCC 2460
Qy 2461 ACACTCTTCATGTGTTAACCACTGCTTCTTCTGACCTTGGAGCCACGGTACTGTATTAC 2520
Db 2461 ACACTCTTCATGTGTTAACCACTGCTTCTTCTGACCTTGGAGCCACGGTACTGTATTAC 2520
Qy 2521 ATGTGTATTAAGAACTGATTTTAAGATCTGATCTTCAAGAGATGATTAATTTAC 2580
Db 2521 ATGTGTATTAAGAACTGATTTTAAGATCTGATCTTCAAGAGATGATTAATTTAC 2580
Qy 2581 ATTTCT 2587
Db 2581 ATTTCT 2587

RESULT 2
AAA70077
ID AAA70077 standard; cDNA; 2627 BP.
XX
AC AAA70077;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide seq ID NO:391.
XX
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN MO200036107-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99MO-US030270.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
XX
DR MPI; 2000-431589/37.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
```

```
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Claim 1; Page 204-205; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
cytostatic activity and can be used in gene therapy and vaccines. Ovarian
carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
for the prevention, diagnosis and treatment of cancer, preferably ovarian
cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
ovarian carcinoma polynucleotides and proteins used in the
exemplification of the present invention
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 99.1%; Score 2565; DB 3; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCACTCAGCCAGTACCAGATACGCTGGGAACCTTCCCAAGCCATGGCTTCCC 71
Db 33 GGCAGCTCACTCAGCCAGTACCAGATACGCTGGGAACCTTCCCAAGCCATGGCTTCCC 92
Qy 72 TGGGGAGATTCCTTCTTGAGGATTAATGATCATCATTAATTTCTGGCTGGAGCAATTG 131
Db 93 TGGGGAGATTCCTTCTTGAGGATTAATGATCATCATTAATTTCTGGCTGGAGCAATTG 152
Qy 132 CACTCATCATTTGGCTTTGGATTTTCAGGAGACATCCATCACTCACTACTGTGGCT 191
Db 153 CACTCATCATTTGGCTTTGGATTTTCAGGAGACATCCATCACTCACTACTGTGGCT 212
Qy 192 CAGCTGGGAACATTTGGGAGAGATGAATCTTGAAGCTGCACTTTGAACTGACATCAAC 251
Db 213 CAGCTGGGAACATTTGGGAGAGATGAATCTTGAAGCTGCACTTTGAACTGACATCAAC 272
Qy 252 TTTCTGATTCGATATCAATAGCTGCAAGAAAGCTTTTAAAGCTTGTGCAAGATTTCA 311
Db 273 TTTCTGATTCGATATCAATAGCTGCAAGAAAGCTTTTAAAGCTTGTGCAAGATTTCA 332
Qy 312 AAGAAAGCAAAAGTGAAGCTGTGCGAGCAGAGATGAATGTTTCAAGAGCCGGAAGCAGATGT 371
Db 333 AAGAAAGCAAAAGTGAAGCTGTGCGAGCAGAGATGAATGTTTCAAGAGCCGGAAGCAGATGT 392
Qy 372 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGCGGCTGAAGAAAGTGCAACGACAG 431
Db 393 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTGCGGCTGAAGAAAGTGCAACGACAG 452
Qy 432 ATGCTGGCACCTTCAAAATGTTATATCATCTTTAAAGCAAGGGGAATGCTTAACCTTG 491
Db 453 ATGCTGGCACCTTCAAAATGTTATATCATCTTTAAAGCAAGGGGAATGCTTAACCTTG 512
Qy 492 AGTATAAACTGGAAGCTTCAGCATCCGGAAGTGAATGGAAGCTTAATGCAAGCTCAG 551
Db 513 AGTATAAACTGGAAGCTTCAGCATCCGGAAGTGAATGGAAGCTTAATGCAAGCTCAG 572
Qy 552 AGAAGCTTGGGATGAGGCTCCCGATGCTTCCCGAGCCCAAGTGTCTGGGCAATCCC 611
Db 573 AGAAGCTTGGGATGAGGCTCCCGATGCTTCCCGAGCCCAAGTGTCTGGGCAATCCC 632
Qy 612 AAGTTGACCAAGGAGCACTTCTCGGAAGTCTCCCAATTCAGAGCTTGAAGCTGAATCTTG 671
Db 633 AAGTTGACCAAGGAGCACTTCTCGGAAGTCTCCCAATTCAGAGCTTGAAGCTGAATCTTG 692
Qy 672 AGAATGTGACATGAAGTGTGTCTGTGCTCTCAATGTTTGAATCAACACATACT 731
Db 693 AGAATGTGACATGAAGTGTGTGTGTGTCTCTCAATGTTTGAATCAACACATACT 752
Qy 732 CCTGTATGATTAAGAAATGACATTTGCCAAGCAACAGGGATATCAAGTGAAGCAATCGG 791
Db 753 CCTGTATGATTAAGAAATGACATTTGCCAAGCAACAGGGATATCAAGTGAAGCAATCGG 812
```

QY 792 AGATCAAAAGGCGAGTACCTACAGCTCTAAACTCAAGGCTTCTGTGTCTCTT 851
| | | | |
Db 813 AGATCAAAAGGCGAGTACCTACAGCTCTAAACTCAAGGCTTCTGTGTCTCTT 872
| | | | |
QY 852 CTTTCTTTGGCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 911
| | | | |
Db 873 CTTTCTTTGGCCATCAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 932
| | | | |
QY 912 GGGCCCTGGCCCAAAAAGCATGCAAGTCATGTTTCAACAGGGATCTACAGAACTAT 971
| | | | |
Db 933 GGGCCCTGGCCCAAAAAGCATGCAAGTCATGTTTCAACAGGGATCTACAGAACTAT 992
| | | | |
QY 972 TTCAACCAAGATATGACCTAGTTTATATTTCTGGAGAAATGATATCATATCTAGA 1031
| | | | |
Db 993 TTCAACCAAGATATGACCTAGTTTATATTTCTGGAGAAATGATATCATATCTAGA 1052
| | | | |
QY 1032 GTCTGGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAGCAGAGAGCTCCAT 1091
| | | | |
Db 1053 GTCTGGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAGCAGAGAGCTCCAT 1112
| | | | |
QY 1092 ATGAACAAGATATATCTATCTTCAAGAGATATTTGAAGTTGGGAAATATTCATGTGA 1151
| | | | |
Db 1113 ATGAACAAGATATATCTATCTTCAAGAGATATTTGAAGTTGGGAAATATTCATGTGA 1172
| | | | |
QY 1152 ACTAGCAAGTGTATGAGAGTATAGTAAATGACAGCTGAGACAGATGATCCGAG 1211
| | | | |
Db 1173 ACTAGCAAGTGTATGAGAGTATAGTAAATGACAGCTGAGACAGATGATCCGAG 1232
| | | | |
QY 1212 ATCTCAGGAGCTCCCTGCTGCTGCTGCTGAGAGTGAAGACAGATATGTCATGTT 1271
| | | | |
Db 1233 ATCTCAGGAGCTCCCTGCTGCTGCTGCTGAGAGTGAAGACAGATATGTCATGTT 1292
| | | | |
QY 1272 CTTTGTCTGTGAATTTTATGTTATATGTCGTAAATGTTGCTGTGAGAAAGCCCTGAA 1331
| | | | |
Db 1293 CTTTGTCTGTGAATTTTATGTTATATGTCGTAAATGTTGCTGTGAGAAAGCCCTGAA 1352
| | | | |
QY 1332 AGTCTATCCCAATATCCCAATCTATATTCACAAATTAAGCTGTATGATGACCTTA 1391
| | | | |
Db 1353 AGTCTATCCCAATATCCCAATCTATATTCACAAATTAAGCTGTATGATGACCTTA 1412
| | | | |
QY 1392 AGACGCTGTAATGACCTGACCTTGCACCTCAGAGGCGGCTGCATTTTATGATGGGT 1451
| | | | |
Db 1413 AGACGCTGTAATGACCTGACCTTGCACCTCAGAGGCGGCTGCATTTTATGATGGGT 1472
| | | | |
QY 1452 CAAATGATCAGCTTTTATGATGCTTCCAAAGTGCTGGCTGCTCCCAACTGACA 1511
| | | | |
Db 1473 CAAATGATCAGCTTTTATGATGCTTCCAAAGTGCTGGCTGCTCCCAACTGACA 1532
| | | | |
QY 1512 AATGCCAAAGTTGAGAAAATATGATCAATATTTAGCATTAACAGACAGTCGCGACACC 1571
| | | | |
Db 1533 AATGCCAAAGTTGAGAAAATATGATCAATATTTAGCATTAACAGACAGTCGCGACACC 1592
| | | | |
QY 1572 GATTTTATATAATTAACCTGACACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
| | | | |
Db 1593 GATTTTATATAATTAACCTGACACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1652
| | | | |
QY 1632 GATGATGTTCAATCCGGAATGATCCAGGAGAGGACCTTTCACCTGACTATATGACATTA 1691
| | | | |
Db 1653 GATGATGTTCAATCCGGAATGATCCAGGAGAGGACCTTTCACCTGACTATATGACATTA 1712
| | | | |
QY 1692 TGTCAATCAGAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGCAGCTAAGACCTCAGT 1751
| | | | |
Db 1713 TGTCAATCAGAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGCAGCTAAGACCTCAGT 1772
| | | | |
QY 1752 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTCCGCCCCCATCTCGGG 1811
| | | | |
Db 1773 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTCCGCCCCCATCTCGGG 1832
| | | | |
QY 1812 GGAATGTCGAAGACAAATTTGGTTACTCAATGAGGAGTGGAGGAGATTCAGTGCCTA 1871
| | | | |
Db 1833 GGAATGTCGAAGACAAATTTGGTTACTCAATGAGGAGTGGAGGAGATTCAGTGCCTA 1892
| | | | |
QY 1872 CTACCAATAGTGATTAAGGCGCAGGAGATGCTGCTCAACTCTCTACCATGTATCAGAGACGT 1931
| | | | |

Db 1893 CTACCAATAGTGATTAAGGCCAGAGATGCTGCTCAACTCTACCATGTATCAGAGACGT 1952
| | | | |
QY 1932 CTCCCATTAATACATACCCATCCGAAGTGTCACTGTGTGAGACCTAAGAAACCTGGT 1991
| | | | |
Db 1953 CTCCCATTAATACATACCCATCCGAAGTGTCACTGTGTGAGACCTAAGAAACCTGGT 2012
| | | | |
QY 1992 TTTGAGTAAAGAGGCGCTGGAAGAGAGGAGCCCAACATCTGTCTGCTT - CTCACAT 2050
| | | | |
Db 2013 TTTGAGTAAAGAGGCGCTGGAAGAGAGGAGCCCAACATCTGTCTGCTTCTCTCACA 2072
| | | | |
QY 2051 AGTCATTTGGCAATTAAGCATTTCTGCTTTTGGCTGCTGCTCAGCAGAGAGCCAGAA 2110
| | | | |
Db 2073 AGTCATTTGGCAATTAAGCATTTCTGCTTTTGGCTGCTGCTCAGCAGAGAGCCAGAA 2132
| | | | |
QY 2111 CTCTATCGGGGACCGAGATTAACATCTCTCAGTGAACAGAGTTGACCAAGGCTATGGGAA 2170
| | | | |
Db 2133 CTCTATCGGGGACCGAGATTAACATCTCTCAGTGAACAGAGTTGACCAAGGCTATGGGAA 2192
| | | | |
QY 2171 TGCCGATGAGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTCATTTCTAAC 2230
| | | | |
Db 2193 TGCCGATGAGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTCATTTCTAAC 2252
| | | | |
QY 2231 CTGCAAGCCAAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
| | | | |
Db 2253 CTGCAAGCCAAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
| | | | |
QY 2291 ATTTGATCTCCAGACCCCTGCTGCGCAATTCATTAAGGCAACAAATATATACCTT 2350
| | | | |
Db 2313 ATTTGATCTCCAGACCCCTGCTGCGCAATTCATTAAGGCAACAAATATATACCTT 2372
| | | | |
QY 2351 CCATGAGCAGACACAGACCTTTTGAAGAGAGCAATGATGCTTGAATGAGGCTTGG 2410
| | | | |
Db 2373 CCATGAGCAGACACAGACCTTTTGAAGAGAGCAATGATGCTTGAATGAGGCTTGG 2432
| | | | |
QY 2411 AGGAATGAAGCTTTGAAGAGAAAGATCTTTGTTTCAAGCCCTTCCACACCTTCA 2470
| | | | |
Db 2433 AGGAATGAAGCTTTGAAGAGAAAGATCTTTGTTTCAAGCCCTTCCACACCTTCA 2492
| | | | |
QY 2471 TGTGTTAACCACTGCTCTGAGACCTTGAAGCCAGGTAAGTATATGATGTTAT 2530
| | | | |
Db 2493 TGTGTTAACCACTGCTCTGAGACCTTGAAGCCAGGTAAGTATATGATGTTAT 2552
| | | | |
QY 2531 AGAAAATGATTTTGAAGCTTGTGATGTTCAAGAGATGATTAATATATATTTCT 2587
| | | | |
Db 2553 AGAAAATGATTTTGAAGCTTGTGATGTTCAAGAGATGATTAATATATATTTCT 2609
| | | | |

RESULT 3
AAH55681
ID AAH55681 standard; DNA; 2627 BP.
XX
AC AAH55681;
XX
DT 04-SEP-2001 (first entry)
XX
DB Human ovarian tumour-derived antigen O8E DNA sequence.
XX
KW Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
XX antigen; O8E; ds.
XX
OS Homo sapiens.
XX
PN MO200140269-A2.
XX
PD 07-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-US032520.
XX
PR 30-NOV-1999; 99US-00451651.
XX 22-FEB-2000; 2000US-00510652.
PR 10-MAR-2000; 2000US-00523586.
PR 07-APR-2000; 2000US-00545068.

PR 15-MAY-2000; 2000US-00571025.
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX WPI: 2001-356154/37.
XX DR N-PSDB; AAB99204, AAB99205.
XX
XX Breast tumor polypeptides and the nucleic acids that encode them, useful
XX PT for the prevention, diagnosis and treatment of breast cancer.
XX
XX Claim 24; Page 189; 221pp; English.
XX
XX The present invention relates to human breast tumour protein coding
XX sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
XX AAH55762). The breast tumour protein DNA sequences may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate expression of the breast tumour protein e.g. breast cancer.
XX The present sequence is a human ovarian tumour-derived antigen coding
XX sequence, which was used in an example from the present invention
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 99.1%; Score 2565; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 12 GGCAGCTCCACAGCCAGTACCCAGATACGCTGGAACTTCCCGCCAGCCATGGCTTCCC 71
DB 33 GGCAGCTCCACAGCCAGTACCCAGATACGCTGGAACTTCCCGCCAGCCATGGCTTCCC 92
QY 72 TGGGGGAGATCTCTTCTTGGAGCATAAATAGCATCATCATTTTCTGGCTGGAGCAATTG 131
DB 93 TGGGGGAGATCTCTTCTTGGAGCATAAATAGCATCATCATTTTCTGGCTGGAGCAATTG 152
QY 132 CACTCATCATTTGGCTTGTGATTTTCAGGGAGACATCCATCAGTACTACTGTGGCCT 191
DB 153 CACTCATCATTTGGCTTGTGATTTTCAGGGAGACATCCATCAGTACTACTGTGGCCT 212
QY 192 CAGCTGGGAACATTTGGGAGATGGAATCCTGAGCTGCATTTTGAACCTGACATCAAC 251
DB 213 CAGCTGGGAACATTTGGGAGATGGAATCCTGAGCTGCATTTTGAACCTGACATCAAC 272
QY 252 TTTTCTGATTCGTGATTCATATGCTGGAAGAGGTGTTTAAAGCTTGTCCATGAGTTCA 311
DB 273 TTTTCTGATTCGTGATTCATATGCTGGAAGAGGTGTTTAAAGCTTGTCCATGAGTTCA 332
QY 312 AAGAAGCAAGATGAGCTGTCGGAAGAGATGAAAATGTTCAAGGCCGGAACAGAGTGT 371
DB 333 AAGAAGCAAGATGAGCTGTCGGAAGAGATGAAAATGTTCAAGGCCGGAACAGAGTGT 392
QY 372 TTGCTGATCAAGTATGATGGAATGCTCTTTGCGGCTGAAAAAGTCAACTCAG 431
DB 393 TTGCTGATCAAGTATGATGGAATGCTCTTTGCGGCTGAAAAAGTCAACTCAG 452
QY 432 ATGCTGGACCTTCAAAATGTTATATCATCTTTAAAGCAAGGGAATGCTAACCTTG 491
DB 453 ATGCTGGACCTTCAAAATGTTATATCATCTTTAAAGCAAGGGAATGCTAACCTTG 512
QY 492 AGATTAATAAAGTGAAGCTTTCAGCATGCGGAAGGAATGGAATTAAGCCAGCTCAG 551
DB 513 AGATTAATAAAGTGAAGCTTTCAGCATGCGGAAGGAATGGAATTAAGCCAGCTCAG 572
QY 552 AGACCTTGGCGGTGAGAGCTCCCGAGATGTTCCCGCCAGCCAGAGTGTGGCAATCCC 611
DB 573 AGACCTTGGCGGTGAGAGCTCCCGAGATGTTCCCGCCAGCCAGAGTGTGGCAATCCC 632
QY 612 AAGTTGACCAAGGAGCACTTCTCGGAAGTCTTCAATACCAAGCTTTGAGCTGAATCTG 671
DB 633 AAGTTGACCAAGGAGCACTTCTCGGAAGTCTTCAATACCAAGCTTTGAGCTGAATCTG 692
QY 672 AGAATGTGACATGAAGGTTGTGTGTGCTTCAATGTTAAGATGAACAACATCACT 731

DB 693 AGAATGTGACATGAAGGTTGTGTGTGCTTCAATGTTAAGATGAACAACATCACTACT 752
QY 732 CCTGTATGATTTGAAAATGATGATTCGCAAGCAACAGGGATATCAAAAGTACAGAAATCGG 791
DB 753 CCTGTATGATTTGAAAATGATGATTCGCAAGCAACAGGGATATCAAAAGTACAGAAATCGG 812
QY 792 AGATCAAAAGGCGGAGCTACCTACAGCTGTAAATCAAAAGGCTTGTGTGTCTCT 851
DB 813 AGATCAAAAGGCGGAGCTACCTACAGCTGTAAATCAAAAGGCTTGTGTGTCTCT 872
QY 852 CTTTCTTGGCATCAAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 911
DB 873 CTTTCTTGGCATCAAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAT 932
QY 912 GTGCTTGGCCACAAAAAAGCATGCAAGATCATTTTACACAGGATCTACCAACTAT 971
DB 933 GTGCTTGGCCACAAAAAAGCATGCAAGATCATTTTACACAGGATCTACCAACTAT 992
QY 972 TTCACACAGATATGACCTAGTTTATATTTCTGGGAGGAATGAATTCATATCTAGAA 1031
DB 993 TTCACACAGATATGACCTAGTTTATATTTCTGGGAGGAATGAATTCATATCTAGAA 1052
QY 1032 GTCTGAGTGAAGCAACAAGCAAGAAACAAGCAAGCCAAAGCCAGAGGCTCCAT 1091
DB 1053 GTCTGAGTGAAGCAACAAGCAAGAAACAAGCAAGCCAAAGCCAGAGGCTCCAT 1112
QY 1092 ATGAACAAGATTAATCTATCTTCAAAAGCATATTTAGAGTTGGGAAATATATCATGTGA 1151
DB 1113 ATGAACAAGATTAATCTATCTTCAAAAGCATATTTAGAGTTGGGAAATATATCATGTGA 1172
QY 1152 ACTAGCAAGTGTGTTAAGATGATAGTAAATGACGTGAGACAGAGCATCCCCAG 1211
DB 1173 ACTAGCAAGTGTGTTAAGATGATAGTAAATGACGTGAGACAGAGCATCCCCAG 1232
QY 1212 ATCTCAGGAGACCTCCCCCTGCTGCTCAGCTGGGAGTGAAGAGACAGATAGTCAATGTT 1271
DB 1233 ATCTCAGGAGACCTCCCCCTGCTGCTCAGCTGGGAGTGAAGAGACAGATAGTCAATGTT 1292
QY 1272 CTTTGTCTGTGAATTTTATGATATGCTGTGATATGTTGCTCTGAGAAAGCCCTGAAA 1331
DB 1293 CTTTGTCTGTGAATTTTATGATATGCTGTGATATGTTGCTCTGAGAAAGCCCTGAAA 1352
QY 1332 AGTCTATCCCAATATCCATCTTATATTCACAAATTAAGCTGTAGATGCTACCTTA 1391
DB 1353 AGTCTATCCCAATATATCCATCTTATATTCACAAATTAAGCTGTAGATGCTACCTTA 1412
QY 1392 AGACGCTGCTAATTTGACCTGCACTTGCAGAACTCAGGGGCGGCTGCATTTTATGATGGGT 1451
DB 1413 AGACGCTGCTAATTTGACCTGCACTTGCAGAACTCAGGGGCGGCTGCATTTTATGATGGGT 1472
QY 1452 CAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1511
DB 1473 CAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1532
QY 1512 AATGCCAAGTTGAGAAAATGATCATATTTTGAATGAAGACAGACAGTGGCGGACACC 1571
DB 1533 AATGCCAAGTTGAGAAAATGATCATATTTTGAATGAAGACAGACAGTGGCGGACACC 1592
QY 1572 GATTTTATTAATAAATGAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
DB 1593 GATTTTATTAATAAATGAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1652
QY 1632 GATGATGTTTCATCGTAATGCTGACAGGAAGACCTTTTACCTTATATATGCAATTA 1691
DB 1653 GATGATGTTTCATCGTAATGCTGACAGGAAGACCTTTTACCTTATATATGCAATTA 1712
QY 1692 TGTGATCAAAAGTCTGAGGCTTCTGCTTCCATCTGTGGTGAAGAGCTTAAGCTCAAGT 1751
DB 1713 TGTGATCAAAAGTCTGAGGCTTCTGCTTCCATCTGTGGTGAAGAGCTTAAGCTCAAGT 1772
QY 1752 TTTCAATAGCATATGAGAGATGGAAGTCTGAGCTGGGATATTTGCCCCCATCTCGGAG 1811

Db 1773 TTTCATATGATCATAGAGGAGTGGGAGCTGAGCTGGGGGTGATTTCCGCCCCCATCTCCGGG 1832
Qy 1812 GGAATGTCGAAAGACAATTTTGGTTAAGCTTCAATGAGGAGTGGAGAGATCACTGCTA 1871
Db 1833 GGAATGTCGAAAGACAATTTTGGTTAAGCTTCAATGAGGAGTGGAGAGATCACTGCTA 1892
Qy 1872 CTACCAACTAGTGGATTAAGGAGCAGGAGATGCTGCTCAACTCTCAATGATGACAGAGAT 1931
Db 1893 CTACCAACTAGTGGATTAAGGAGCAGGAGATGCTGCTCAACTCTCAATGATGACAGAGAT 1952
Qy 1932 CTCCCCATTACAACTAACCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTGTGT 1991
Db 1953 CTCCCCATTACAACTAACCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTGTGT 2012
Qy 1992 TTTGAGTAAAGAGGCTTGGAAAGAGGAGAGCTCAAAATCTGTCTGCTT-CTCAACT 2050
Db 2013 TTTGAGTAAAGAGGCTTGGAAAGAGGAGAGCTCAAAATCTGTCTGCTTCTCAACT 2072
Qy 2051 AGTCATTTGGCAATTAAGCATCTGTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2110
Db 2073 AGTCATTTGGCAATTAAGCATCTGTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2132
Qy 2111 CTCTATCGGAGCACAGATTAACATCTCTAGTGAAGAGATTAAGAGCTTAAGGAGAA 2170
Db 2133 CTCTATCGGAGCACAGATTAACATCTCTAGTGAAGAGATTAAGAGCTTAAGGAGAA 2192
Qy 2171 TGGCTATGGGATTAATCTTCAAGTGTGAGCTTCAAGTTCTTCCCTTCACTTAC 2230
Db 2193 TGGCTATGGGATTAATCTTCAAGTGTGAGCTTCAAGTTCTTCCCTTCACTTAC 2252
Qy 2231 CTGCAAGCCAAAGTTCTGTGAAGAAATGCTGATCTAGCTCAGGCTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAAGTTCTGTGAAGAAATGCTGATCTAGCTCAGGCTTCTTACTCTGA 2312
Qy 2291 ATTATGATCTCCAGACCTTCTCTGAGCACAAATTAAGGCAACAAATATACCTT 2350
Db 2313 ATTATGATCTCCAGACCTTCTCTGAGCACAAATTAAGGCAACAAATATACCTT 2372
Qy 2351 CCATGAGACACACAGACTTTTGAAGCAAGACATGACTTGAATGAGGCTTG 2410
Db 2373 CCATGAGACACACAGACTTTTGAAGCAAGACATGACTTGAATGAGGCTTG 2432
Qy 2411 AGGAATGAGCTTTGAAGAAAGAAATCTTGTTCAGACCCCTTCCCACTCTTCA 2470
Db 2433 AGGAATGAGCTTTGAAGAAAGAAATCTTGTTCAGACCCCTTCCCACTCTTCA 2492
Qy 2471 TGTGTTAACCACTGCTTCTCTGAGCCTTGAAGCCAGCTGATGTAATCATGTTGTAT 2530
Db 2493 TGTGTTAACCACTGCTTCTCTGAGCCTTGAAGCCAGCTGATGTAATCATGTTGTAT 2552
Qy 2531 AGAAACTGATTTTGAAGTTCTGATGTTCAAGAGATGTAATATATCATTTCT 2587
Db 2553 AGAAACTGATTTTGAAGTTCTGATGTTCAAGAGATGTAATATATCATTTCT 2609

RESULT 4
ABN72971
ID ABN72971 standard; DNA; 2627 BP.
XX
AC ABN72971;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma polynucleotide O8B.
XX
KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; de.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX

PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00678857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
XX (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Piling SP, Retler MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill F, Albone E;
XX
DR WPI; 2002-164781/21.
P-PSDB; ABP30900, ABP30901.
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
PS Example 2; Page 319-320; 408pp; English.
XX
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents DNA related
CC to the invention
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 99.1%; Score 2565; DB 6; Length 2627;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;

Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCCACTCAGCAGCAGTACCCAGATACGCTGGAACTTCCCACTGCTTCC 71
Db 33 GGCAGCTCCACTCAGCAGCAGTACCCAGATACGCTGGAACTTCCCACTGCTTCC 92
Qy 72 TGGGCGAGATCTCTTCTGAGACATTAATGATCATATTTCTGCTGGAGCAATTG 131
Db 93 TGGGCGAGATCTCTTCTGAGACATTAATGATCATATTTCTGCTGGAGCAATTG 152
Qy 112 CACTCATGATGGCTTGGTATTTTCAAGGAGACATCTCATGACTGCTGCT 191
Db 153 CACTCATGATGGCTTGGTATTTTCAAGGAGACATCTCATGACTGCTGCTGCT 212
Qy 192 CAGCTGGAAACATTTGGGAGAGATGGAATCTGAGCTGACCTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGGAAACATTTGGGAGAGATGGAATCTGAGCTGACCTTTGAACCTGACATCAAC 272
Qy 252 TTTCTGATATCTGATTAACAATGCTGAAGAAAGTGTTTTGAAGCTTGTGATGATGCTCA 311
Db 273 TTTCTGATATCTGATTAACAATGCTGAAGAAAGTGTTTTGAAGCTTGTGATGATGCTCA 332
Qy 312 AAGAAAGCAAGATGAGCTGCTGAGCAGATGAATGTTCAAGAGCCGAGCAGAGTGT 371
Db 333 AAGAAAGCAAGATGAGCTGCTGAGCAGATGAATGTTCAAGAGCCGAGCAGAGTGT 392
Qy 372 TTTGCTATCAATGATTAAGTTGCAATGCTTCTTGGCTGAAACCTGCACTCAAG 431
Db 393 TTTGCTATCAATGATTAAGTTGCAATGCTTCTTGGCTGAAACCTGCACTCAAG 452
Qy 432 ATGCTGGACCTTAACAATGTTATATCATCTTTAAAGGCAAGGGAATGTTAATCTTG 491
Db 453 ATGCTGGACCTTAACAATGTTATATCATCTTTAAAGGCAAGGGAATGTTAATCTTG 512
Qy 492 AGTATTAACCTGAGACCTTCAAGCATGCCGGAAGTAATGAGCTATTAATGACAGTNG 551
Db 513 AGTATTAACCTGAGACCTTCAAGCATGCCGGAAGTAATGAGCTATTAATGACAGTNG 572
Qy 552 AGACCTTGGGATGATGAGGCTCCCGATGATTCCTCCAGCCCAAGTGTCTTGGGATCCC 611

Db 573 AGACCTGGCGGTGGAAGCTCCCGATGGTTCCTCCCGACCCCAAGTGTGTCTGGGCATCCC 632
Qy 612 AAGTTGACGAGGAGCCCACTTCTCGGAAGTCTCCATACCAGTTTGAAGTGAAGTCTG 671
Db 633 AAGTTGACGAGGAGCCCACTTCTCGGAAGTCTCCATACCAGTTTGAAGTGAAGTCTG 692
Qy 672 AGATGAGCATGAAGTGTGTGTCTGTGCTGCAATGTTAGATGAACAACATACCT 731
Db 693 AGAATGAGCATGAAGT 752
Qy 732 CCTGTATGATGAAATGACATTCGCAAGCAACAGGGATATCAAGATGACAGATCG 791
Db 753 CCGTATGATGAAATGACATTCGCAAGCAACAGGGATATCAAGATGACAGATCG 812
Qy 792 AGATCAAAAGGCGAGTCACTTACAGTGTCTAACTCAAGGCTTCTGTGTGTCTT 851
Db 813 AGATCAAAAGGCGAGTCACTTACAGTGTCTAACTCAAGGCTTCTGTGTGTCTT 872
Qy 852 CTTTCTTGTGCTAGCTGGGCACTTGTGCTGTACGCTTACCTGATGCTAAATAT 911
Db 873 CTTTCTTGTGCTAGCTGGGCACTTGTGCTGTACGCTTACCTGATGCTAAATAT 932
Qy 912 GTGCTTGGCCACAAAAAGCATGCAAGTCAATGTTTACAAAGGATCTACAGAACTAT 971
Db 933 GTGCTTGGCCACAAAAAGCATGCAAGTCAATGTTTACAAAGGATCTACAGAACTAT 992
Qy 972 TTTCAACCAAGATATGACCTAGTTTATTTCTGGAGAGAAATGAAATCATATCTAGAA 1031
Db 993 TTTCAACCAAGATATGACCTAGTTTATTTCTGGAGAGAAATGAAATCATATCTAGAA 1052
Qy 1032 GTCTGGAGTGAAGCAACAGACAGAAACAAAAGAGCCAAAGAGAGAGCTCCAT 1091
Db 1053 GTCTGGAGTGAAGCAACAGACAGAAACAAAAGAGCCAAAGAGAGAGCTCCAT 1112
Qy 1092 ATGAACAAGATTAATCTATCTTCAAAAGACATATTAGAAATGGGAAATATTCATGTGA 1151
Db 1113 ATGAACAAGATTAATCTATCTTCAAAAGACATATTAGAAATGGGAAATATTCATGTGA 1172
Qy 1152 ACTAGACAGTGTGTTAAGAGTATAGTAAATGACGTTGAGACAGATGCAATCCCGAG 1211
Db 1173 ACTAGACAGTGTGTTAAGAGTATAGTAAATGACGTTGAGACAGATGCAATCCCGAG 1232
Qy 1212 ATCTCAGGAGCTCCCCCTGCTGTACCTGGGAGTGAAGAGACAGATAGTGCAT 1271
Db 1233 ATCTCAGGAGCTCCCCCTGCTGTACCTGGGAGTGAAGAGACAGATAGTGCAT 1292
Qy 1272 CTTTGTCTCTGAATTTTAACTTATATGTGCTGTATGTTGCTCTGAGGAAAGCCCTGGAA 1331
Db 1293 CTTTGTCTCTGAATTTTAACTTATATGTGCTGTATGTTGCTCTGAGGAAAGCCCTGGAA 1352
Qy 1332 AGTCTATCCCAACATATCCATCTTATATTCACAAATTAAGCTGTATGATATACCTTA 1391
Db 1353 AGTCTATCCCAACATATCCATCTTATATTCACAAATTAAGCTGTATGATATACCTTA 1412
Qy 1392 AGAGCTGCTAATTTGATGCTGCACTGCACTGAGGAGGAGCTGCAATTTAATGATAGGCT 1451
Db 1413 AGAGCTGCTAATTTGATGCTGCACTGCACTGAGGAGGAGCTGCAATTTAATGATAGGCT 1472
Qy 1452 CAATGATTTCACTTTTATGATGCTTCAAAAGTGTGCTTCTCTTCCCACTGAC 1511
Db 1473 CAATGATTTCACTTTTATGATGCTTCAAAAGTGTGCTTCTCTTCCCACTGAC 1532
Qy 1512 AATGCCAAAGTTGAGAAAAATGATCATATTTTAAAGATAACAGAGAGTGGCGACACC 1571
Db 1533 AATGCCAAAGTTGAGAAAAATGATCATATTTTAAAGATAACAGAGAGTGGCGACACC 1592
Qy 1572 GATTTATATAAATAACAGAGACCTTCTTTTAAACAAATGAGGAGTTATTTCTCA 1631
Db 1593 GATTTATATAAATAACAGAGACCTTCTTTTAAACAAATGAGGAGTTATTTCTCA 1652
Qy 1632 GATGATGTTCACTCGTGAATGTCTCAGGAGAGACCTTTCACCTGATGCTATGCACTTA 1691

Db 1653 GATGATGTTCACTCGTGAATGTCTCAGGAGAGACCTTTCACCTGATGCTATGCACTTA 1712
Qy 1692 TGTATATCAAGAGTCTGAGGCTTCTCTTCCATCTCTGGTGAAGAGTGAAGCTTCACT 1751
Db 1713 TGTATATCAAGAGTCTGAGGCTTCTCTTCCATCTCTGGTGAAGAGTGAAGCTTCACT 1772
Qy 1752 TTTCAATAGCATATGAGAGAGTGGAGCTCAGAGTGGGAGTATTTGAGGAGGAGTGGAG 1811
Db 1773 TTTCAATAGCATATGAGAGAGTGGAGCTCAGAGTGGGAGTATTTGAGGAGGAGTGGAG 1832
Qy 1812 GGAATGTCTGAGACAAATTTTGGTTACTTCAATGAGGAGTGAAGAGATACAGTGTCTA 1871
Db 1833 GGAATGTCTGAGACAAATTTTGGTTACTTCAATGAGGAGTGAAGAGATACAGTGTCTA 1892
Qy 1872 CTACCAACTAGTGAATTAAGAGGCGAGGAGTGTCTCAACTCTTACCATGTATACAGAGCT 1931
Db 1893 CTACCAACTAGTGAATTAAGAGGCGAGGAGTGTCTCAACTCTTACCATGTATACAGAGCT 1952
Qy 1932 CTCCCATTTACAACTACCCCAATCCGAAGTGTCACTGTGTCAAGAGCTTAAGAAACCTGT 1991
Db 1953 CTCCCATTTACAACTACCCCAATCCGAAGTGTCACTGTGTCAAGAGCTTAAGAAACCTGT 2012
Qy 1992 TTTGAGTGAAGAAAGGCTGGAAGAGGAGGAGCCAAATCTGTCTCTT-CTCACTT 2050
Db 2013 TTTGAGTGAAGAAAGGCTGGAAGAGGAGGAGCCAAATCTGTCTCTTCACTT 2072
Qy 2051 AGTCAATTTGCAATTAAGCAATCTGTCTCTTGTGCTGTCTGTCTGTCTGTCTGTCTGT 2110
Db 2073 AGTCAATTTGCAATTAAGCAATCTGTCTCTTGTGCTGTCTGTCTGTCTGTCTGTCTGT 2132
Qy 2111 CTCTATCGGAGCACAGAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTATGGGAAA 2170
Db 2133 CTCTATCGGAGCACAGAGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTATGGGAAA 2192
Qy 2171 TGCCTGATGGAGTTATCTTCAAGTGTGTGAGCTTCTAAGTTCTTCCCTCACTTAC 2230
Db 2193 TGCCTGATGGAGTTATCTTCAAGTGTGTGAGCTTCTAAGTTCTTCCCTCACTTAC 2252
Qy 2231 CTGCAAGCCCAAGTCTGTGAAGAGAAATGCTGTGAGTCTAGCTCAAGTCTTCTTCACTGTA 2290
Db 2253 CTGCAAGCCCAAGTCTGTGAAGAGAAATGCTGTGAGTCTAGCTCAAGTCTTCTTCACTGTA 2312
Qy 2291 ATTATGATCTCCAGACCTTCTGAGCACAATTCATTAAGGCAACAATATATACCTT 2350
Db 2313 ATTATGATCTCCAGACCTTCTGAGCACAATTCATTAAGGCAACAATATATACCTT 2372
Qy 2351 CCATGAAGCACACAGACTTTTGAAGAGAGACATATGCTTGAATGAGGCTTG 2410
Db 2373 CCATGAAGCACACAGACTTTTGAAGAGAGACATATGCTTGAATGAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAGAAATACCTTGTTCAGGCCCTTCCCACTTCTTA 2470
Db 2433 AGGAATGAAGCTTTGAAGAGAAATACCTTGTTCAGGCCCTTCCCACTTCTTA 2492
Qy 2471 TGTGTAAACACGCTCTCTGAGCCTTGGAGCAGGAGTGTATCATGTTGTAT 2530
Db 2493 TGTGTAAACACGCTCTCTGAGCCTTGGAGCAGGAGTGTATCATGTTGTAT 2552
Qy 2531 AGAAAACTGATTTTGAAGTCTGATGCTTCAAGAGATGATTAATATATCATTTCT 2587
Db 2553 AGAAAACTGATTTTGAAGTCTGATGCTTCAAGAGATGATTAATATATCATTTCT 2609

RESULT 5
ADA08544
ID ADA08544 standard; cDNA; 2627 BP.

ADA08544:

AC ADA08544:
XX
XX 06-NOV-2003 (first entry)
XX
XX Human ovarian carcinoma polynucleotide OBE.
XX

KW ss; human; gene therapy; ovarian cancer; cancer.

OS Homo sapiens.

PN US2003091580-A1.

PD 15-MAY-2003.

AA 17-JUL-2001; 2001US-00907969.

PR 18-JUN-2001; 2001US-00884441.

XX
PA (MITC/) MITCHAM J L.

PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.

PA (ELIN/) ELING S P.
PA (RETT/) RETTER M W.

PA (FANG/) FANGER G R.
PA (REED/) REED S G.

PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D

PA (HILL/) HILL P.
PA (ALBO/) ALBONE E

XX	Mitcham	TT	Vino	CE
BT				

PI Reed SG, Vedvick TS

DR WPI; 2003-532352/50.

PT New isolated 0772P

PT cancer.

PS	Example 2; SEQ ID NO
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

The invention relates to

the polypeptides, pc

CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen polynucleotide.

Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 99.1%; Score 2565; DB 9; Length 2627;

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

QY	12	GGCAGCTCCACTCAGCCAGTACCAGATACGCTGGGAACCTTCCCGAGCATGGCTTCCC	71
Db	33	GGCAGCTCCACTCAGCCAGTACCAGATACGCTGGGAACCTTCCCGAGCATGGCTTCCC	92
QY	72	TGGGGCAGATCCTCTTCGTGAGCATTAATAGATCTACTTATTCGTGGCTGGAGCAATTG	131
Db	93	TGGGGCAGATCCTCTTCGTGAGCATTAATAGATCTACTTATTCGTGGCTGGAGCAATTG	152
QY	132	CACCTGATCATTTGGCTTTGGTATTTACGGAGACATCCATCAGTCAGTCAGTCAGCT	191
Db	153	CACCTGATCATTTGGCTTTGGTATTTACGGAGACATCCATCAGTCAGTCAGTCAGCT	212
QY	192	CAGCTGGGAACATTTGGGGAGATGGAATCCTGAGCTGCACCTTTGAACCTGCATCAAAC	251
Db	213	CAGCTGGGAACATTTGGGGAGATGGAATCCTGAGCTGCACCTTTGAACCTGCATCAAAC	272
QY	252	TTTTCGATATCGATGATACATGGCTGAAGGAAGGTGTTTAAGGCTGGTCCATGAGTCA	311
Db	273	TTTTCGATATCGATGATACATGGCTGAAGGAAGGTGTTTAAGGCTGGTCCATGAGTCA	332
QY	312	AAGAAAGCAAAAGATGAGCTGTGCGAGCAGAGTGAATGTTTCAGAGGCGGACACGACGTG	371

Db	333	AAGAAGCAAAAGATGAGCTGTGCGAGCAGAGATGAAATGTTTCAGAGGCCGAGCAGCACTGT	392
Qy	372	TTGCGATCAAGTATAGTTGGCAATGCTCTTTGGGCTGTGAAAACTGCAACTCAAG	431
Db	393	TTGCGATCAAGTATAGTTGGCAATGCTCTTTGGGCTGTGAAAACTGCAACTCAAG	452
Qy	432	ATGCTGGGCACTCAAAATGTTATATCATCTTTAAAGGCAAGGGGAATGCTAACCTTG	491
Db	453	ATGCTGGGCACTCAAAATGTTATATCATCTTTAAAGGCAAGGGGAATGCTAACCTTG	512
Qy	492	AGTATPAAAACCTGGAGCCCTTCAGATGCGCGAAGGAATGTGACTATATATGCCAGCTCAG	551
Db	513	AGTATPAAAACCTGGAGCCCTTCAGATGCGCGAAGGAATGTGACTATATATGCCAGCTCAG	572
Qy	552	AGACCTTGCGGATGTGAGGCTCCCGATGTTTCCCGACGCCACAGTGGTCTGGGCATCCC	611
Db	573	AGACCTTGCGGATGTGAGGCTCCCGATGTTTCCCGACGCCACAGTGGTCTGGGCATCCC	632
Qy	612	AAAGTTGACCAAGGAGCCCACTTCTCGGAAGTCTCCATATCCAGCTTTGAGTGAACCTCG	671
Db	633	AAAGTTGACCAAGGAGCCCACTTCTCGGAAGTCTCCATATCCAGCTTTGAGTGAACCTCG	692
Qy	672	AGAAATGTCACATGAAAGGTTGTCTGTGCTCTCAATGTTACATGATCAACACATCACT	731
Db	693	AGAAATGTCACATGAAAGGTTGTGTCTGTGCTCTCAATGTTACATGATCAACACATCACT	752
Qy	732	CCTGTATGATTTGAAAATATGACATTGTCCAAAGCACAAGGGGATATCAAAAGTACAGAACTCG	791
Db	753	CCTGTATGATTTGAAAATATGACATTGTCCAAAGCACAAGGGGATATCAAAAGTACAGAACTCG	812
Qy	792	AGATTAATAAGGCGGAGTCACTTACAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTCTT	851
Db	813	AGATTAATAAGGCGGAGTCACTTACAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTCTT	872
Qy	852	CTTTCTTTTGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAAAATAT	911
Db	873	CTTTCTTTTGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAAAATAT	932
Qy	912	GTGCTTGCGCCACAATAAAAGCATCAAAAGTCAATGTTTACAACAGGAGTCTACAGAACTAT	971
Db	933	GTGCTTGCGCCACAATAAAAGCATCAAAAGTCAATGTTTACAACAGGAGTCTACAGAACTAT	992
Qy	972	TTTACCAACAAGATATGACCTTATGTTTATATTTCTGGGAGGAATGAATTCATATCTTGAA	1031
Db	993	TTTACCAACAAGATATGACCTTATGTTTATATTTCTGGGAGGAATGAATTCATATCTTGAA	1052
Qy	1032	GTTCTGGAATGTAGCAAAACAAGCAAGAAACAATAAAGCAACCAAGAGAGAAAGGCTCAAT	1091
Db	1053	GTTCTGGAATGTAGCAAAACAAGCAAGAAACAATAAAGCAACCAAGAGAGAAAGGCTCAAT	1112
Qy	1092	ATGAACAAGATPAAATCTATCTTCAAAGCATATTTAGAAAGTTGGGAAAATATTCATGTGA	1151
Db	1113	ATGAACAAGATPAAATCTATCTTCAAAGCATATTTAGAAAGTTGGGAAAATATTCATGTGA	1172
Qy	1152	ACTAGACAAGTGTGTTAAGAGTGAATAGTAAATATGACAGTGGAGACAAGTGCACTCCAG	1211
Db	1173	ACTAGACAAGTGTGTTAAGAGTGAATAGTAAATATGACAGTGGAGACAAGTGAATGTGCA	1232
Qy	1212	ATTCACAGGAGCTCCCGCTGCTGTACCTGGGGAGTGAAGGACAGGATATGTCATGTT	1271
Db	1233	ATTCACAGGAGCTCCCGCTGCTGTACCTGGGGAGTGAAGGACAGGATATGTCATGTT	1292
Qy	1272	CTTTGTCTCTGAATTTTAAAGTTATATGTCGTATGTGCTCTGAGGAAGCCCTTGAA	1331
Db	1293	CTTTGTCTCTGAATTTTAAAGTTATATGTCGTATGTGCTCTGAGGAAGCCCTTGAA	1352
Qy	1332	AGCTATATCCAAATATACATCTTATATTCACAAATTAAGCTGTATGATGACCTTA	1391
Db	1353	AGCTATATCCAAATATACATCTTATATTCACAAATTAAGCTGTATGATGACCTTA	1412
Qy	1392	AGACGCTGCTAATTTGACCTGCACTTTCCGAATCAGGGGGCGGCTGCATTTTAAGTAAATGGGT	1451
Db	1413	AGACGCTGCTAATTTGACCTGCACTTTCCGAATCAGGGGGCGGCTGCATTTTAAGTAAATGGGT	1472

QY 1452 CAATGATTCATTTTATGATGCTTCCAAAGGCTGGCTTCTTCCCACTGACA 1511
DB 1473 CAATGATTCATTTTATGATGCTTCCAAAGGCTGGCTTCTTCCCACTGACA 1532
QY 1512 AATGCCAAAGTTGAGAAAATGATCATATTTTATGATTAAGAGAGAGTGGCGACACC 1571
DB 1533 AATGCCAAAGTTGAGAAAATGATCATATTTTATGATTAAGAGAGAGTGGCGACACC 1592
QY 1572 GATTTTATTAATTAAGTACGACACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCA 1631
DB 1593 GATTTTATTAATTAAGTACGACACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCA 1652
QY 1632 GATGATGTTGATCGGTAATGTCGAGGGAAGACCTTTCACCTTGATCTATATGGAATTA 1691
DB 1653 GATGATGTTGATCGGTAATGTCGAGGGAAGACCTTTCACCTTGATCTATATGGAATTA 1712
QY 1692 TGTTCATCACAAGCTGTGAGGCTTCTCTTTCATCTCGTGAAGAGTAAAGACTCAGT 1751
DB 1713 TGTTCATCACAAGCTGTGAGGCTTCTCTTTCATCTCGTGAAGAGTAAAGACTCAGT 1772
QY 1752 TTTCAATAGCATTTAGAGCAGTGGGACTCAGCTGGGGTGATTTTGGCCCCCATCTCGGG 1811
DB 1773 TTTCAATAGCATTTAGAGCAGTGGGACTCAGCTGGGGTGATTTTGGCCCCCATCTCGGG 1832
QY 1812 GGAATGTCGAGAACATTTTGGTTACCTCAATGAGGAGATGAGAGATAGAGTCTTA 1871
DB 1833 GGAATGTCGAGAACATTTTGGTTACCTCAATGAGGAGATGAGAGATAGAGTCTTA 1892
QY 1872 CTACCAACTAGTGAATTAAGGCGAGGATCTGCTCAACTCTTACCATATAGAGACGT 1931
DB 1893 CTACCAACTAGTGAATTAAGGCGAGGATCTGCTCAACTCTTACCATATAGAGACGT 1952
QY 1932 CTCCCATTTTCAACTCACTCCCAATCCGAACTGTCACTGTGTCAAGACTAAGAAACCTGTGT 1991
DB 1953 CTCCCATTTTCAACTCACTCCCAATCCGAACTGTGTCAAGACTAAGAAACCTGTGT 2012
QY 1992 TTTGAGTGAAGAAAGGCGTGGAAAGAGGGGACCAAAATCTGTCTGCTT-CTCACTT 2050
DB 2013 TTTGAGTGAAGAAAGGCGTGGAAAGAGGGGACCAAAATCTGTCTGCTTCTCACTT 2072
QY 2051 AGTCATTTGGCAAAATTAAGCATTTCTGTCTTTTGGCTGTGCTGAGACAGAGAGCCAGAA 2110
DB 2073 AGTCATTTGGCAAAATTAAGCATTTCTGTCTTTTGGCTGTGCTGAGACAGAGAGCCAGAA 2132
QY 2111 CTCTATCGGGCACAGGATTAATCTCTCTCACTGTAAGAGTGAACAAGGCTTATGGGAAA 2170
DB 2133 CTCTATCGGGCACAGGATTAATCTCTCTCACTGTAAGAGTGAACAAGGCTTATGGGAAA 2192
QY 2171 TGGCTGATGGGATTAATCTCTCACTGTAAGGCTTCTTAACTTCTTCCCTCACTTAC 2230
DB 2193 TGGCTGATGGGATTAATCTCTCACTGTAAGGCTTCTTAACTTCTTCCCTCACTTAC 2252
QY 2231 CTGCAAGCCAAAGTTCTGTAAGAAAATGCTGAGTTCTAGGCTTCTTCTTCTTCTGTA 2290
DB 2253 CTGCAAGCCAAAGTTCTGTAAGAAAATGCTGAGTTCTAGGCTTCTTCTTCTTCTGTA 2312
QY 2291 ATTTAGATCTCGAGACCTTCTCTGCGCACAATTCAAATTAAGCAACAACATATACCTT 2350
DB 2313 ATTTAGATCTCGAGACCTTCTCTGCGCACAATTCAAATTAAGCAACAACATATACCTT 2372
QY 2351 CCATTAAGGACACACAGACTTTTGAAGGAAAGACATATGCTTGAATTAAGGAGCTTG 2410
DB 2373 CCATTAAGGACACACAGACTTTTGAAGGAAAGACATATGCTTGAATTAAGGAGCTTG 2432
QY 2411 AGGAATGAAGCTTTGAAGGAAAGAAATACCTTTTTCAGAGCCCTTCCCACTCTTCA 2470
DB 2433 AGGAATGAAGCTTTGAAGGAAAGAAATACCTTTTTCAGAGCCCTTCCCACTCTTCA 2492
QY 2471 TGTGTTAAACCACTGCTTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTGTAT 2530
DB 2493 TGTGTTAAACCACTGCTTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTGTAT 2552

QY 2531 AGAAACGATTTTATGATGCTTCAAGAGATGATTAATATATATTCCT 2587
DB 2553 AGAAACGATTTTATGATGCTTCAAGAGATGATTAATATATATTCCT 2609

RESULT 6
ADF08887
ID ADF08887 standard; cDNA; 2627 BP.
XX
AC ADF08887;
XX
DT 12-FEB-2004 (first entry)
XX
DE cDNA encoding secreted ovarian carcinoma antigen seqid 391.
XX
KW gene therapy; protein therapy; vaccine; antibody inhibition;
KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
KW secreted ovarian carcinoma antigen; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003124140-A1.
XX
PD 03-JUL-2003.
XX
PF 17-JUL-2002; 2002US-00198053.
XX
PR 17-DEC-1998; 98US-00215681.
XX
PR 17-DEC-1998; 98US-00216003.
XX
PR 23-JUN-1999; 99US-00338933.
XX
PR 24-SEP-1999; 99US-00404879.
XX
PR 17-JUL-2000; 2000US-00617747.
XX
PR 10-AUG-2000; 2000US-00636801.
XX
PR 20-SEP-2000; 2000US-00667857.
XX
PR 04-APR-2001; 2001US-00827271.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PR 17-JUL-2001; 2001US-00907969.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Retter MW, Fanger GR, Hill P;
XX
DR WPI; 2003-897152/82.
XX
PT P-PSDB; ADF08888, ADF08889.
XX
PT Oncogenic nucleic acids useful for the prevention, diagnosis and
XX treatment of breast cancer.
XX
PS Example 2; SEQ ID NO 391; 399pp; English.
XX
XX The invention describes nucleic acids (I) and the polypeptides (II) they
XX encode. The nucleic acids (I) may be used for preventing, diagnosing and
XX treating diseases related to their aberrant expression i.e. breast
XX cancers. For example, (I) and (II) may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of (II) by expressing
XX inactive proteins or to supplement the patient's own production of (II).
XX Additionally, (I) may be used to produce (II), by inserting (I) into a
XX host cell and culturing the cell to express the protein (II). (I) and its
XX complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantify the presence of similar nucleic acids in
XX samples, and therefore which patients may be in need of restorative
XX therapy. The host cell may also be used as antigens in the production of
XX antibodies against (II) and in assays to identify modulators of (II)'s
XX expression and activity. The anti-(II) antibodies, agonists and
XX antagonists may be used to regulate expression and activity and as
XX diagnostic agents for detecting the presence of (II) in samples (e.g. by
XX immunoassay). This sequence represents a polynucleotide encoding a
XX secreted ovarian carcinoma antigen.
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 99.1%; Score 2565; DB 10; Length 2627;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 12 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCAGCATGGCTTCCC 71
Db 33 GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCAGCATGGCTTCCC 92
QY 72 TGGGGCAGATCCTCTTCTGAGCATTAATAGCATCATTAATTCTGGCTGGAGCAATTG 131
Db 93 TGGGGCAGATCCTCTTCTGAGCATTAATAGCATCATTAATTCTGGCTGGAGCAATTG 152
QY 132 CACTCATCTTGGCTTGGTATTTTCAAGGAGACATCCATCAAGTCACTACTGTGCGCT 191
Db 153 CACTCATCTTGGCTTGGTATTTTCAAGGAGACATCCATCAAGTCACTACTGTGCGCT 212
QY 192 CAGCTGGGAACTTGGGGAGATGGAATCTGAGCTGCATTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGGAACTTGGGGAGATGGAATCTGAGCTGCATTTTGAACCTGACATCAAC 272
QY 252 TTTCTGATTCGTGATACAAATGGCTGAAGGAAGTGTATTAGGCTTGGTCCATGAGTTCA 311
Db 273 TTTCTGATTCGTGATACAAATGGCTGAAGGAAGTGTATTAGGCTTGGTCCATGAGTTCA 332
QY 312 AAGAAAGCAAGATGAGCTGTGAGCAGAGATGAAATGTTCAAGGCGCGAGCAGAGTGT 371
Db 333 AAGAAAGCAAGATGAGCTGTGAGCAGAGATGAAATGTTCAAGGCGCGAGCAGAGTGT 392
QY 372 TTGCTGATCAATGATAGTTGGCAATGCTCTTTTGGGCTGAAAAACCTGACATCAAG 431
Db 393 TTGCTGATCAATGATAGTTGGCAATGCTCTTTTGGGCTGAAAAACCTGACATCAAG 452
QY 432 ATGCTGGCAGCTACAAATGTTATATCATCACTCTTAAAGCAAGGGAAATGCTAACTTG 491
Db 453 ATGCTGGCAGCTACAAATGTTATATCATCACTCTTAAAGCAAGGGAAATGCTAACTTG 512
QY 492 AGTATPAAACTGAGAGCTTTCAGCATGCGGAAGTGAATGATGATTAATATGCTCACTG 551
Db 513 AGTATPAAACTGAGAGCTTTCAGCATGCGGAAGTGAATGATGATTAATATGCTCACTG 572
QY 552 AAGCTTGGGGTGTAGAGCTTCCCGCATGTTTCCCGACGCCACAGTGTCTGGGCACTCC 611
Db 573 AAGCTTGGGGTGTAGAGCTTCCCGCATGTTTCCCGACGCCACAGTGTCTGGGCACTCC 632
QY 612 AAGTTGACAGGAGGCACTTCTCGGAAGTCTCCAAATCAGACTTGGAGTGAAGTCTG 671
Db 633 AAGTTGACAGGAGGCACTTCTCGGAAGTCTCCAAATCAGACTTGGAGTGAAGTCTG 692
QY 672 AAGATGTGACATGAAAGTGTGTCTGCTCTTCAATGTTTACATCAACACACTACT 731
Db 693 AAGATGTGACATGAAAGTGTGTCTGCTCTTCAATGTTTACATCAACACACTACT 752
QY 732 CCTGTATGATTTGAAAATGACATTTGCCAAGCAACAGGGATATCAAAAGTGAACAGATCG 791
Db 753 CCTGTATGATTTGAAAATGACATTTGCCAAGCAACAGGGATATCAAAAGTGAACAGATCG 812
QY 792 AGATCAAAAGGCGAGTCACTTACAGCTGCTAAACTCAAAAGGCTTCTGTGTCTCTT 851
Db 813 AGATCAAAAGGCGAGTCACTTACAGCTGCTAAACTCAAAAGGCTTCTGTGTCTCTT 872
QY 852 CTTTCTTTTGCATCAGCTGGGACATTTCTGCTCTCAGGCCCTTACCTGATGCTAAATAAT 911
Db 873 CTTTCTTTTGCATCAGCTGGGACATTTCTGCTCTCAGGCCCTTACCTGATGCTAAATAAT 932
QY 912 GTGCTTGGCCCAAAAAAGCATGCAAGTCAATGTTTACACAGGATCTACAGAACTAT 971
Db 933 GTGCTTGGCCCAAAAAAGCATGCAAGTCAATGTTTACACAGGATCTACAGAACTAT 992
QY 972 TTCAACACAGATATGACCTAGTTTATATTTCTGGGAGAAATGAATCATATCTAGAA 1031
Db 993 TTCAACACAGATATGACCTAGTTTATATTTCTGGGAGAAATGAATCATATCTAGAA 1052
QY 1032 GTCTGAGTGAACAAACAGAGCAAGAAACAAAAGAACCCAAAAGCAGAGGCTTCAAT 1091
Db 1053 GTCTGAGTGAACAAACAGAGCAAGAAACAAAAGAACCCAAAAGCAGAGGCTTCAAT 1091
```

```
Db 1053 GTCTGAGTGAACAAACAGAGCAAGAAACAAAAGAACCCAAAAGCAGAGGCTTCAAT 1112
QY 1092 ATGAACAGATPAAATCTATCTTCAAGAATATTAAGATTTAGGAAATTAATTCATGTA 1151
Db 1113 ATGAACAGATPAAATCTATCTTCAAGAATATTAAGATTTAGGAAATTAATTCATGTA 1172
QY 1152 ACTAGCAAGTGTGTTAAGATGATTAAGTAAATGACAGTGGAGCAAGTCAATCCGAG 1211
Db 1173 ACTAGCAAGTGTGTTAAGATGATTAAGTAAATGACAGTGGAGCAAGTCAATCCGAG 1232
QY 1212 ATCTAGAGGACCTCCCGCTGCTGTCACTGGGAGTGAAGACAGATAGTGAATTT 1271
Db 1233 ATCTAGAGGACCTCCCGCTGCTGTCACTGGGAGTGAAGACAGATAGTGAATTT 1292
QY 1272 CTTTGTCTCTGAAATTTTATGATATGCTGTATAGTTGTGCTGAGAGAACCCCTGAA 1331
Db 1293 CTTTGTCTCTGAAATTTTATGATATGCTGTATAGTTGTGCTGAGAGAACCCCTGAA 1352
QY 1332 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATGATCCCTA 1391
Db 1353 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATGATCCCTA 1412
QY 1392 AGAGCTGCTTAATTAAGTCCCACTTCCGACATCAGAGGGGCGCTGCATTTTATGATGGT 1451
Db 1413 AGAGCTGCTTAATTAAGTCCCACTTCCGACATCAGAGGGGCGCTGCATTTTATGATGGT 1472
QY 1452 CAATATGATTCATTTTATGATGCTTCCAAAGTGTGCTTCCAACTGCTCTTCCAACTGACA 1511
Db 1473 CAATATGATTCATTTTATGATGCTTCCAAAGTGTGCTTCCAACTGCTCTTCCAACTGACA 1532
QY 1512 AATGCAAAAGTTGAGAAAATATGATCATTAATTTTATGATTAACAGAGAGTGGGACACC 1571
Db 1533 AATGCAAAAGTTGAGAAAATATGATCATTAATTTTATGATTAACAGAGAGTGGGACACC 1592
QY 1572 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1631
Db 1593 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1652
QY 1632 GATGATGTTCAATCCGTGAATGGTCCAGGAGAGAGACCTTTCACCTTATATGATGATTA 1691
Db 1653 GATGATGTTCAATCCGTGAATGGTCCAGGAGAGAGACCTTTCACCTTATATGATGATTA 1712
QY 1692 TGTCAATCAAGAGCTGAGGCTTCTCTTTCATCTGCTGAGACAGTAAAGACTCACT 1751
Db 1713 TGTCAATCAAGAGCTGAGGCTTCTCTTTCATCTGCTGAGACAGTAAAGACTCACT 1772
QY 1752 TTTCAATAGCATCTTACAGAGTGGGACCTCACTGGGGTGAATTTGGCCCCCATCTCGGG 1811
Db 1773 TTTCAATAGCATCTTACAGAGTGGGACCTCACTGGGGTGAATTTGGCCCCCATCTCGGG 1832
QY 1812 GGAATGTCTGAAGACAAATTTTGTGTTACTCAATGAGGAGTGAAGAGATACAGTGTCTA 1871
Db 1833 GGAATGTCTGAAGACAAATTTTGTGTTACTCAATGAGGAGTGAAGAGATACAGTGTCTA 1892
QY 1872 CTACCACTAGTGAATTAAGGCGAGGATGCTGCTCAACTCTTACATGATACAGAGAGT 1931
Db 1893 CTACCACTAGTGAATTAAGGCGAGGATGCTGCTCAACTCTTACATGATACAGAGAGT 1952
QY 1932 CTCCCATTTTACACATCCCAATCCGAAAGTGTCACTGTGTCAAGACTAAAGAAACCTGTGT 1991
Db 1953 CTCCCATTTTACACATCCCAATCCGAAAGTGTCACTGTGTCAAGACTAAAGAAACCTGTGT 2012
QY 1992 TTTGATGAAGAAAGGCGCTGGAAGAGAGGAGCCAAACAAATCTGTCTGCTT-CTCACATT 2050
Db 2013 TTTGATGAAGAAAGGCGCTGGAAGAGGAGGAGCCAAACAAATCTGTCTGCTTCTCACTT 2072
QY 2051 AGTCAATTTGGCAAAATTAAGCAATCTGTCTTTGGCTGTGCTGCTCAGACAGAGAGCAGAA 2110
Db 2073 AGTCAATTTGGCAAAATTAAGCAATCTGTCTTTGGCTGTGCTGCTCAGACAGAGAGCAGAA 2132
QY 2111 CTCTATTCGGGACCCAGATTAACATCTCTCAGTGAACAGAGTTTGAACAAGGCTTATGGGAAA 2170
Db 2133 CTCTATTCGGGACCCAGATTAACATCTCTCAGTGAACAGAGTTTGAACAAGGCTTATGGGAAA 2192
```

QY 2171 TGGCTGATGGGATTATCTTACGCTTGTAGAGCTTCTTAAGTTCTTCCCTTCAATTCACC 2230
DB 2193 TGGCTATGGGATTATCTTACGCTTGTAGAGCTTCTTAAGTTCTTCCCTTCAATTCACC 2252
QY 2231 CTGCAAGCCAGTCTGTAGAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTCTGA 2290
DB 2253 CTGCAAGCCAGTCTGTAGAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTCTGA 2312
QY 2291 ATTGATCTCCAGACCTTCTGCGCAATTCAAATTAAAGCAACAAATATACCTT 2350
DB 2313 ATTGATCTCCAGACCTTCTGCGCAATTCAAATTAAAGCAACAAATATACCTT 2372
QY 2351 CCAATGAGCAACACAGACTTTTGAAGCAAGACATGACTGTTGAATTTAGAGCCCTTG 2410
DB 2373 CCAATGAGCAACACAGACTTTTGAAGCAAGACATGACTGTTGAATTTAGAGCCCTTG 2432
QY 2411 AGGAATGAAGCTTTGAAGAAAGAAATATCTTGTTCACAGCCCTTCCCACTCTTCA 2470
DB 2433 AGGAATGAAGCTTTGAAGAAAGAAATATCTTGTTCACAGCCCTTCCCACTCTTCA 2492
QY 2471 TGTGTTAACCACTGCTTCTGGAACCTTGGAGCCAGGTGACTGTATTTACATGTTTAT 2530
DB 2493 TGTGTTAACCACTGCTTCTGGAACCTTGGAGCCAGGTGACTGTATTTACATGTTTAT 2552
QY 2531 AGAAATCTGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCT 2587
DB 2553 AGAAATCTGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCT 2609

RESULT 7
AD646174
ID AD646174 standard; cDNA; 2627 BP.
AC AD646174;
XX 26-FEB-2004 (first entry)
DT Human ovarian carcinoma polynucleotide #387.
DE Human ovarian carcinoma polynucleotide #387.
XX
XX Human; ovarian carcinoma; gene; ss; OBE; ovarian cancer;
KM secreted tumour antigen; cytosolic; 0772P.
XX
OS Homo sapiens.
XX
XX US2003165504-A1.
XX
XX 04-SEP-2003.
PD
XX 04-APR-2001; 2001US-00827271.
PF
XX 17-DEC-1998; 980US-00215681.
PR 17-DEC-1998; 980US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-0067857.
XX
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
XX
PI Retter MW, Fanger GR;
XX
XX MPI; 2003-898035/82.
DR
XX
XX New isolated OBE or 0772P polypeptides, useful for diagnosing,
PT preventing, treating and monitoring cancer, e.g. ovarian cancer,
PT stimulating the immune response in patient.
XX
XX Example 2; SEQ ID NO 391; 290bp; English.
PS
XX The invention relates to human ovarian carcinoma polypeptides, designated

CC OBE or 0772P, and the polynucleotides encoding them. The invention also
CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC methods for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polynucleotide of the invention.
XX
XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
SQ
Query Match 99.1%; Score 2565; DB 10; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 12 GGCAGCTCCAGCTCAGCAGATCCAGATACGCTGGAACTTCCAGCCATGGCTTCC 71
DB 33 GGCAGCTCCAGCTCAGCAGATCCAGATACGCTGGAACTTCCAGCCATGGCTTCC 92
QY 72 TGGGGCAATCCTCTTCTGAGCATATTAACATCATATTTCTGGTGGAGCAATTG 131
DB 93 TGGGGCAATCCTCTTCTGAGCATATTAACATCATATTTCTGGTGGAGCAATTG 152
QY 132 CACTCATCAATGGCTTGGATTTTCAGGGAGACATCCATCAAGTCACTACTGTGCGCT 191
DB 153 CACTCATCAATGGCTTGGATTTTCAGGGAGACATCCATCAAGTCACTACTGTGCGCT 212
QY 192 CAGCTGGAAATTTGGGGAGATGATGATCTGAGCTGCACTTTTGAACCTGATCAAA 251
DB 213 CAGCTGGAAATTTGGGGAGATGATGATCTGAGCTGCACTTTTGAACCTGATCAAA 272
QY 252 TTTCTGATTCGTGATTAACAATGCTGAAGAGGTGTTTGAAGCTTGTCTCATGATTC 311
DB 273 TTTCTGATTCGTGATTAACAATGCTGAAGAGGTGTTTGAAGCTTGTCTCATGATTC 332
QY 312 AAGAAGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAAGGCCGAGACAGAGTGT 371
DB 333 AAGAAGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAAGGCCGAGACAGAGTGT 392
QY 372 TTGCTATCAAGTATGTTGGCAATGCTCTTTGGCGGTGAAGAAAGTGCATCTACAG 431
DB 393 TTGCTATCAAGTATGTTGGCAATGCTCTTTGGCGGTGAAGAAAGTGCATCTACAG 452
QY 432 ATGCTGGACACTTAACAATGTTATATCATCACTTTAAAGCAAGGGAATGCTAACCTTG 491
DB 453 ATGCTGGACACTTAACAATGTTATATCATCACTTTAAAGCAAGGGAATGCTAACCTTG 512
QY 492 AGTATTAACCTGAGGCTTCAGCATGCCGGAAGTGAATGAGCTTAATATGCCAGCTCAG 551
DB 513 AGTATTAACCTGAGGCTTCAGCATGCCGGAAGTGAATGAGCTTAATATGCCAGCTCAG 572
QY 552 AGACTTGGCGTGTGAGGCTCCCGATGTTCCCGCAGCCACAGTGTCTGGCATCC 611
DB 573 AGACTTGGCGTGTGAGGCTCCCGATGTTCCCGCAGCCACAGTGTCTGGCATCC 632
QY 612 AAGTTGACCAAGGAGCAACTTTCGGAAGTCTTCAATACAGCTTTGAGCTGAATCTTG 671
DB 633 AAGTTGACCAAGGAGCAACTTTCGGAAGTCTTCAATACAGCTTTGAGCTGAATCTTG 692
QY 672 AGAATGAGCAATGAAGGTGTGTCTGTCTCAAGATGTTAGATCAACACATACT 731
DB 693 AGAATGAGCAATGAAGGTGTGTCTGTCTCAAGATGTTAGATCAACACATACT 752
QY 732 CCTGTATGATTTGAAAATGACATTTGCCAAAGCAACAGGGATATCAAGTACAGAAATCGG 791
DB 753 CCTGTATGATTTGAAAATGACATTTGCCAAAGCAACAGGGATATCAAGTACAGAAATCGG 812
QY 792 AGATCAAAAGGCGAGTCACTTAACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTT 851
DB 813 AGATCAAAAGGCGAGTCACTTAACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTT 872
QY 852 CTTTCTTTCGCAATCAGCTGGGACCTTCTGCTCTGAGCCCTTACATGATCTAAATAT 911

```

Db      873 CTTTCTTTCGCACTGAGTGGGACCTTCTGCTCTGAGCCCTTACCTGATGTAATAATAT 932
Qy      912 GTGCGCTTGGCCGCAAAAAAGCATGCAAAATCATTTGTTACACAGGATCTACAGAACTAT 971
Db      933 GTGCGCTTGGCCGCAAAAAAGCATGCAAAATCATTTGTTACACAGGATCTACAGAACTAT 992
Qy      972 TTACACACAGATATGATGATGATTTTATTTATTTCTGGAGGAATGAAATCATATCTAGAA 1031
Db      993 TTACACACAGATATGATGATGATTTTATTTATTTCTGGAGGAATGAAATCATATCTAGAA 1052
Qy      1032 GTTGTGAGTGAGCAACAAAGCAAGAAACAAAAAGAGCCAAAGCAGAGGCTTCCAAAT 1091
Db      1053 GTCTGGAGTGAGCAACAAAGCAAGAAACAAAAAGAGCCAAAGCAGAGGCTTCCAAAT 1112
Qy      1092 ATGAAACAGATATATCTATCTTCAAGACATATTTAGAAATTTGGGAAAAATTTCAATGTA 1151
Db      1113 ATGAAACAGATATATCTATCTTCAAGACATATTTAGAAATTTGGGAAAAATTTCAATGTA 1172
Qy      1152 ACTAGACAGTGTGTTAAGATGATTAAGTAAATGACCTGGAGACAAATGATCCCGAG 1211
Db      1173 ACTAGACAGTGTGTTAAGATGATTAAGTAAATGACCTGGAGACAAATGATCCCGAG 1232
Qy      1212 ATCTCAGGAGCCTCCCTGCTGTCACCTGGGAGTGAGAGACAGATTAATGATGTT 1271
Db      1233 ATCTCAGGAGCCTCCCTGCTGTCACCTGGGAGTGAGAGACAGATTAATGATGTT 1292
Qy      1272 CTTTGTCTCTGAATTTTGTATTAATGTCGTGAATGTTGCTGTGAGAAAGCCCTGGAA 1331
Db      1293 CTTTGTCTCTGAATTTTGTATTAATGTCGTGAATGTTGCTGTGAGAAAGCCCTGGAA 1352
Qy      1332 AGTCTATCCCAACATATCCATCTATATTTCCACAAATTAAGCTGTATATGATCCCTA 1391
Db      1353 AGTCTATCCCAACATATCCATCTATATTTCCACAAATTAAGCTGTATATGATCCCTA 1412
Qy      1392 AGACGCTGTAAATGATGATGCACTTTCGCACTCAGGAGCGGCTGCATTTTAAATGGGT 1451
Db      1413 AGACGCTGTAAATGATGATGCACTTTCGCACTCAGGAGCGGCTGCATTTTAAATGGGT 1472
Qy      1452 CAAAGATCATCTTTTATGATGCTTCCAAAGTGTGCTGCTGCTCCCAACGAGA 1511
Db      1473 CAAAGATCATCTTTTATGATGCTTCCAAAGTGTGCTGCTGCTCCCAACGAGA 1532
Qy      1512 AATGCCAAAGTTGAGAAATATGATCATATTTTATGATTAAGACAGACATCGGCGACACC 1571
Db      1533 AATGCCAAAGTTGAGAAATATGATCATATTTTATGATTAAGACAGACATCGGCGACACC 1592
Qy      1572 GATTTTATAATTAACCTGAGCACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
Db      1593 GATTTTATAATTAACCTGAGCACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1652
Qy      1632 GATGATGTTCAATCCCGATGATGTCAGGAGGACCTTTCACCTTGACATATATGATTA 1691
Db      1653 GATGATGTTCAATCCCGATGATGTCAGGAGGACCTTTCACCTTGACATATATGATTA 1712
Qy      1692 TGTATCATCAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGTAAAGCTCACT 1751
Db      1713 TGTATCATCAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGTAAAGCTCACT 1772
Qy      1752 TTTCAATAGCATCTAGAGCAATTTGGTTACCTCAATGAGGAGTGGAGGATTCAGTGTA 1811
Db      1773 TTTCAATAGCATCTAGAGCAATTTGGTTACCTCAATGAGGAGTGGAGGATTCAGTGTA 1832
Qy      1812 GGAATGTCTGAGAGCAATTTGGTTACCTCAATGAGGAGTGGAGGATTCAGTGTA 1871
Db      1833 GGAATGTCTGAGAGCAATTTGGTTACCTCAATGAGGAGTGGAGGATTCAGTGTA 1892
Qy      1872 CTACCAACTAGTGAATAAGGCGCAGGAGTGTGCTCAACCTCTCAATCATATGACAGACCT 1931
Db      1893 CTACCAACTAGTGAATAAGGCGCAGGAGTGTGCTCAACCTCTCAATCATATGACAGACCT 1952
Qy      1932 CTCCTCATTTACAACTAACCAATTCGAATGTCACTGTCTCAGGACTTAAGAAACCTGTGT 1991

```

```

Db      1953 CTCCTCATTTACAACTAACCAATTCGAATGTCACTGTCTCAGGACTTAAGAAACCTGTGT 2012
Qy      1992 TTTGATGAAAGAGGCGCTGGAAAGAGGAGGCCAAACAAATCTGTCTGCTT-CTGACATTT 2050
Db      2013 TTTGATGAAAGAGGCGCTGGAAAGAGGAGGCCAAACAAATCTGTCTGCTTCTCTCACTTT 2072
Qy      2051 AGTCATTTGGCAAAATTAAGCATTTCTGTCTCTTTGGCTGTGCTCTCAGACAGAGAGCCAGAA 2110
Db      2073 AGTCATTTGGCAAAATTAAGCATTTCTGTCTCTTTGGCTGTGCTCTCAGACAGAGAGCCAGAA 2132
Qy      2111 CTCTATCGGAGCACCGAGTAAACATCTCTCAGTGAACAAAGTTGACAAAGGCTTAAGGAAA 2170
Db      2133 CTCTATCGGAGCACCGAGTAAACATCTCTCAGTGAACAAAGTTGACAAAGGCTTAAGGAAA 2192
Qy      2171 TGCCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTTCCCTTCATTTCACTAC 2230
Db      2193 TGCCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTTCCCTTCATTTCACTAC 2252
Qy      2231 CTGCAAGCCAAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
Db      2253 CTGCAAGCCAAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
Qy      2291 ATTTGATCTCGAGACCTTCTCTGCGCACATTTGAAATTAAGGCAACAAATATATACCTT 2350
Db      2313 ATTTGATCTCGAGACCTTCTCTGCGCACATTTGAAATTAAGGCAACAAATATATACCTT 2372
Qy      2351 CCATGAGACACACACAGACTTTTGAAGCAAGACAAATGATCTGTTGAATTTAGGCGCTTG 2410
Db      2373 CCATGAGACACACACAGACTTTTGAAGCAAGACAAATGATCTGTTGAATTTAGGCGCTTG 2432
Qy      2411 AGGAATGAAGCTTTGAAGGAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCA 2470
Db      2433 AGGAATGAAGCTTTGAAGGAAAGAAATCTTTGTTTCCAGCCCTTCCACACTCTTCA 2492
Qy      2471 TGTGTTAACCACTGCTTCTCTGAGACCTTGGAGCCAGGCTGATATTAACATGTTGTTAT 2530
Db      2493 TGTGTTAACCACTGCTTCTCTGAGACCTTGGAGCCAGGCTGATATTAACATGTTGTTAT 2552
Qy      2531 AGAAATGATGATTTTGAATGATCTGATCTGTTCAAGAGAAATGATTAATATACATTTCT 2587
Db      2553 AGAAATGATGATTTTGAATGATCTGATCTGTTCAAGAGAAATGATTAATATACATTTCT 2609

```

```

RESULT 8
ADN40452
ID      ADN40452 strand: cdNA; 2627 BP.
XX
AC      ADN40452;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Human breast cancer associated cdNA sequence #203.
XX
KW      Human; breast cancer; T cell; tumour protein; antigen presenting cell;
KW      Immune response; CD4+; CD8+; cytostatic; gene therapy; gene; ss.
OS      Homo sapiens.
PN      US2004101899-A1.
XX
PD      27-MAY-2004.
XX
PF      13-NOV-2003; 2003US-00714389.
XX
PR      30-NOV-1999; 99US-00451651.
PR      22-FEB-2000; 2000US-00510662.
PR      10-MAR-2000; 2000US-00523586.
PR      07-APR-2000; 2000US-00545068.
PR      15-MAY-2000; 2000US-00571025.
PR      06-FEB-2001; 2001US-00778320.
XX
PA      (CORI-) CORIXA CORP.
XX

```



```

QY 1632 GATGATGTTTCATCCGTAAGTGTCCAGGAAAGACCTTTCACTTGACTATATGACATTA 1691
   |||
   |||
Db 1653 GATGATGTTTCATCCGTAAGTGTCCAGGAAAGACCTTTCACTTGACTATATGACATTA 1712
   |||
   |||
QY 1692 TGTGATCACAAGCTTGAGGCTTCTCTTTCATCTCTGCGAAGCTAAGACCTCACT 1751
   |||
   |||
Db 1713 TGTGATCACAAGCTTGAGGCTTCTCTTTCATCTCTGCGAAGCTAAGACCTCACT 1772
   |||
   |||
QY 1752 TTTGCAATGATCTGAGAGAGTGGAGCTGAGCTGGGGTGAATTTCCGCCCCCACTCCGGG 1811
   |||
   |||
Db 1773 TTTGCAATGATCTGAGAGAGTGGAGCTGAGCTGGGGTGAATTTCCGCCCCCACTCCGGG 1832
   |||
   |||
QY 1812 GGAATGTCGAAGACAATTTTGGTTTACTCAATGAGGAGTGGAGAGGATACAGTGCTA 1871
   |||
   |||
Db 1833 GGAATGTCGAAGACAATTTTGGTTTACTCAATGAGGAGTGGAGAGGATACAGTGCTA 1892
   |||
   |||
QY 1872 CTACCAACTAGTGTGATTAAGGCGCAGGAGTGTCTCAACCTCTCAATGTAACAGACGT 1931
   |||
   |||
Db 1893 CTACCAACTAGTGTGATTAAGGCGCAGGAGTGTCTCAACCTCTCAATGTAACAGACGT 1952
   |||
   |||
QY 1932 CTCCCACTTACAACTAACCCCAATCCGAAAGTGTCAACGTGTCTAGGACTAAGAAACCTGGT 1991
   |||
   |||
Db 1953 CTCCCACTTACAACTAACCCCAATCCGAAAGTGTCAACGTGTCTAGGACTAAGAAACCTGGT 2012
   |||
   |||
QY 1992 TTTGAGTGAAGAAAGGCGCTGAAAGAGGAGGACCAACAATCTGTCTGCTT-CTGACAT 2050
   |||
   |||
Db 2013 TTTGAGTGAAGAAAGGCGCTGAAAGAGGAGGACCAACAATCTGTCTGCTTCTCTGACAT 2072
   |||
   |||
QY 2051 AGTCATTTGGCAATAAGACATTTCTCTTTTGGCTGCTGCTCTGACAGACAGAGGCCAGAA 2110
   |||
   |||
Db 2073 AGTCATTTGGCAATAAGACATTTCTCTTTTGGCTGCTGCTCTGACAGACAGAGGCCAGAA 2132
   |||
   |||
QY 2111 CTCTATCGGGGACACAGGATTAATCTCTGATGTAACAGAGTGAACAAGGCGTATGGGAAA 2170
   |||
   |||
Db 2133 CTCTATCGGGGACACAGGATTAATCTCTGATGTAACAGAGTGAACAAGGCGTATGGGAAA 2192
   |||
   |||
QY 2171 TGCCTGATGGAGATTATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCCCTTATTTTAC 2230
   |||
   |||
Db 2193 TGCCTGATGGAGATTATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCCCTTATTTTAC 2252
   |||
   |||
QY 2231 CTGCAAGCCAAAGTTCTGTAAGAGAAATGCTGATTTCTGAGCTTCTTCTTCTTCTGTA 2290
   |||
   |||
Db 2253 CTGCAAGCCAAAGTTCTGTAAGAGAAATGCTGATTTCTGAGCTTCTTCTTCTTCTGTA 2312
   |||
   |||
QY 2291 ATTATGATCTCCAGACCTTCTCTGCGCAATTAATTAAGGCAACAACATATATCTT 2350
   |||
   |||
Db 2313 ATTATGATCTCCAGACCTTCTCTGCGCAATTAATTAAGGCAACAACATATATCTT 2372
   |||
   |||
QY 2351 CCATGAAGACACACAGACTTTTGAAGCAAGACATGCTTGAATTAAGGCGCTTG 2410
   |||
   |||
Db 2373 CCATGAAGACACACAGACTTTTGAAGCAAGACATGCTTGAATTAAGGCGCTTG 2432
   |||
   |||
QY 2411 AGGAATGAAGCTTTGAAGAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCAACTCTTGA 2470
   |||
   |||
Db 2433 AGGAATGAAGCTTTGAAGAAAGAAATACCTTTGTTTCCAGCCCCCTTCCCAACTCTTGA 2492
   |||
   |||
QY 2471 TGTGTTAACCATGCTCTCTCTGAGACCTTGAAGCAGAGTGACTGTATTAATGTTTAT 2530
   |||
   |||
Db 2493 TGTGTTAACCATGCTCTCTCTGAGACCTTGAAGCAGAGTGACTGTATTAATGTTTAT 2552
   |||
   |||
QY 2531 AGAAAACTGATTTTGAAGTTCGATGCTTCAAGAGATGTTAAATATACATTTCT 2587
   |||
   |||
Db 2553 AGAAAACTGATTTTGAAGTTCGATGCTTCAAGAGATGTTAAATATACATTTCT 2609
   |||
   |||

```

```

DE Human B7-H8 gene.
KW Human; B7-like protein; inflammation; tissue damage; immune disorder;
KW Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis;
KW diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer;
KW rheumatoid arthritis; cardiovascular disorder; nervous system disorder;
KW myocardial ischaemia; ulcerative colitis; reproductive system disorder;
KW Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis;
KW diabetes mellitus; Grave's disease; Paget's disease; liver disorder;
KW gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia;
KW dysphagia; hepatomegaly; neurological disease; infectious disease;
KW epilepsy; gene therapy; B7-H8 protein; chromosome 1; gene; ds.
OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 419..1267
FT /tag= a
FT /product= "Human B7-H8 protein"
FT sig_peptide 419..490
FT /tag= b
FT mat_peptide 491..1264
FT /tag= c
FT /product= "Human mature B7-H8 protein"
PD WO200202587-A1.
PD 10-JUN-2002.
PF 29-JUN-2001; 2001WO-US020917.
PR 30-JUN-2000; 2000US-025133P.
PR 14-AUG-2000; 2000US-0225266P.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Fiscella M, Ni J, Ruben SM;
PI MPI: 2002-257198/30.
DR P-PSDB; MAE20311.
XX Isolated nucleic acids encoding human B7-like polypeptides, useful for
XX diagnosis and treatment of e.g. inflammation, cancer, immune disorders
XX such as Addison's disease, and cardiovascular disorders such as
XX myocardial ischaemia.
XX Example 1; Fig 1; 493bp; English.
XX
XX The present invention relates to novel human B7-like polypeptides and
XX polynucleotides encoding such proteins. Sequences of the invention are
XX used for preventing, treating or ameliorating a medical condition in a
XX mammalian subject. The polynucleotides and polypeptides are administered
XX to subjects having a disorder related to B-7 like polypeptides, such as
XX inappropriate or excessive inflammation which can lead to tissue damage
XX or even death, where the inflammation is brought about by the activation
XX of certain cells in the body e.g. T cells and may involve disorders
XX related to immune system. The nucleic acids, proteins, antibodies,
XX agonists and antagonists of the invention are useful in the diagnosis,
XX treatment and prevention of cancer (e.g. cancers of the adrenal gland,
XX bone, bone marrow, breast, gastrointestinal tract, liver, urogenital or
XX lung), immune disorders (e.g., Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis, ulcerative colitis),
XX cardiovascular disorders (e.g., myocardial ischaemia), nervous system
XX disorders (Alzheimer's disease, Parkinson's disease), endocrine disorders
XX (e.g., diabetes mellitus, Grave's disease), reproductive system disorders
XX (e.g., cryptorchism, Paget's disease), gastrointestinal disorders (e.g.,
XX dysphagia, irritable bowel syndrome), liver disorders (e.g., hepatitis,
XX hepatomegaly), neurological diseases (e.g., cerebral anoxia and epilepsy)
XX and infectious diseases such as viral, bacterial, fungal and parasitic
XX infections. Sequences of the invention are also used in gene therapy. The
XX present sequence is a DNA encoding human B7-H8 protein. B7-H8 gene is
XX located on chromosome 1

```

XX Sequence 3357 BP; 956 A; 784 C; 761 G; 855 T; 0 U; 1 Other:
Query Match 99.1%; Score 2563.4; DB 6; Length 3357;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2575; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 12 GGGAGCTCCACTGAGCCAGTACCAGATAGCTGGGAACCTTCCCGACCATGGCTTCCC 71
DB 369 GGGAGCTCCACTGAGCCAGTACCAGATAGCTGGGAACCTTCCCGACCATGGCTTCCC 428
QY 72 TGGGGAGATCTCTTCTGGAGCATTAATTAGCATCATTAATTCTGGCTGGAGCAATTG 131
DB 429 TGGGGAGATCTCTTCTGGAGCATTAATTAGCATCATTAATTCTGGCTGGAGCAATTG 488
QY 132 CACTCATCATTTGGCTTTGTAATTTCAGGAGACATCTCATCAAGTCACTAGTGGCT 191
DB 489 CACTCATCATTTGGCTTTGTAATTTCAGGAGACATCTCATCAAGTCACTAGTGGCT 548
QY 192 CAGCTGGGAACATTTGGGGAGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAC 251
DB 549 CAGCTGGGAACATTTGGGGAGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAC 608
QY 252 TTTCTGATATCGTATACAAATGAGCTGAGAGAGAGTGTATTAGCTTGGTTCATGAGTTCA 311
DB 609 TTTCTGATATCGTATACAAATGAGCTGAGAGAGAGTGTATTAGCTTGGTTCATGAGTTCA 668
QY 312 AAGAGGCAAAAGATGAGCTGTCCGAGAGATGAAATGTTCAAGGCCGGAACAGAGTGT 371
DB 669 AAGAGGCAAAAGATGAGCTGTCCGAGAGATGAAATGTTCAAGGCCGGAACAGAGTGT 728
QY 372 TTGCTGATCAAGATGATGTTGGCAATGCCCTTTCGGCTGGAAGAAAGTGCATCTCAAG 431
DB 729 TTGCTGATCAAGATGATGTTGGCAATGCCCTTTCGGCTGGAAGAAAGTGCATCTCAAG 788
QY 432 ATGCTGGACCTCAAAATGTTATATCATCTTCTAAGGCAAGGGAAATGCTAACCTTG 491
DB 789 ATGCTGGACCTCAAAATGTTATATCATCTTCTAAGGCAAGGGAAATGCTAACCTTG 848
QY 492 AGTATAAACTGAGACCTTCAGACATGCCGGAAGTGAATGTAATATATGCAAGCTCAG 551
DB 849 AGTATAAACTGAGACCTTCAGACATGCCGGAAGTGAATGTAATATATGCAAGCTCAG 908
QY 552 AGACCTTGGCGTGTGAGAGCTCCCGAATGTTCCCGACCGCAAGTGTCTGGCAATCCC 611
DB 909 AGACCTTGGCGTGTGAGAGCTCCCGAATGTTCCCGACCGCAAGTGTCTGGCAATCCC 968
QY 612 AAGTTGACGAGGAGCCAACTTCTCGGAAGTCTCAATAACAGCTTTGAGCTGAACCTTG 671
DB 969 AAGTTGACGAGGAGCCAACTTCTCGGAAGTCTCAATAACAGCTTTGAGCTGAACCTTG 1028
QY 672 AGAATGTGACATGAAGGTTGTGTCTGTGTCTCAATGTTACGATCAACAAACATACT 731
DB 1029 AGAATGTGACATGAAGGTTGTGTGTGTCTCAATGTTACGATCAACAAACATACT 1088
QY 732 CCTGTATGATTTGAAATGATGATGCGCAAGCAAGGGGATATCAAAAGTGAAGCAATCGG 791
DB 1089 CCTGTATGATTTGAAATGATGATGCGCAAGCAAGGGGATATCAAAAGTGAAGCAATCGG 1148
QY 792 AGATCAAAAGGCGAGTCACTTCAAGCTGCTAAACTCAAGAGCTTCTGTGTGTCTCT 851
DB 1149 AGATCAAAAGGCGAGTCACTTCAAGCTGCTAAACTCAAGAGCTTCTGTGTGTCTCT 1208
QY 852 CTTTCTTTTGGCATCAAGCTGGGCACTTCTGCTCTCAAGCCCTTACCTGATCTAAATAT 911
DB 1209 CTTTCTTTTGGCATCAAGCTGGGCACTTCTGCTCTCAAGCCCTTACCTGATCTAAATAT 1268
QY 912 GTGCTTTGGCGCAAAAGATGCAATGCTATTTGTTAACAAGGATCTACAGAACTAT 971
DB 1269 GTGCTTTGGCGCAAAAGATGCAATGCTATTTGTTAACAAGGATCTACAGAACTAT 1328
QY 972 TTCACCAACGATATGACTAGTTTATATTTCTGGAGGAAATGAATCATATCTAGAA 1031

DB 1329 TTCACCAACGATATGACTAGTTTATATTTCTGGAGGAAATGAATCATATCTAGAA 1388
QY 1032 GTCTGAGTGAAGCAAAACAGAGCAAAACAAAGAACCCAAACCAAGGCTCCAAAT 1091
DB 1389 GTCTGAGTGAAGCAAAACAGAGCAAAACAAAGAACCCAAACCAAGGCTCCAAAT 1448
QY 1092 ATGAACAAGTAAATCTATCTTCAAGACATATTTAAGTGGGAAATTAATTCATGTGA 1151
DB 1449 ATGAACAAGTAAATCTATCTTCAAGACATATTTAAGTGGGAAATTAATTCATGTGA 1508
QY 1152 ACTAGAACAAGTGTTAAGAGTATTAAGTAAATGCAAGCTGAGACAGTCAATCCCAG 1211
DB 1509 ACTAGAACAAGTGTTAAGAGTATTAAGTAAATGCAAGCTGAGACAGTCAATCCCAG 1568
QY 1212 ATCTCAGGAGCTCCCTGCTGTGTCACTGGGAGTGAAGAGACAGATAGCATGTT 1271
DB 1569 ATCTCAGGAGCTCCCTGCTGTGTCACTGGGAGTGAAGAGACAGATAGCATGTT 1628
QY 1272 CTTTGTCTGAAATTTTGTATATATGCTGTGAATGTTGCTGTGAGAAAGCCCTGGAA 1331
DB 1629 CTTTGTCTGAAATTTTGTATATATGCTGTGAATGTTGCTGTGAGAAAGCCCTGGAA 1688
QY 1332 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTATGTACCTTA 1391
DB 1689 AGTCTATCCCAACATATTCACATCTTATATTCACAAATTAAGCTGTATGTACCTTA 1748
QY 1392 AAGCGTGTCTAATTGATCTGCACTTGGCACTCAAGGGGGGCTGCAATTTAGTAATGGGT 1451
DB 1749 AAGCGTGTCTAATTGATCTGCACTTGGCACTCAAGGGGGGCTGCAATTTAGTAATGGGT 1808
QY 1452 CAAATGATTCACCTTTTATGATGCTTCAAAAGGTGCTTGGCTTCTTCCCAACTGACA 1511
DB 1809 CAAATGATTCACCTTTTATGATGCTTCAAAAGGTGCTTGGCTTCTTCCCAACTGACA 1868
QY 1512 AATGCCAAAGTTGAGAAAAATGATCATTAATTTTGAATAAACAGACAGTGGCGACCC 1571
DB 1869 AATGCCAAAGTTGAGAAAAATGATCATTAATTTTGAATAAACAGACAGTGGCGACCC 1928
QY 1572 GATTTTATTAATTAATCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
DB 1929 GATTTTATTAATTAATCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1988
QY 1632 GATGATGTTCAATCCGGAATGATCCAGGAGAGACCTTTCACCTTGAATATATGAGCTTA 1691
DB 1989 GATGATGTTCAATCCGGAATGATCCAGGAGAGACCTTTCACCTTGAATATATGAGCTTA 2048
QY 1692 TGTATCAACAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGTAAAGCTCAGT 1751
DB 2049 TGTATCAACAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGTAAAGCTCAGT 2108
QY 1752 TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGG 1811
DB 2109 TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGGTGAATTTCCGCCCATCTCCGGG 2168
QY 1812 GGAATGTCTGAAGACAAATTTTGGTTACTCAANTGAAGGAGTGAAGGATACAGTGCTTA 1871
DB 2169 GGAATGTCTGAAGACAAATTTTGGTTACTCAANTGAAGGAGTGAAGGATACAGTGCTTA 2228
QY 1872 CTACCAATAGTGAATAAAGGCGAGGAGTGTGCTCAACCTCTCAATGATACAGACGT 1931
DB 2229 CTACCAATAGTGAATAAAGGCGAGGAGTGTGCTCAACCTCTCAATGATACAGACGT 2288
QY 1932 CTCCCAATTAACAATCAACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGGT 1991
DB 2289 CTCCCAATTAACAATCAACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGGT 2348
QY 1992 TTTGATGAGAAAGGCGCTGGAAGGAGGAGCAACAATCTGTCTGCTTCTCACTT 2050
DB 2349 TTTGATGAGAAAGGCGCTGGAAGGAGGAGCAACAATCTGTCTGCTTCTCACTT 2408
QY 2051 AGTCATTTGCAATTAAGCAATTTCTCTTTGGCTGTCTCTAGACAGAGGCCAGAA 2110
DB 2409 AGTCATTTGCAATTAAGCAATTTCTCTTTGGCTGTCTCTCTAGACAGAGGCCAGAA 2468

QY 312 AGAAGGCAAAAGATGAGCTGTCGGAGCAGGATGAAATGTTCAAGAGCCGGAACAGAGTGT 371
| | | | |
Db 303 AAGAGGCAAAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGAGCCGGAACAGAGTGT 362
| | | | |
QY 372 TTGCTGATCAAGATGATGTCGCAATGCTCTTTCGCGCTGAAAAAGTGCACCTCAG 431
| | | | |
Db 363 TTGCTGATCAAGATGATGTCGCAATGCTCTTTCGCGCTGAAAAAGTGCACCTCAG 422
| | | | |
QY 432 ATGCTGGCACCTACAAATGTTTATATCATCTTCTTAAAGCAAGGGGAATGCTAACCTTG 491
| | | | |
Db 423 ATCTGGCACCTACAAATGTTTATATCATCTTCTTAAAGCAAGGGGAATGCTAACCTTG 482
| | | | |
QY 492 AGATATAAAGCTGAGCCTTACAGATGCGGAAAGGAATGGAAGTAAATGAGCAAGCTCAG 551
| | | | |
Db 483 AGATATAAAGCTGAGCCTTACAGATGCGGAAAGGAATGGAAGTAAATGAGCAAGCTCAG 542
| | | | |
QY 552 AGACCTTTCGCGTGTGAGGCTCCCGATGTTCCCGCAGCCAGAGTGTCTGGGCAATCCC 611
| | | | |
Db 543 AGACCTTTCGCGTGTGAGGCTCCCGATGTTCCCGCAGCCAGAGTGTCTGGGCAATCCC 602
| | | | |
QY 612 AAGTTGACCAAGGAGCCAACTTCTCGGAAGTCTTCAATACGAGCTTGAAGCTGAATCTTG 671
| | | | |
Db 603 AAGTTGACCAAGGAGCCAACTTCTCGGAAGTCTTCAATACGAGCTTGAAGCTGAATCTTG 662
| | | | |
QY 672 AGAATGACCATGAGAGT 731
| | | | |
Db 663 AGAATGACCATGAGAGT 722
| | | | |
QY 732 CCTGTATGATTGAAATATGATTCGCAATGTCGCAAGGAGATATCAAAAGTACAGAACTCG 791
| | | | |
Db 723 CCTGTATGATTGAAATATGATTCGCAATGTCGCAAGGAGATATCAAAAGTACAGAACTCG 782
| | | | |
QY 792 AGATCAAAAGGCGAGTCACTTACAGTCTTAACTCAAAAGCTTCTGTGTGTCTCTT 851
| | | | |
Db 783 AGATCAAAAGGCGAGTCACTTACAGTCTTAACTCAAAAGCTTCTGTGTGTCTCTT 842
| | | | |
QY 852 CTTTCTTGTGCATGAGTGGGCACTTGTGCTGTGAGGCTTACCTGATCTTAAATTAAT 911
| | | | |
Db 843 CTTTCTTGTGCATGAGTGGGCACTTGTGCTGTGAGGCTTACCTGATCTTAAATTAAT 902
| | | | |
QY 912 GTGCTTGTGCGCACAAAAAAGCATGCAAGTCAATGTTTACAAAGGAGTCTACAGAACTAT 971
| | | | |
Db 903 GTGCTTGTGCGCACAAAAAAGCATGCAAGTCAATGTTTACAAAGGAGTCTACAGAACTAT 962
| | | | |
QY 972 TTCAACAACGATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA 1031
| | | | |
Db 963 TTCAACAACGATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA 1022
| | | | |
QY 1032 GTCTGAGTGAAGGAAACAAAGCAAGAAACAAAAAGGCCAAAGCAGAGGCTCCAT 1091
| | | | |
Db 1023 GTCTGAGTGAAGGAAACAAAGCAAGAAACAAAAAGGCCAAAGCAGAGGCTCCAT 1082
| | | | |
QY 1092 ATGAACAAGATTAATCTATCTTCAAGAATATTAGAAATGGGAAAAATTAATCATGTGA 1151
| | | | |
Db 1083 ATGAACAAGATTAATCTATCTTCAAGAATATTAGAAATGGGAAAAATTAATCATGTGA 1142
| | | | |
QY 1152 ACTAGCAAGTGTGTTAAGAGTAAATGAATGACGTTGAGACAAAGTCAATCCCGAG 1211
| | | | |
Db 1143 ACTAGCAAGTGTGTTAAGAGTAAATGAATGACGTTGAGACAAAGTCAATCCCGAG 1202
| | | | |
QY 1212 ATCTCAGGAGCCTCCCGTGCCTGTGACCTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1271
| | | | |
Db 1203 ATCTCAGGAGCCTCCCGTGCCTGTGACCTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1262
| | | | |
QY 1272 CTTTGTCTCTGAATTTTATGTTATATGTCGTATATGTTGCTCTGAGGAAGCCCTGGA 1331
| | | | |
Db 1263 CTTTGTCTCTGAATTTTATGTTATATGTCGTATATGTTGCTCTGAGGAAGCCCTGGA 1322
| | | | |
QY 1332 AGTCTATCCCAATATCCATCTTATATTCACAAATTAAGCTGTAGTATGACCTTA 1391
| | | | |
Db 1323 AGTCTATCCCAATATCCATCTTATATTCACAAATTAAGCTGTAGTATGACCTTA 1382
| | | | |

QY 1392 AGACGCTGCTAATTGATGCTGCACCTTGCACACTCAGAGGCGGCTGATTTTATGTAATGGGT 1451
| | | | |
Db 1383 AGACGCTGCTAATTGATGCTGCACCTTGCACACTCAGAGGCGGCTGATTTTATGTAATGGGT 1442
| | | | |
QY 1452 CAATGATTCATCTTTTATGATGCTTCAAAAGTGTGCTTGTCTTCTTCCACCTGAC 1511
| | | | |
Db 1443 CAATGATTCATCTTTTATGATGCTTCAAAAGTGTGCTTGTCTTCTTCCACCTGAC 1502
| | | | |
QY 1512 AATGCCAAAGTTGAGAAAAATGATCTAATTTTATGATTAACAGACACTGCGGACAC 1571
| | | | |
Db 1503 AATGCCAAAGTTGAGAAAAATGATCTAATTTTATGATTAACAGACACTGCGGACAC 1562
| | | | |
QY 1572 GATTTATATAATTAATCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
| | | | |
Db 1563 GATTTATATAATTAATCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1622
| | | | |
QY 1632 GATGATGTTTATCTCCGTAATGCTCAGGAGAGAGACCTTTCACCTTGATATATGAGCATTA 1691
| | | | |
Db 1623 GATGATGTTTATCTCCGTAATGCTCAGGAGAGAGACCTTTCACCTTGATATATGAGCATTA 1682
| | | | |
QY 1692 TGTATCAACAAGCTCTGAGGCTTCTCTTTCATCTGCTGTGACAGCTAAGACCTCAGT 1751
| | | | |
Db 1683 TGTATCAACAAGCTCTGAGGCTTCTCTTTCATCTGCTGTGACAGCTAAGACCTCAGT 1742
| | | | |
QY 1752 TTTCAATAGATCTAGAGCAGTGGAGCTCAGAGTGGGATGATTTGGCCCCCATCTCCGG 1811
| | | | |
Db 1743 TTTCAATAGATCTAGAGCAGTGGAGCTCAGAGTGGGATGATTTGGCCCCCATCTCCGG 1802
| | | | |
QY 1812 GGAATGTGGAAGACAAATTTTGTGTTACTCAATGAGGAGTGGAGAGATACAGTCTTA 1871
| | | | |
Db 1803 GGAATGTGGAAGACAAATTTTGTGTTACTCAATGAGGAGTGGAGAGATACAGTCTTA 1862
| | | | |
QY 1872 CTACCACTAGTGGATTAAGAGGCGCAGGAGTGTCTTCACTCTTACATATGACAGACGT 1931
| | | | |
Db 1863 CTACCACTAGTGGATTAAGAGGCGCAGGAGTGTCTTCACTCTTACATATGACAGACGT 1922
| | | | |
QY 1932 CTCGCCATTACAACTACCCCAATCCGAAGTGTCAACTGTGTGAGGACTAAGAAACCTGTGT 1991
| | | | |
Db 1923 CTCGCCATTACAACTACCCCAATCCGAAGTGTCAACTGTGTGAGGACTAAGAAACCTGTGT 1982
| | | | |
QY 1992 TTTGATGAGAAAAAGGCGCTGAAAGAGGAGGCAACAAATCTGTGTGCTT - CTCACATT 2050
| | | | |
Db 1983 TTTGATGAGAAAAAGGCGCTGAAAGAGGAGGCAACAAATCTGTGTGCTTCTTCAATT 2042
| | | | |
QY 2051 AGTCATTTGGCAATTAAGCATTTCTGTCTCTTTGTGCTGTCTGTCTGTCTGTCTGTCTGT 2110
| | | | |
Db 2043 AGTCATTTGGCAATTAAGCATTTCTGTCTCTTTGTGCTGTCTGTCTGTCTGTCTGTCTGT 2102
| | | | |
QY 2111 CTCTATCGGGCACAGGATTAATCTCTCAGTGAACAGAGTTGACAAGGCTATGGGAAA 2170
| | | | |
Db 2103 CTCTATCGGGCACAGGATTAATCTCTCAGTGAACAGAGTTGACAAGGCTATGGGAAA 2162
| | | | |
QY 2171 TGCCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCAC 2230
| | | | |
Db 2163 TGCCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCAC 2222
| | | | |
QY 2231 CTGCAAGCCAAAGTCTGTAGAGAAATGCTCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
| | | | |
Db 2223 CTGCAAGCCAAAGTCTGTAGAGAAATGCTCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2282
| | | | |
QY 2291 ATTTAGATCTCCAGACCTTCTCGGCAATTTCAATTAAGGCAACAAATATATACCTT 2350
| | | | |
Db 2283 ATTTAGATCTCCAGACCTTCTCGGCAATTTCAATTAAGGCAACAAATATATACCTT 2342
| | | | |
QY 2351 CCATGAAGCACACACAGCTTTTGAAGAGAGACAAATGACCTTGAATGAGGCTTGG 2410
| | | | |
Db 2343 CCATGAAGCACACACAGCTTTTGAAGAGAGACAAATGACCTTGAATGAGGCTTGG 2402
| | | | |
QY 2411 AGGAATGAAGCTTTGAAGAGAAAGATATCTTTGTTTCAGGCCCTTCCCAACTCTTA 2470
| | | | |
Db 2403 AGGAATGAAGCTTTGAAGAGAAAGATATCTTTGTTTCAGGCCCTTCCCAACTCTTGA 2462
| | | | |
QY 2471 TGTGTTAACCATGCTTCTGTGAACCTTGGAGCCACGAGTGTATATCATGTTGTAT 2530
| | | | |

```

|||||
DB      2463 TGTGTTAAACCACTGCTTCCTGACCTTGAGCCAGCGGACTGATTTACATGTTGTAAT 2522
QY      2531 AAAAAACGATTTTGAAGTTTCGATCGCTTCAGAGAAATGATTAATATCATTTTCT 2587
DB      2523 AGAAAACTGATTTTAAAGTTTCGATCGCTTCAGAGAAATGATTAATATCATTTTCT 2579

RESULT 11
ABLS7354
ID      ABL57354 standard; cDNA; 2591 BP.
XX
AC      ABL57354;
XX
DT      12-AUG-2002 (first entry)
XX
DE      Breast BS265 gene EST clone 3038129.
XX
KW      BS265; human; breast; cancer; tumour; metastasis; diagnosis;
KM      gene therapy; expressed sequence tag; EST; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      61..909
FT      FT      /*tag= a
FT      ET      /product= "BS265"
XX
PN      US2002034749-A1.
XX
PD      21-MAR-2002.
XX
PF      07-MAY-2001; 2001US-00850178.
XX
PR      18-NOV-1997; 97US-00972376.
PR      18-NOV-1998; 98US-00193944.
XX
PA      (BILL/) BILLINGEL P A.
PA      (COHE/) COHEN M.
PA      (COLE/) COLPITTS T L.
PA      (FRIE/) FRIEDMAN P N.
PA      (GORD/) GORDON J.
PA      (GRAN/) GRANADOS E N.
PA      (HODG/) HODGES S C.
PA      (KIAS/) KIAS M R.
PA      (KRAT/) KRATOCHVIL J D.
PA      (ROBE/) ROBERTS-RAPP L A.
PA      (RUSSE/) RUSSELL J C.
PA      (STRO/) STROUPE S D.
XX
PI      Billngel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI      Grandos EN, Hodges SC, Kias MR, Kratochvil JD, Roberts-Rapp LA,
PI      Russell JC, Stroupe SD;
XX
DR      WPI; 2002-403712/43.
DR      P-PSDB; ABB76274.
XX
PT      New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
PT      staging, monitoring, prognosticating, in vivo imaging, preventing,
PT      treating, or determining the predisposition of an individual to breast
PT      cancer.
XX
PS      Claim 52; Page 41-42; 52pp; English.
XX
CC      The present sequence is of human breast BS265 gene expressed sequence tag
CC      (EST) clone 3038129. ESTs were derived from cDNA libraries made from
CC      breast tumour tissues, breast non-tumour tissues and numerous other
CC      tissues, and entered into a database as gene transcript images. They were
CC      then evaluated to identify EST sequences that were representative
CC      primarily of the breast tissue libraries, and were ranked according to
CC      their abundance in the target libraries and absence from background
CC      libraries. 4 Partial clones (see ABLS7345-48) represented the minimum
CC      number of clones that, together with the full-length sequence of clone

```

```

CC      3090752H1 (see ABL57349), were needed to form a contig and from which a
CC      consensus sequence (see ABL57350) for BS265 was derived. Other clones
CC      appeared at positions in the assembly upstream of the above sequences.
CC      Clone 3038129 spanned the entire assembly, and encoded the protein given
CC      in ABB76274. The set of contiguous and partially overlapping cDNA
CC      sequences, designated as BS265 and transcribed from breast tissue, and
CC      the polypeptides encoded by them, are useful for detecting, diagnosing,
CC      staging, monitoring, prognosticating, in vivo imaging, preventing,
CC      treating, or determining the predisposition of an individual to diseases
CC      and conditions of the breast, especially tumours and metastases
XX
SQ      Sequence 2591 BP; 739 A; 591 C; 579 G; 682 T; 0 U; 0 Other;
XX
Query Match      98.7%; Score 2554; DB 6; Length 2591;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY      12 GGCAGCTCCACTCAGCCAGTACCCAGATACCGTGGAACTTCCCGACCAATGGCTTCCC 71
DB      11 GGCAGCTCCACTCAGCCAGTACCCAGATACCGTGGAACTTCCCGACCAATGGCTTCCC 70
QY      72 TGGGGCAGATCCCTCTTCGAGCATATTAAGCATCATATTCTGCTGGAGCAATTG 131
DB      71 TGGGGCAGATCCCTCTTCGAGCATATTAAGCATCATATTCTGCTGGAGCAATTG 130
QY      132 CACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCACTCACTGCTGCGCT 191
DB      131 CACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCACTCACTGCTGCGCT 190
QY      192 CAGCTGGGAACTTGGGGAGATGGAAATCTCGAGCTGCACCTTTTGAACCTGACATCAAAAC 251
DB      191 CAGCTGGGAACTTGGGGAGATGGAAATCTCGAGCTGCACCTTTTGAACCTGACATCAAAAC 250
QY      252 TTTCTGATATCGTATATCAATATGCTGAGAGAAAGGTTTGGAGCTTGGTCCATGAGTTCA 311
DB      251 TTTCTGATATCGTATATCAATATGCTGAGAGAAAGGTTTGGAGCTTGGTCCATGAGTTCA 310
QY      312 AAGAAAGCAAGATGAGCTGTGCGAGAGATGAATGTTAGAGCCGGAACAGAGTGT 371
DB      311 AAGAAAGCAAGATGAGCTGTGCGAGAGATGAATGTTAGAGCCGGAACAGAGTGT 370
QY      372 TTGCTGATCAAGTATATGTTGGCAATGCTCTTTGGCGCTGAAAAAGCTGCACTCAAG 431
DB      371 TTGCTGATCAAGTATATGTTGGCAATGCTCTTTGGCGCTGAAAAAGCTGCACTCAAG 430
QY      432 ATGCTGGACCTACCAATGTTATATCATCACTTCAAGGCAAGGGAGATGTAACCTTG 491
DB      431 ATGCTGGACCTACCAATGTTATATCATCACTTCAAGGCAAGGGAGATGTAACCTTG 490
QY      492 AGTATAAACTGGAACCTTCAGCATGCGGAAAGTGAATGTGACATTAATGCAAGCTCAG 551
DB      491 AGTATAAACTGGAACCTTCAGCATGCGGAAAGTGAATGTGACATTAATGCAAGCTCAG 550
QY      552 AGACCTTGGGCTGTAGAGCTCCCGATGTTCCCGACCAAGTGTCTGGGATCCC 611
DB      551 AGACCTTGGGCTGTAGAGCTCCCGATGTTCCCGACCAAGTGTCTGGGATCCC 610
QY      612 AAGTTGACAGGAGACCAACTTCTGGAAGTGTCCAAATACAGCTTGAAGCTGAAGCTCG 671
DB      611 AAGTTGACAGGAGACCAACTTCTGGAAGTGTCCAAATACAGCTTGAAGCTGAAGCTCG 670
QY      672 AGAATGTGACCATGAAGGTTGTCTGTGCTCTCAATATGTAAGTCAACAACATCACT 731
DB      671 AGAATGTGACCATGAAGGTTGTGTGTGTCTCTCAATATGTAAGTCAACAACATCACT 730
QY      732 CCTGTATGATTAATAATGATATGCTGCAAGCAAGGGAGATATCAAGTGAAGATGCG 791
DB      731 CCTGTATGATTAATAATGATATGCTGCAAGCAAGGGAGATATCAAGTGAAGATGCG 790
QY      792 AGATCAAAAGGGAGTCACTACAGCTGCTTAACTCAAGGCTTCTGTGTCTCTT 851
DB      791 AGATCAAAAGGGAGTCACTACAGCTGCTTAACTCAAGGCTTCTGTGTCTCTT 850

```

QY 852 CTTTCTTGGCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAAT 911
 DB 851 CTTTCTTGGCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATGCTAAATAAT 910
 QY 912 GTGCTTGGCCACAAAAGCATGCAAGTCAATTTGTTACACAGGGATCTACAGAACTAT 971
 DB 911 GTGCTTGGCCACAAAAGCATGCAAGTCAATTTGTTACACAGGGATCTACAGAACTAT 970
 QY 972 TTACACACAGATTTGACCTAGTTTTTATTTCTGGGAGGAAAATGATTCATATCTTGAA 1031
 DB 971 TTACACACAGATTTGACCTAGTTTTTATTTCTGGGAGGAAAATGATTCATATCTTGAA 1030
 QY 1032 GTCTGAGTGAAGCAACAGAGCAAGAAACAAAAGAGCCAAAAGCAGAGAGCTCCAT 1091
 DB 1031 GTCTGAGTGAAGCAACAGAGCAAGAAACAAAAGAGCCAAAAGCAGAGAGCTCCAT 1090
 QY 1092 ATGACCAAGTAAATCTATCTTCAAGACATATTAGAACTTGGAAAATATTCATGTGA 1151
 DB 1091 ATGACCAAGTAAATCTATCTTCAAGACATATTAGAACTTGGAAAATATTCATGTGA 1150
 QY 1152 ACTAGACAAAGTGTAAAGTGAATAGTAAATGACGCTGAGACAAAGTGCATCCCGAG 1211
 DB 1151 ACTAGACAAAGTGTAAAGTGAATAGTAAATGACGCTGAGACAAAGTGCATCCCGAG 1210
 QY 1212 ATCTCAGGGACCTCCCGCTGCTGCTCAGCTGGGAGTGAAGAGCAGAGATAGTGCATGT 1271
 DB 1211 ATCTCAGGGACCTCCCGCTGCTGCTCAGCTGGGAGTGAAGAGCAGAGATAGTGCATGT 1270
 QY 1272 CTTTGTCTGAAATTTTAACTTATATGTGCTGTAATGTGCTCTGAGAAAGCCCTGGA 1331
 DB 1271 CTTTGTCTGAAATTTTAACTTATATGTGCTGTAATGTGCTCTGAGAAAGCCCTGGA 1330
 QY 1332 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAATGTAACCTTA 1391
 DB 1331 AGTCTATCCCAACATATCCACATCTTATATTCACAAATTAAGCTGTAATGTAACCTTA 1390
 QY 1392 AGAGCTGCTAAATTTGACCTGCACTTGGCACTGAGGGGCGGCTGCAATTTAGTAATGGGT 1451
 DB 1391 AGAGCTGCTAAATTTGACCTGCACTTGGCACTGAGGGGCGGCTGCAATTTAGTAATGGGT 1450
 QY 1452 CAAATGATTCATTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1511
 DB 1451 CAAATGATTCATTTTATGATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACA 1510
 QY 1512 AATGCCAAAGTTGAGAAAATGATCATATTTTAACTAAACAGAGAGTGGCGACACC 1571
 DB 1511 AATGCCAAAGTTGAGAAAATGATCATATTTTAACTAAACAGAGAGTGGCGACACC 1570
 QY 1572 GATTTTATAATTAACCTGAGCACCTTCTTTTAAACAAATGCGGGTTATTTCTCA 1631
 DB 1571 GATTTTATAATTAACCTGAGCACCTTCTTTTAAACAAATGCGGGTTATTTCTCA 1630
 QY 1632 GATGATGTTGATCGTGAATGTCAGAGGAAGACCTTTGACCTTGACTATATGACATTA 1691
 DB 1631 GATGATGTTGATCGTGAATGTCAGAGGAAGACCTTTGACCTTGACTATATGACATTA 1690
 QY 1692 TGTGATCACAAGCTGAGGCTTCTCTTCCATCTGCTGAGCAGCTAAGACCTCAGT 1751
 DB 1691 TGTGATCACAAGCTGAGGCTTCTCTTCCATCTGCTGAGCAGCTAAGACCTCAGT 1750
 QY 1752 TTTCAATAGCATCTAGAGCAGTGGGACTGAGCTGGGGTGATTTGCGCCCCCATCTCCG 1810
 DB 1751 TTTCAATAGCATCTAGAGCAGTGGGACTGAGCTGGGGTGATTTGCGCCCCCATCTCCG 1810
 QY 1811 GGGAAATGCTGAAGACAAATTTTGTTAACCTCAATGAGAGAGTGAAGAGATACAGTGTCT 1870
 DB 1811 GGGAAATGCTGAAGACAAATTTTGTTAACCTCAATGAGAGAGTGAAGAGATACAGTGTCT 1870
 QY 1871 ACTACCAACTAGTGAATGAAGGCGCAGGAGTGTGCTCAACTCTTACCATGTACAGAGAG 1930
 DB 1871 ACTACCAACTAGTGAATGAAGGCGCAGGAGTGTGCTCAACTCTTACCATGTACAGAGAG 1930
 QY 1931 TCTCCCATTTACAACTAACCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTCTGG 1990

DB 1931 TCTCCCATTTAGACACTAACCAATCCGAAGTGTCACTGTGTGACGACTAAGAAACCTCTGG 1990
 QY 1991 TTTTGAATGAAAAGGCTCTGAAAAGAGGGAGCCAAACAATCTGTCTGCTT-CTCACAT 2049
 DB 1991 TTTTGAATGAAAAGGCTCTGAAAAGAGGGAGCCAAACAATCTGTCTGCTTCTCACAT 2050
 QY 2050 TAGTCATGAGCAATTAAGATCTGTCTCTTTGGCTGCTGCTCAGACACAGAGAGCCAG 2109
 DB 2051 TAGTCATGAGCAATTAAGATCTGTCTCTTTGGCTGCTGCTCAGACACAGAGAGCCAG 2110
 QY 2110 ACTCTATCGGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGAA 2169
 DB 2111 ACTCTATCGGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGAA 2170
 QY 2170 ATGCTGATGAGATTAATCTTCACTGCTGTTGAGCTTCTTAAGTTCTTTCCCTCATCTAC 2229
 DB 2171 ATGCTGATGAGATTAATCTTCACTGCTGTTGAGCTTCTTAAGTTCTTTCCCTCATCTAC 2230
 QY 2230 CCTGCAAGCCAAAGTCTGTAAAGAAATGCTGAGTCTTGAAGTCTCAGGTTTCTTACTCTG 2289
 DB 2231 CCTGCAAGCCAAAGTCTGTAAAGAAATGCTGAGTCTTGAAGTCTCAGGTTTCTTACTCTG 2290
 QY 2290 AATTAGATCTCCAGACCTCTCTGAGCACAATTCAAATTAAGGCAACAATATACCT 2349
 DB 2291 AATTAGATCTCCAGACCTCTCTGAGCACAATTCAAATTAAGGCAACAATATACCT 2350
 QY 2350 TCCATGAAACACACACAGACTTTTGAACCAAGAACATGACTGCTGTAATGAGGCTT 2409
 DB 2351 TCCATGAAACACACACAGACTTTTGAACCAAGAACATGACTGCTGTAATGAGGCTT 2410
 QY 2410 GAGGAATGAAGCTTTGAAGAAAAGATCTTTGTTCCAGGCCCTTCCACACTCTTC 2469
 DB 2411 GAGGAATGAAGCTTTGAAGAAAAGATCTTTGTTCCAGGCCCTTCCACACTCTTC 2470
 QY 2470 ATGTGTTAACCACTGCTCTCTGAGACCTTGAAGCCAGGCTGACTGATTAATGTTGTTA 2529
 DB 2471 ATGTGTTAACCACTGCTCTCTGAGACCTTGAAGCCAGGCTGACTGATTAATGTTGTTA 2530
 QY 2530 TAGAAAACCTGATTTTGAAGTCTGATCGTTCAAGAAATGATTAATATACATTTCTT 2587
 DB 2531 TAGAAAACCTGATTTTGAAGTCTGATCGTTCAAGAAATGATTAATATACATTTCTT 2588

RESULT 12
 ABL56582
 ID ABL56582 standard; cDNA; 2626 BP.
 AC ABL56582;
 XX
 AC
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Complete nucleotide sequence of the OREO gene (gene B) cDNA.
 XX
 KW Human; gene A; ovarian tumour; gene B; OREO; gene; ovarian cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 61..909
 FT /tag= a
 FT /product= "OREO protein"
 FT
 XX
 PN WO200194641-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 11-JUN-2001; 2001WO-US018700.
 XX
 PR 09-JUN-2000; 2000US-0210451P.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX

PI Ople E, McLachlan K, Heard C;
 XX WPI, 2002-404365/43.
 DR P-PSDB; ABB09879.

XX New polynucleotide and corresponding antigens from human ovarian cancer
 PT cells, useful for treatment and diagnosis of ovarian cancer.

XX Claim 1, Fig 7a; 71pp; English.

XX The present sequence encodes a protein, designated ORO. The ORO (Ople
 CC RDA of Epithelial Tissue vs. Ovary tumour) gene is a novel gene, also
 CC designated gene B. This gene was identified by representational
 CC difference analysis (RDA) screening, and is selectively expressed by
 CC certain human ovarian tumours. The specification also describes gene A,
 CC identified by the same method. Gene A and B polynucleotides are useful
 CC for detecting ovarian cancer. Their polypeptides are useful for treating
 CC ovarian cancer

XX Sequence 2626 BP; 776 A; 589 C; 579 G; 680 T; 0 U; 2 Other;

Query Match 97.7%; Score 2527.2; DB 6; Length 2626;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2565; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

QY 12 GGGAGTCGACCTGAGCAGTACCAGATAGGCTGGGACCTTCCCGAGCATGGCTCC 71
 DB 11 GGGAGTCGACCTGAGCAGTACCAGATAGGCTGGGACCTTCCCGAGCATGGCTCC 70
 QY 72 TGGGGGAGATCCCTCTTCTGGAGCATTAATAGCATCATTAATTCCTGGAGCAATG 131
 DB 71 TGGGGGAGATCCCTCTTCTGGAGCATTAATAGCATCATTAATTCCTGGAGCAATG 130
 QY 132 CACTCATCATTCGCTTGGTATTTTCAGGGAGACCTCATCAAGTCATCACTGCTGCT 191
 DB 131 CACTCATCATTCGCTTGGTATTTTCAGGGAGACCTCATCAAGTCATCACTGCTGCT 190
 QY 192 CAGCTGGGAAACATTTGGGGAGATGAGTAATCTGAGCTGCACTTTTGAACCTGACATCAAC 251
 DB 191 CAGCTGGGAAACATTTGGGGAGATGAGTAATCTGAGCTGCACTTTTGAACCTGACATCAAC 250
 QY 252 TTTCTGATTCGTGATACATAGCTGAGGAAGTCTTTTGAAGCTTGTGCTCATGAGTTCA 311
 DB 251 TTTCTGATTCGTGATACATAGCTGAGGAAGTCTTTTGAAGCTTGTGCTCATGAGTTCA 310
 QY 312 AAGAGGCAAGATGAGCTGTCCGAGCAGATGAATGTTCAAGGCCCGGACAGCATGT 371
 DB 311 AAGAGGCAAGATGAGCTGTCCGAGCAGATGAATGTTCAAGGCCCGGACAGCATGT 370
 QY 372 TTGCTGATCAAGTATGATTTGGCAATGCTTTTGGGGTGAAAAAGTGCATCAG 431
 DB 371 TTGCTGATCAAGTATGATTTGGCAATGCTTTTGGGGTGAAAAAGTGCATCAG 430
 QY 432 ATGCTGGACCTTCAATATGTTATATCATCACTTCTAAGGCAAGGGAAATGCTAACCTTG 491
 DB 431 ATGCTGGACCTTCAATATGTTATATCATCACTTCTAAGGCAAGGGAAATGCTAACCTTG 490
 QY 492 AGATATAAACTGAGCTTACAGATGCGGAAGTGAATGATCTAATATGCCAGCTCAG 551
 DB 491 AGATATAAACTGAGCTTACAGATGCGGAAGTGAATGATCTAATATGCCAGCTCAG 550
 QY 552 AGACCTTGGGGTGAAGGCTCCCGAGTGTTCGCCAGGCCACAGAGTGTCTGGGCAATCC 611
 DB 551 AGACCTTGGGGTGAAGGCTCCCGAGTGTTCGCCAGGCCACAGAGTGTCTGGGCAATCC 610
 QY 612 AAGTTGACGAGGAGCACTTCTCGGAAGTCTCAATACCAAGCTTTGAGCTGAACCTTG 671
 DB 611 AAGTTGACGAGGAGCACTTCTCGGAAGTCTCAATACCAAGCTTTGAGCTGAACCTTG 670
 QY 672 AGAATGTGACATGAAGTGTGTCTGTGCTTCAATATGTTACGATCAACACACACTACT 731
 DB 671 AGAATGTGACATGAAGTGTGTCTGTGCTTCAATATGTTACGATCAACACACACTACT 730

QY 732 CCTGATGATTTAAAAATGACATTTGCCAAGGCAAGGGGATATCAAGTGAACAGATCCG 791
 DB 731 CCTGATGATTTAAAAATGACATTTGCCAAGGCAAGGGGATATCAAGTGAACAGATCCG 790
 QY 792 AGATCAAAAGGCGGAGTCACTTACAGCTGCTTAACTCAAGGCTTCTGTGTCTCTT 851
 DB 791 AGATCAAAAGGCGGAGTCACTTACAGCTGCTTAACTCAAGGCTTCTGTGTCTCTT 850
 QY 852 CTTTCTTTGGCATAGGCTGGGACCTTGTGCTCTCAGCCCTTACTGATGCTAAATAT 911
 DB 851 CTTTCTTTGGCATAGGCTGGGACCTTGTGCTCTCAGCCCTTACTGATGCTAAATAT 910
 QY 912 GTGCTTTGGGAC-AAAAAGCATGCAAGTCAATTTTACACAGGATCTACAGACTA 970
 DB 911 GTGCTTTGGGACAAAAAGCATGCAAGTCAATTTTACACAGGATCTACAGACTA 970
 QY 971 TTTTCCACCGAGATATGACCTTAAATTTATTTCTGGAGAGAAATGAATTCATATGA 1030
 DB 971 TTTTCCACCGAGATATGACCTTAAATTTATTTCTGGAGAGAAATGAATTCATATGA 1030
 QY 1031 AGTGGAGTGGCAAAACAGGCAAGAAACAAAAGGCCAAAAGCAGAAAGGCTCCAA 1090
 DB 1031 AGTGGAGTGGCAAAACAGGCAAGAAACAAAAGGCCAAAAGCAGAAAGGCTCCAA 1090
 QY 1091 TATGAACAAGATTAATCTATCTTCAAGACATATTAGAAATTTGGGAAAAATATCATGTG 1150
 DB 1091 TATGAACAAGATTAATCTATCTTCAAGACATATTAGAAATTTGGGAAAAATATCATGTG 1150
 QY 1151 AACTGACAAATGTGTTAAGAGTATTAAGTAAATGACCTGGAGACAAAGGCAATCCCA 1210
 DB 1151 AACTGACAAATGTGTTAAGAGT-ATAAGTAAATGACAGTGGAGACAAAGGCAATCCCA 1209
 QY 1211 GATCTCAGGAGCCTCCCTGCTGTCACTCGGGAGTGAAGAGACAGATATGTCATGT 1270
 DB 1210 GATCTCAGGAGCCTCCCTGCTGTCACTCGGGAGTGAAGAGACAGATATGTCATGT 1269
 QY 1271 TCTTGTCTGAAATTTTAAATATATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGA 1330
 DB 1270 TCTTGTCTGAAATTTTAAATATATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGA 1329
 QY 1331 AAGTCTATCCCAACATATTCACATTTATTTCCCAAAATTAAGTGTATATGATACCT 1390
 DB 1330 AAGTCTATCCCAACATATTCACATTTATTTCCCAAAATTAAGTGTATATGATACCT 1389
 QY 1391 AAGAGCTGCTAATGACATGCGCACTTCCCACTCAGGGGCGGCTGATTTAGTATGG 1450
 DB 1390 AAGAGCTGCTAATGACATGCGCACTTCCCACTCAGGGGCGGCTGATTTAGTATGG 1449
 QY 1451 TCAAAATGATTCATTTTATATGATGCTTCCAAAGTGCTTGTGCTTCCCACTGAC 1510
 DB 1450 TCAAAATGATTCATTTTATATGATGCTTCCAAAGTGCTTGTGCTTCCCACTGAC 1509
 QY 1511 AAATGCCAAAGTGGAAAAATGATCAATTTTATGATTAACAGAGAGTCCGGGACAC 1570
 DB 1510 AAATGCCAAAGTGGAAAAATGATCAATTTTATGATTAACAGAGAGTCCGGGACAC 1569
 QY 1571 CGATTTTAAATAAATGAGACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTC 1630
 DB 1570 CGATTTTAAATAAATGAGACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTC 1629
 QY 1631 AGATGATGTTCACTCGGTAAATGATCAGGAAAGACCTTTTCACTTGAATATGACATT 1690
 DB 1630 AGATGATGTTCACTCGGTAAATGATCAGGAAAGACCTTTTCACTTGAATATGACATT 1689
 QY 1691 ATGTATCACAAGCTCTGAGGCTTCTCTTTTCCATCTCTGCTGGAACACTTAAGACTCAG 1750
 DB 1690 ATGTATCACAAGCTCTGAGGCTTCTCTTTTCCATCTCTGCTGGAACACTTAAGACTCAG 1749
 QY 1751 TTTTCAATATGACATTAAGAGAGTGGAGTCAAGCTGGGGTGAATTTGCCCCCATCTCCGG 1810
 DB 1750 TTTTCAATATGACATTAAGAGAGTGGAGTCAAGCTGGGGTGAATTTGCCCCCATCTCCGG 1809
 QY 1811 GGAATATGCTGAAGCAATTTTGTTAACCTCAATGAGGAGTGAAGAGATATACAGTCT 1870

```
Db 1810 GGGATATCTGAGAGACATTTTGGTTACCTCAATGAGAGAGTGGAGAGATACAGTCT 1869
Qy 1871 ACTACCACTAGTGTGATTAAGGCCAGGATGTCTCAACCTCTCATCTATGACAGAGC 1930
Db 1870 ACTACCACTAGTGTGATTAAGGCCAGGATGTCTCAACCTCTCATCTATGACAGAGC 1929
Qy 1931 TCTCCCATTAACAATCTCCCAATCCGAAGTGTCACTGTGTGACGAGTAAAGAAACCTGG 1990
Db 1930 TCTCCCATTAACAATCTCCCAATCCGAAGTGTCACTGTGTGACGAGTAAAGAAACCTGG 1989
Qy 1991 TTTTGTAGTAAAGAGGCTGTGAAAGAGGAGCCAAATCTGTCTGCTT-CTCACAT 2049
Db 1990 TTTTGTAGTAAAGAGGCTGTGAAAGAGGAGCCAAATCTGTCTGTCTCTCTCAT 2049
Qy 2050 TAGCTATGGCAATTAAGCAATCTGTCTCTTTGGCTCTGCTGACAGACAGAGCCAGA 2109
Db 2050 TAGCTATGGCAATTAAGCAATCTGTCTCTTTGGCTCTGCTGACAGACAGAGCCAGA 2109
Qy 2110 ACTCTATCGGGGACCAAGATTAACATCTCTGAGTGAACAGAGTGAACAAAGCCATAGGAA 2169
Db 2110 ACTCTATCGGGGACCAAGATTAACATCTCTGAGTGAACAGAGTGAACAAAGCCATAGGAA 2169
Qy 2170 ATGCTGTAGTGGATTAATCTTCAAGCTGTGTGAGCTTCTAAAGTCTTCTCCCTCATTTTAC 2229
Db 2170 ATGCTGTAGTGGATTAATCTTCAAGCTGTGTGAGCTTCTAAAGTCTTCTCCCTCATTTTAC 2229
Qy 2230 CTGCAAGCAAGTCTGTGAAGAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 2289
Db 2230 CTGCAAGCAAGTCTGTGAAGAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 2289
Qy 2290 AATTTGATCTCCAGACCTTCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCA 2349
Db 2290 AATTTGATCTCCAGACCTTCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCA 2349
Qy 2350 TCCATGAGACACACAGACTTTTGAAGAGAAAGAAATCTGTTTCCAGCCCCCTTCCACACTCTTC 2409
Db 2350 TCCATGAGACACACAGACTTTTGAAGAGAAAGAAATCTGTTTCCAGCCCCCTTCCACACTCTTC 2409
Qy 2410 GAGGAATGAAGCTTTGAAGAGAAAGAAATCTGTTTCCAGCCCCCTTCCACACTCTTC 2469
Db 2410 GAGGAATGAAGCTTTGAAGAGAAAGAAATCTGTTTCCAGCCCCCTTCCACACTCTTC 2469
Qy 2470 ATGTGTTAAACACCTGCTTCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCA 2529
Db 2470 ATGTGTTAAACACCTGCTTCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCAATCTGAGCA 2529
Qy 2530 TAGAAAACTGATTTTGAAGTCTGATCTGATCAAGAGATGATTAATATCAATTTCTCT 2587
Db 2530 TAGAAAACTGATTTTGAAGTCTGATCTGATCTGATCAAGAGATGATTAATATCAATTTCTCT 2587
```

RESULT 13

ADP81075 standard; DNA; 2690 BP.

ADP81075;

09-SEP-2004 (first entry)

Human ovarian specific gene, SEQ ID No 109.

normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;

metastatic; cancer; vaccine; cytosolic; human; gene; ds.

Homo sapiens.

WO2004053079-A2.

24-JUN-2004.

08-DEC-2003; 2003WO-US038855.

```
PR 06-DEC-2002; 2002US-0431301P.
PR 06-DEC-2002; 2002US-0431321P.
PR 30-JUN-2003; 2003US-0484584P.
PR 07-NOV-2003; 2003US-0518607P.
PA (DIAD-) DIADEXUS INC.
PI Medina RA, Turner LR, Sun Y, Liu S, Chen H;
XX WPI; 2004-468850/44.
DR P-PSDB; ADP81235, ADP81236.
XX
PT New ovarian specific nucleic acid molecules and polypeptides useful for
PT diagnosing, preventing or treating ovarian cancer, for producing
PT transgenic animals or cells, or for research purposes.
XX
PS Claim 1; SEQ ID NO 109; 754pp; English.
CC The invention relates to novel isolated nucleic acid molecules and
CC polypeptides present in normal and neoplastic ovarian cells. These
CC comprise a nucleic acid sequence encoding any of the 167 amino acid
CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
CC further comprises: a method for determining the presence of a ovarian
CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
CC nucleic acid molecule; a host cell comprising the vector; a method for
CC producing a polypeptide encoded by the above nucleic acid molecule; a
CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
CC or its fragment that specifically binds to the above polypeptide; a
CC method for determining the presence of an ovarian specific protein in a
CC sample; a method for diagnosing or monitoring the presence and metastases
CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
CC presence of cancer in a patient; a kit for detecting a means for
CC determining the presence of the above nucleic acid molecule or
CC polypeptide; a method of treating a patient with ovarian cancer; and a
CC vaccine comprising the above polypeptide or nucleic acid encoding the
CC polypeptide. The isolated nucleic acid molecules and polypeptides have
CC cytostatic activity. The isolated polypeptides may be used to create a
CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
CC for diagnosing or monitoring the presence and metastases of ovarian
CC cancer and treating ovarian cancer. This polynucleotide sequence
CC represents an ovarian specific gene of the invention.
XX
SQ Sequence 2690 BP; 760 A; 611 C; 603 G; 716 T; 0 U; 0 Other;
Query Match 95.1%; Score 2460; DB 12; Length 2690;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2571; Conservative 0; Mismatches 0; Indels 91; Gaps 2;
Qy 17 CTCACCTAGCCAGTACCCAGATACGCTGGAACTTCCCAAGCATGCTTCCCTGGGG 76
Db 28 CTCACCTAGCCAGTACCCAGATACGCTGGAACTTCCCAAGCATGCTTCCCTGGGG 87
Qy 77 CAGATCTCTTCTGAGCATTAATTAACATCAATTAATTTGCTGTGAGCAATTTGCACTC 136
Db 88 CAGATCTCTTCTGAGCATTAATTAACATCAATTAATTTGCTGTGAGCAATTTGCACTC 147
Qy 137 ATCATGGCTTGGTATTTT----- 155
Db 148 ATCATGGCTTGGTATTTTCAAGATCTCTGTGCTTTCAGCAATGAAGGTTTGTT 207
Qy 156 -----CAGGAGACAC 166
Db 208 GTAGAAGTTCAGAGCTTCCCTTAGCATTAATTTGCTTCTGCAATGACAGGAGACAC 267
Qy 167 TCCATGACAGTCACTCTGCTGAGTGGAAATTTGGGAGAGATGAATTCCTGAGC 226
Db 268 TCCATGACAGTCACTCTGCTGAGTGGAAATTTGGGAGAGATGAATTCCTGAGC 327
Qy 227 TGCACTTTGAACCTACATCAAACTTTGATATGATGATCAATGAGCTGAAGAGGT 286
```

Db 328 TGCACCTTTGAACCTGCACATCAAACTTTCGTATATCGTATCAAAATGCGTCGAAGAAAGGT 387
Qy 287 GTTTTAAGGCTTGTCATAGATTTCAAGAGGCAAAAGATGAGCTGTCGAGAGAGATGAA 346
Db 388 GTTTTAAGGCTTGTCATAGATTTCAAGAGGCAAAAGATGAGCTGTCGAGAGAGATGAA 447
Qy 347 ATGTTCAAGAGGCGGACAGACAGTGTGTTGCTGATCAAGTATGTTGGCAATGCTCTTTG 406
Db 448 ATGTTCAAGAGGCGGACAGACAGTGTGTTGCTGATCAAGTATGTTGGCAATGCTCTTTG 507
Qy 407 CGGCTGAAAAACGTGCACCTCAACAGATGCTGACCTTACAAATGTTATATCATCTTCT 466
Db 508 CGGCTGAAAAACGTGCACCTCAACAGATGCTGACCTTACAAATGTTATATCATCTTCT 567
Qy 467 AAGAGCAAGGGGAATGCTAAGCTTGATGATTAACCTGAGCCTTACAGATGCGGAAAGT 526
Db 568 AAGAGCAAGGGGAATGCTAAGCTTGATGATTAACCTGAGCCTTACAGATGCGGAAAGT 627
Qy 527 AATGTGACTATATATGCTCAGACCTTGCAGACCTTGCAGGCTTCCCGATGCTTCC 586
Db 628 AATGTGACTATATATGCTCAGACCTTGCAGACCTTGCAGGCTTCCCGATGCTTCC 687
Qy 587 CAGCCCAACGTGCTGCGGCTCCCAAGTTGACAGGAGCCAACTTCTCGAAGTCTCC 646
Db 688 CAGCCCAACGTGCTGCGGCTCCCAAGTTGACAGGAGCCAACTTCTCGAAGTCTCC 747
Qy 647 AATACAGCTTTGAGCTGTAAGCTCTGAGATGTAACCATGAAGTGTGTCGTGCTAC 706
Db 748 AATACAGCTTTGAGCTGTAAGCTCTGAGATGTAACCATGAAGTGTGTCGTGCTAC 807
Qy 707 AATGTTCAGTCAACACACATACCTCTGATGATTTGAATGACATTGCCAAGCAACA 766
Db 808 AATGTTCAGTCAACACACATACCTCTGATGATTTGAATGACATTGCCAAGCAACA 867
Qy 767 GGGGATATCAAAAGTGCAGAAATCGAGATCAAAAGCGAGTCACTTAAGCTGCTAAC 826
Db 868 GGGGATATCAAAAGTGCAGAAATCGAGATCAAAAGCGAGTCACTTAAGCTGCTAAC 927
Qy 827 TCAAAAGGCTTCTGTGTGCTCTTCTTCTTGGCAGTGGGCACTTCTGCTCTC 886
Db 928 TCAAAAGGCTTCTGTGTGCTCTTCTTCTTGGCAGTGGGCACTTCTGCTCTC 987
Qy 887 AGCCCTTACCTGATGCTAAATATATGCTTGGCCCAAAAAAGCATGCAATG 946
Db 988 AGCCCTTACCTGATGCTAAATATATGCTTGGCCCAAAAAAGCATGCAATG 1047
Qy 947 TTAACAACAGGATCTACAGAACTATTTCAACACAGATGTAAGTATTTATTTCTG 1006
Db 1048 TTAACAACAGGATCTACAGAACTATTTCAACACAGATGTAAGTATTTATTTCTG 1107
Qy 1007 GGAGGAAATGAATTCATCTGAAGTCTGAGTGAAGCAAGAGCAAGAAACAAA 1066
Db 1108 GGAGGAAATGAATTCATCTGAAGTCTGAGTGAAGCAAGAGCAAGAAACAAA 1167
Qy 1067 GAAGCCAAAGAGAGAGGCTCCAAATATGAACAAGATTAATCTATCTTCAAGACATATTA 1126
Db 1168 GAAGCCAAAGAGAGAGGCTCCAAATATGAACAAGATTAATCTATCTTCAAGACATATTA 1227
Qy 1127 GAAGTTGGAAAAATTAATCATGTGAACTTGACAAAGTGTGTTAAGAGTAAAGTAAATG 1186
Db 1228 GAAGTTGGAAAAATTAATCATGTGAACTTGACAAAGTGTGTTAAGAGTAAAGTAAATG 1287
Qy 1187 CAGGTGAGACAAAGTGCATCCCAAGTCTCAGGGAAGCTCCCGCTGCTGACCTGAGGA 1246
Db 1288 CAGGTGAGACAAAGTGCATCCCAAGTCTCAGGGAAGCTCCCGCTGCTGACCTGAGGA 1347
Qy 1247 GTGAGAGACAGAGATAGTCAATGTTCTTGTCTGTGAATTTTATATATGCTGTA 1306
Db 1348 GTGAGAGACAGAGATAGTCAATGTTCTTGTCTGTGAATTTTATATATGCTGTA 1407
Qy 1307 TGTGCTCTGAGAGAGCCCTGGAAGTCTATCCCAACATTCACATCTTATATTTCCAC 1366
Db 1408 TGTGCTCTGAGAGAGCCCTGGAAGTCTATCCCAACATTCACATCTTATATTTCCAC 1467

Qy 1367 AAATTAAGCTGATGATGTAACCTTAAGAGCGCTGCTAATTTGACTGCCACTTGAC 1426
Db 1468 AAATTAAGCTGATGATGTAACCTTAAGAGCGCTGCTAATTTGACTGCCACTTGAC 1527
Qy 1427 GGGCGGCTGCATTTTATGATAGGGTCAAAATGATCACTTTTATATGATGCTTCAAGGTG 1486
Db 1528 GGGCGGCTGCATTTTATGATAGGGTCAAAATGATCACTTTTATATGATGCTTCAAGGTG 1587
Qy 1487 CCTTGGCTTCTTCCCACTGACAAATGCCAAGTTGAGAAAAATGATCAATATTTAG 1546
Db 1588 CTTGGCTTCTTCTTCCCACTGACAAATGCCAAGTTGAGAAAAATGATCAATATTTAG 1647
Qy 1547 CATAAACAGACAGTGGCGGACACCGATTTTATTAATTAACCTGACACTTCTTTTAAA 1606
Db 1648 CATAAACAGACAGTGGCGGACACCGATTTTATTAATTAACCTGACACTTCTTTTAAA 1707
Qy 1607 CAACAAATGCGGGTTATTTTCTCATGATGATGTTCAATCGTGAATGTCAGAGAGAC 1666
Db 1708 CAACAAATGCGGGTTATTTTCTCATGATGATGTTCAATCGTGAATGTCAGAGAGAC 1767
Qy 1667 CTTTCACTGATCTATATGAGATTAATGATCAACAGCTGAGAGCTTCTCTTCCATC 1726
Db 1768 CTTTCACTGATCTATATGAGATTAATGATCAACAGCTGAGAGCTTCTCTTCCATC 1827
Qy 1727 CTGCGTGAACAGCTTAAGACCTCAGTTTCAATAGCATTAAGAGAGTGGGACTCAGCTGG 1786
Db 1828 CTGCGTGAACAGCTTAAGACCTCAGTTTCAATAGCATTAAGAGAGTGGGACTCAGCTGG 1887
Qy 1787 GGTGATTTGCCCCCATCTCCGGGGGAATGTCGAGACAAATTTTGGTTACCTCAATGA 1846
Db 1888 GGTGATTTGCCCCCATCTCCGGGGGAATGTCGAGACAAATTTTGGTTACCTCAATGA 1947
Qy 1847 GGGAGTGAAGAGGATACAGTCTACTACAACTAGTGATTAAGGCCAGGAGATGCTCT 1906
Db 1948 GGGAGTGAAGAGGATACAGTCTACTACAACTAGTGATTAAGGCCAGGAGATGCTCT 2007
Qy 1907 CAACCTCTTACCATGATACAGACGCTTCCCATTAACAATCCCAATCCGAATGTCAC 1966
Db 2008 CAACCTCTTACCATGATACAGACGCTTCCCATTAACAATCCCAATCCGAATGTCAC 2067
Qy 1967 TGTGTACAGACTAAGAAACCTGTTTGAATGAGAAAAGGCTCTGAAAAGGGAGCCA 2026
Db 2068 TGTGTACAGACTAAGAAACCTGTTTGAATGAGAAAAGGCTCTGAAAAGGGAGCCA 2127
Qy 2027 ACAATCTGTCGCTT-CTCACTAATGATTTGCAATTAAGCAATCTGCTCTTGGCT 2085
Db 2128 ACAATCTGTCGCTTCTCACTAATGATTTGCAATTAAGCAATCTGCTCTTGGCT 2187
Qy 2086 GCTGCTCAGACAGAGAGCCAGAACTCTATCGGCAACAGAGATTAACATCTCTCAGTGA 2145
Db 2188 GCTGCTCAGACAGAGAGCCAGAACTCTATCGGCAACAGAGATTAACATCTCTCAGTGA 2247
Qy 2146 CAGAGTTGAACAAGCTTATGAGAAATGCTGATGAGGATTAATCTTCAAGTTGTGAGCTTC 2205
Db 2248 CAGAGTTGAACAAGCTTATGAGAAATGCTGATGAGGATTAATCTTCAAGTTGTGAGCTTC 2307
Qy 2206 TAAGTTCTTTCCTTCAATTCACCTGCAAGCCAAAGTTCTGTAAAGAAAATGCTGAGT 2265
Db 2308 TAAGTTCTTTCCTTCAATTCACCTGCAAGCCAAAGTTCTGTAAAGAAAATGCTGAGT 2367
Qy 2266 TCTAGCTCAGGTTTCTTACTGTGAATTTAGATCTCAGACCTTCTGAGCCAAATTC 2325
Db 2368 TCTAGCTCAGGTTTCTTACTGTGAATTTAGATCTCAGACCTTCTGAGCCAAATTC 2427
Qy 2326 AATTAAGCAACAAACATATACCTTCAATGAAGCACACAGACTTTTGAAGAGAGAC 2385
Db 2428 AATTAAGCAACAAACATATACCTTCAATGAAGCACACAGACTTTTGAAGAGAGAC 2487
Qy 2386 AATGATGCTTGAATGAGGCTTGAAGAAATGAAGCTTGAAGAAAAGAAATCTTGT 2445
Db 2488 AATGATGCTTGAATGAGGCTTGAAGAAATGAAGCTTGAAGAAAAGAAATCTTGT 2547


```

1257 TGGGGA-TGAGAGGACAGAGTAGTGATGCTTTGTCTCTGAATTTTGTAGTAAATG 1315
1301 CTGTATATGTTGCTCGAGGAGACCCCTGGAAGTCTATCCCAATATCATCTTATA 1360
1316 CTGTATATGTTGCTCGAGGAGACCCCTGGAAGTCTATCCCAATATCATCTTATA 1375
1361 TTCCCAAAATTAAGCTGTAGTATGTACCTTAAGACGCTGTATAGTACCTGCGA 1420
1376 TTCCCAAAATTAAGCTGTAGTATGTACCTTAAGACGCTGTATAGTACCTGCGA 1435
1421 ACTCAGGGGCGGCTGATTTTGTATGGGTCAATGATTCATTTTATGATGCTTCA 1480
1436 ACTCAGGGGCGGCTGATTTTGTATGGGTCAATGATTCATTTTATGATGCTTCA 1495
1481 AAGGAGCCCTGCTTCTTCCCACTGACCAATGCG- AAGTGTAGAAAATGATCATA 1539
1496 AAGGAGCCCTGCTTCTTCCCACTGACCAATGCG- AAGTGTAGAAAATGATCATA 1555
1540 ATTTTAGCATAAACAGAGC-AGTCGGCGACACCGATTTTAAATTAAGTACGACCTTC 1598
1556 ATTTTAGCATAAACAGAGCAAGTCGGCGACACCGATTTTAAATTAAGTACGACCTTC 1615
1599 TTTTAAACAAACAAATGCGGGTTTATTTCTAGATGATGTCAT- CCGTGAATGCTCCA 1657
1616 TTTTAAACAAACAAATGCGGGTTTATTTCTAGATGATGTCATCCCGTGAATGCTCCA 1675
1658 GGGAGGACCTTTCACCTTATATGAGATTAATGATCAACAGCTCGAGGCTTCTC 1717
1676 GGGAGGACCTTTCACCTTATATGAGATTAATGATCAACAGCTCGAGGCTTCTC 1735
1718 CTTCATCTCTCGTGAAGAGCTTAAGACCTCAGTTTCAATAGCATCTAGACAGTGGGA 1777
1736 CTTCATCTCTCGTGAAGAGCTTAAGACCTCAGTTTCAATAGCATCTAGACAGTGGGA 1795
1778 CTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTCTGAAGACAAATTTGGTTA 1837
1796 CTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTCTGAAGACAAATTTGGTTA 1855
1838 CCTCATAGGAGGAGTGAAGAGATACAGTGTCACTACCAACATAGGTAAGGCGCAGG 1897
1856 CCTCATAGGAGGAGTGAAGAGATACAGTGTCACTACCAACATAGGTAAGGCGCAGG 1915
1898 GATGCTGCTCAA-CTCTCTACCATGTACAGACGTCTCCCATTAACAATCCCAATCCG 1956
1916 GATGCTGCTCAACCTCTCTACCATGTACAGACGTCTCCCATTAACAATCCCAATCCG 1975
1957 AAGTGTCA- AACTGTGTCAAGACTAAGAAACCTGTTTGAATGAAAAAGGCTCGAAA 2015
1976 AAGTGTCAACCTGTGTCAAGACTAAGAAACCTGTTTGAATGAAAAAGGCTCGAAA 2035
2016 GAGGGGAGCCAAATCTGTGCGCTT-CTCAATTAGCATTTGGCAATAGCATTTCCG 2074
2036 GAGGGGAGCCAAATCTGTGCTGCTCTCAATTAGCATTTGGCAATAGCATTTCCG 2095
2075 TCTCTTTGGCTGCTGCTCAAGACAGAGCCAGAACTCTATCGGCGACACAGATTAACAT 2134
2096 TCTCTTTGGCTGCTGCTCAAGACAGAGCCAGAACTCTATCGGCGACACAGATTAACAT 2155
2135 CTCTCAGTGAACAGAGTTGACAGAGCCATATGGAATAATGCTGATGGATTAATCTTCAAGCT 2194
2156 CTCTCAGTGAACAGAGTTGACAGAGCCATATGGAATAATGCTGATGGATTAATCTTCAAGCT 2215
2195 TGTTAGGCTTCAAGTTCTTTCCCTCAATGCTACCCCTGCAAGCCAAAGTTCTGTAGAGA 2254
2216 TGTTAGGCTTCAAGTTCTTTCCCTCAATGCTACCCCTGCAAGCCAAAGTTCTGTAGAGA 2275
2255 AATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCCAGACCTTCCG 2314
2276 AATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCCAGACCTTCCG 2335
2315 GCCAATTTCAATTAAGGCAACAAATATATCTTCAATGAAGACACACAGACTTTTG 2374

```

```

Db 2336 GCCAATTTCAATTAAGGCAACAAATATATCTTCCATGAAGACACACAGACTTTTG 2395
QY 2375 AAAGCAGAGACATGACTGCTTGAATTAAGAGCTTGAAGAAATGAAGCTTTGAAGAAAG 2434
Db 2386 AAAGCAGAGACATGACTGCTTGAATTAAGAGCTTGAAGAAATGAAGCTTTGAAGAAAG 2455
QY 2435 AATACCTTTGTTCCAGCCCCCTTCCACACTCTTTCATGTTTAACTGCTTCTGGA 2494
Db 2456 AATACCTTTGTTCCAGCCCCCTTCCACACTCTTTCATGTTTAACTGCTTCTGGA 2515
QY 2495 CCTTGAGCCACAGGAGCTGATTAATCAATGTTTATATAAAATGATTTTGAAGTTCGA 2554
Db 2516 CCTTGAGCCACAGGAGCTGATTAATCAATGTTTATATAAAATGATTTTGAAGTTCGA 2575
QY 2555 TCGTTCAAGAGATGATTAATATATCATTTCT 2587
Db 2576 TCGTTCAAGAGATGATTAATATATCATTTCT 2608

RESULT 15
AAD32526
ID AAD32526 standard; DNA; 2626 BP.
XX
AC AAD32526;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human B7-H8 gene #2.
XX
KW Human; B7-like protein; inflammation; tissue damage; immune disorder;
KW Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis;
KW diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer;
KW rheumatoid arthritis; cardiovascular disorder; nervous system disorder;
KW myocardial ischaemia; ulcerative colitis; reproductive system disorder;
KW Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis;
KW diabetes mellitus; Grave's disease; Paget's disease; liver disorder;
KW gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia;
KW dysphagia; hepatomegaly; neurological disease; infectious disease;
KW epilepsy; gene therapy; B7-H8 protein; chromosome 1; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 74..115
FT FT /*tag=a
FT FT /product="Human B7-H8 protein"
XX
FN WO200202587-A1.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US020917.
XX
PR 30-JUN-2000; 2000US-0215135P.
XX
PR 14-AUG-2000; 2000US-0225266P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Piscella M, Ni J, Ruben SM;
XX
DR WPI; 2002-257198/30.
XX
DR P-PsDB; AAE20318.
XX
PT Isolated nucleic acids encoding human B7-like polypeptides, useful for
PT diagnosis and treatment of e.g. inflammation, cancer, immune disorders
PT such as Addison's disease, and cardiovascular disorders such as
PT myocardial ischaemia.
XX
PS Example 1; Page 457-458; 493bp; English.
XX
CC The present invention relates to novel human B7-like polypeptides and
CC polynucleotides encoding such proteins. Sequences of the invention are
CC used for preventing, treating or ameliorating a medical condition in a

```

CC mammalian subject. The polynucleotides and polypeptides are administered
CC to subjects having a disorder related to B-7 like polypeptides, such as
CC inappropriate or excessive inflammation which can lead to tissue damage
CC or even death, where the inflammation is brought about by the activation
CC of certain cells in the body e.g. T cells and may involve antibodies
CC related to immune system. The nucleic acids, proteins, antibodies,
CC agonists and antagonists of the invention are useful in the diagnosis,
CC treatment and prevention of cancer (e.g. cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, urogenital or
CC lung), immune disorders (e.g., Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis, ulcerative colitis),
CC cardiovascular disorders (e.g., myocardial ischaemias), nervous system
CC disorders (Alzheimer's disease, Parkinson's disease), endocrine disorders
CC (e.g., diabetes mellitus, Grave's disease), reproductive system disorders
CC (e.g., cryptorchidism, Paget's disease), gastrointestinal disorders (e.g.,
CC dysphagia, irritable bowel syndrome), liver disorders (e.g., hepatitis,
CC hepatomegaly), neurological diseases (e.g., cerebral anoxia and epilepsy)
CC and infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Sequences of the invention are also used in gene therapy. The
CC present sequence is a DNA encoding human B7-H8 protein

XX Sequence 2626 BP; 761 A; 598 C; 582 G; 685 T; 0 U; 0 Other;

Query Match 93.6%; Score 2421.8; DB 6; Length 2626;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2535; Conservative 0; Mismatches 7; Indels 11; Gaps 11;

QY 45 GGGAACTTCCCAAGCCAGTGGCTTCTGGGGAGATCTTCTGGAGATTA-TTAC 103
DB 57 GGAACCTTCCCAAGCCAGTGGCTTCTGGGGAGATCTTCTGGAGATTA-TTAC 116
QY 104 ATATATATTTTGTGGTGAGCAATTTGATCATCATTTGGCTTTGGTATTTCAAGGAGA 163
DB 117 ATATATATTTTGTGGTGAGCAATTTGATCATCATTTGGCTTTGGTATTTCAAGGAGA 176
QY 164 CACTCATCAGATCATCATCTGTGCTGCTGAGTGGGAACTTGGGGAGATTTGATCTGT 223
DB 177 CACTCATCAGATCATCATCTGTGCTGCTGAGTGGGAACTTGGGGAGATTTGATCTGT 236
QY 224 AGCTGCACTTTGAACCTGATCAAACTTTGTGATATCGTATACATAGCTGAAGAA 283
DB 237 AGCTGCACTTTGAACCTGATCAAACTTTGTGATATCGTATACATAGCTGAAGAA 296
QY 284 GGTGTTTGAAGCTTGTGCTGATGATCAAGAAAGG-CAAGATGAGCTGCGAGAGAGA 342
DB 297 GGTGTTTGAAGCTTGTGCTGATGATCAAGAAAGG-CAAGATGAGCTGCGAGAGAGA 356
QY 343 TGAATGTTGAGAGGC-GGACAGAGAGTGTGCTGATCAAGTATGATGGCATGCTT 401
DB 357 TGAATGTTGAGAGGC-GGACAGAGAGTGTGCTGATCAAGTATGATGGCATGCTT 416
QY 402 C-TTGGGGCTGAAAAAGTGAACCTGACAGATGCTGGCACTTAAATGTTATATCATC 460
DB 417 CTTTGGGGCTGAAAAAGTGAACCTGACAGATGCTGGCACTTAAATGTTATATCATC 476
QY 461 ACTTCTAAAGGCAAGGGAATGCTTAACCTTGAATTAACCTGAGCTTCAAGATGCC 520
DB 477 ACTTCTAAAGGCAAGGGAATGCTTAACCTTGAATTAACCTGAGCTTCAAGATGCC 536
QY 521 GAAGTGAATGTGACTTAATGCAAGCTGAGAGCTTGGGATGTGAGGCTCCCGATGG 580
DB 537 GAAGTGAATGTGACTTAATGCAAGCTGAGAGCTTGGGATGTGAGGCTCCCGATGG 596
QY 581 TTCCCAAGCCCAAGTGTCTGGGCAATCCAAATTTGACAGGAGGCAATTTCTGGAA 640
DB 597 TTCCCAAGCCCAAGTGTCTGGGCAATCCAAATTTGACAGGAGGCAATTTCTGGAA 656
QY 641 GTTCTCAATTCAGCTTTGAGCTGAATCTGAGAAATGTGACATGAAGGTTGTCTGTG 700
DB 657 GTTCTCAATTCAGCTTTGAGCTGAATCTGAGAAATGTGACATGAAGGTTGTCTGTG 716
QY 701 CTCACAAATGTGATCAACAACATCTCTGTATGATGAAAAATGATTCATTCGCAAA 760

DB 717 CTCACAAATGTGATCAACAACATCTCTGTATGATGAAAAATGATTCATTCGCAAA 776
QY 761 GCACAGGGGATTCAAAGTGAACAGATTTGGAGATTAAGAGGGAGTCACTTACAGCTG 820
DB 777 GCACAGGGGATTCAAAGTGAACAGATTTGGAGATTAAGAGGGAGTCACTTACAGCTG 836
QY 821 CTAAATCTAAAGGCTTCTGTGTGCTCTTCTTTTGGCATGAGCTGGGCACTTCTG 880
DB 837 CTAAATCTAAAGGCTTCTGTGTGCTCTTCTTTTGGCATGAGCTGGGCACTTCTG 896
QY 881 CCTCTCAGCCCTTACCTGATGCTAAATATATGCTTGGCCCAAAAAAGCATGCAAG 940
DB 897 CCTCTCAGCCCTTACCTGATGCTAAATATATGCTTGGCCCAAAAAAGCATGCAAG 956
QY 941 TCATTTGTACACAGGATCTACAGACTTATTTACCAACCAATATAGCTTATTTATTA 1000
DB 957 TCATTTGTACACAGGATCTACAGACTTATTTACCAACCAATATAGCTTATTTATTA 1016
QY 1001 TTTCTGGAGGAAATGATATCTATGATGATGAGTGGAGCAACAAGAGCAAGAA 1060
DB 1017 TTTCTGGAGGAAATGATATCTATGATGATGAGTGGAGCAACAAGAGCAAGAA 1076
QY 1061 CAAAAAGAGCCAAAAAGCAGAAAGCTCAATATGAAACAAGATTAATCTTCAAAAGC 1120
DB 1077 CAAAAAGAGCCAAAAAGCAGAAAGCTCAATATGAAACAAGATTAATCTTCAAAAGC 1136
QY 1121 ATATTGAAAGTTGGGAAATTAATTCATGTGAACTGACAAAGTGTGTAAGATGATTA 1180
DB 1137 ATATTGAAAGTTGGGAAATTAATTCATGTGAACTGACAAAGTGTGTAAGATGATTA 1196
QY 1181 AAAATGACAGTGGAGACAAGTGATCCAGATCTGAGGAGCCTCCCGGCTGTCAAC 1240
DB 1197 AAAATGACAGTGGAGACAAGTGATCCAGATCTGAGGAGCCTCCCGGCTGTCAAC 1256
QY 1241 TGGGAGTGAAGAGCAGAGATAGTGCATTTCTTGTCTGTGAATTTTATGATATG 1300
DB 1257 TGGGAG-TGAGAGAGAGATAGTGCATTTCTTGTCTGTGAATTTTATGATATG 1315
QY 1301 CTGTAAATGTTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCCACTTTTA 1360
DB 1316 CTGTAAATGTTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCCACTTTTA 1375
QY 1361 TTCCACAAATTAAGCTGTGATATGATCCTTAAGAGCTGTATGATGACCTGGCA 1420
DB 1376 TTCCACAAATTAAGCTGTGATATGATCCTTAAGAGCTGTATGATGACCTGGCA 1435
QY 1421 ACTCAGGGCGGCTGATTTTATGATATGAGTCACTTTTATGATGCTTCCA 1480
DB 1436 ACTCAGGGCGGCTGATTTTATGATATGAGTCACTTTTATGATGCTTCCA 1495
QY 1481 AAGTCCCTTGGCTTCTTCTTCCCACTGACAAATGCC-AAAGTGAAGAAAATGATCAT 1539
DB 1496 AAGTCCCTTGGCTTCTTCTTCCCACTGACAAATGCC-AAAGTGAAGAAAATGATCAT 1555
QY 1540 AATTTGACATTAACAGAGC-AATCGGCGCACCGAATTTTATTAATACTGACACTTC 1598
DB 1556 AATTTGACATTAACAGAGC-AATCGGCGCACCGAATTTTATTAATACTGACACTTC 1615
QY 1599 TTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAAT-CCGTGAATGTTCA 1657
DB 1616 TTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAAT-CCGTGAATGTTCA 1675
QY 1658 GGGAGAGACCTTTACCTTGAATATGAGCAATTAATGATCAACAGCTCTGAGGCTTCTC 1717
DB 1676 GGGAGAGACCTTTACCTTGAATATGAGCAATTAATGATCAACAGCTCTGAGGCTTCTC 1735
QY 1718 CTTTCATCTCTGAGAGAGCTTAAGACTGAGTTTCAATGAGCATCTGAGAGAGTGGGA 1777
DB 1736 CTTTCATCTCTGAGAGAGCTTAAGACTGAGTTTCAATGAGCATCTGAGAGAGTGGGA 1795
QY 1778 CTCAGCTGGGGTGAATTTCCGCCCACTCTCGGGGGAATGTCTGAAGCAATTTGGTTA 1837

Db 1796 CTGAGCTGGGGTGAATTTCCGCCCCCATCTCCGGGGGAATGCTGAAGACAATTTTGTTA 1855
QY 1838 CCTCAATGAGGGAGTGGAGGAGATACAGTGTACTACCACTAGTGTGATAAGGCCAGG 1897
Db 1856 CCTCAATGAGGGAGTGGAGGAGATACAGTGTACTACCACTAGTGTGATAAGGCCAGG 1915
QY 1898 GATGCTGCTCAA-CCTCTACCATGTACAGAGCTCTCCCATTTACAATACCAATCCG 1956
Db 1916 GATGCTGCTCAACCTCTACCATGTACAGAGCTCTCCCATTTACAATACCAATCCG 1975
QY 1957 AAGTGT-C-AAGTGTGACGACTAAGAAAACCTGGTTTGTAGTAAAGGGCTGGAAA 2015
Db 1976 AAGTGTCAAACTGTGTACAGACTAAGAACCCCTGGTTTGTAGTAAAGGGCTGGAAA 2035
QY 2016 GAGGGAGGCAACAATCTGTCTGCTT-CTCAATTAAGTCAATTGGCAATAAGCAATTCG 2074
Db 2036 GAGGGAGGCAACAATCTGTCTGCTTCTCTCAATTAAGTCAATTGGCAATAAGCAATTCG 2095
QY 2075 TCTCTTTGSGCTGCTGCTGACAGACAGAGCCAGAACTCTATCGGCAACAGATTAACAT 2134
Db 2096 TCTCTTTGSGCTGCTGCTGACAGACAGAGCCAGAACTCTATCGGCAACAGATTAACAT 2155
QY 2135 CTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTTATGGGATTAATCTTCACT 2194
Db 2156 CTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTTATGGGATTAATCTTCACT 2215
QY 2195 TGTGAGCTTCAAGTTCTTCCCTTCACTTCACTGACCAAGTCTGTAGAGA 2254
Db 2216 TGTGAGCTTCAAGTTCTTCCCTTCACTTCACTGACCAAGTCTGTAGAGA 2275
QY 2255 AATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCAGACCTTCTG 2314
Db 2276 AATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCAGACCTTCTG 2335
QY 2315 GCCACAAATTCAAATTAAGGCAACAACATATACCTTCCATGAGACACACAGACTTTG 2374
Db 2336 GCCACAAATTCAAATTAAGGCAACAACATATACCTTCCATGAGACACACAGACTTTG 2395
QY 2375 AAGCAAGGACAATGACTGCTGAATTGAGGCTTGAGGAATGAAGCTTGAAGGAAAG 2434
Db 2396 AAGCAAGGACAATGACTGCTGAATTGAGGCTTGAGGAATGAAGCTTGAAGGAAAG 2455
QY 2435 AATACTTTGTTTCAAGCCCCCTTCCACACTCTTCAATGTGTTAACCACTGCCTCTGGA 2494
Db 2456 AATACTTTGTTTCAAGCCCCCTTCCACACTCTTCAATGTGTTAACCACTGCCTCTGGA 2515
QY 2495 CCTTGAGCCACGGTACTGTATTAATCATGTTGTTATAGAAAATGATTTTATAGATTCTGA 2554
Db 2516 CCTTGAGCCACGGTACTGTATTAATCATGTTGTTATAGAAAATGATTTTATAGATTCTGA 2575
QY 2555 TCGTTCAAGAAATGATTAATTAATTAATTCCT 2587
Db 2576 TCGTTCAAGAAATGATTAATTAATTAATTCCT 2608

Search completed: May 30, 2005, 10:27:07
Job time : 1597.66 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 17:54:16 ; Search time 1774.97 Seconds
(without alignments)
8948.327 Million cell updates/sec

Title: US-09-763-978B-1

Perfect score: 2587
Sequence: 1 ggaagagcagcggcagctcc.....tgatataacatacttccct 2587

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 306979757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2565	99.1	2627	9	US-09-778-320-207 Sequence 207, App
2	2565	99.1	2627	9	US-09-910-689-207 Sequence 207, App
3	2565	99.1	2627	9	US-09-884-441-391 Sequence 391, App
4	2565	99.1	2627	10	US-09-807-969-391 Sequence 391, App
5	2565	99.1	2627	10	US-09-827-271-391 Sequence 391, App
6	2565	99.1	2627	13	US-10-010-742-207 Sequence 207, App
7	2565	99.1	2627	15	US-10-198-053-391 Sequence 391, App
8	2565	99.1	2627	18	US-10-714-389-207 Sequence 207, App
9	2565	99.1	2627	18	US-10-717-296-207 Sequence 207, App
10	2565	99.1	2627	19	US-10-860-790-391 Sequence 391, App
11	2563.4	99.1	3357	17	US-10-023-339-2 Sequence 2, Appl

12	2563	99.1	2603	9	US-09-896-738-1 Sequence 1, Appl
13	2554	98.7	2591	9	US-09-850-178-23 Sequence 23, Appl
14	2527.2	97.7	2626	9	US-09-877-065-7 Sequence 7, Appl
15	2421.8	93.6	2626	17	US-10-023-339-9 Sequence 9, Appl
16	1921.4	74.3	1965	10	US-09-814-353-19262 Sequence 19262, A
17	1599.8	61.8	1658	9	US-09-889-722-290 Sequence 290, App
18	1599.8	61.8	1658	9	US-09-889-723-290 Sequence 290, App
19	1599.8	61.8	1658	9	US-09-889-723-290 Sequence 290, App
20	1599.8	61.8	1658	9	US-09-889-727-290 Sequence 290, App
21	1599.8	61.8	1658	9	US-09-889-731-290 Sequence 290, App
22	1599.8	61.8	1658	9	US-09-889-732-290 Sequence 290, App
23	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
24	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
25	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
26	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
27	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
28	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
29	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
30	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
31	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
32	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
33	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
34	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
35	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
36	1599.8	61.8	1658	9	US-09-911-163-290 Sequence 290, App
37	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
38	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
39	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
40	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
41	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
42	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
43	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
44	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App
45	1599.8	61.8	1658	10	US-09-989-734-290 Sequence 290, App

ALIGNMENTS

RESULT 1
US-09-778-320-207
Sequence 207, Application US/09778320
Patent No. US20010034052A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: 210121.491C5
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 207
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-778-320-207
Query Match 99.1%; Score 2565; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 256; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 12 GCGAGTCACTCAGCAGCAGTACCGATACGCTGGGAACTTCCCGAGCAATGGCTTCCC 71
DB 33 GCGAGTCACTCAGCAGCAGTACCGATACGCTGGGAACTTCCCGAGCAATGGCTTCCC 92
QY 72 TGGGAGATCCCTCTTGGAGCATATAGATCATATATTTCTGGCTGGAGCAATGG 131

Db 93 TGGGGAGATCCCTCTCTGAGACATPATAGCATCATTAATTCGGCTGGAGCAATG 152
Qy 132 CACTCATCTTGGCTTTGGTATTTTCAAGGAGACATCCCATCAAGCATCTACTGCGCT 191
Db 153 CACTCATCTTGGCTTTGGTATTTTCAAGGAGACATCCCATCAAGCATCTACTGCGCT 212
Qy 192 CAGCTGGGAACATTGGGGAGATGGAATCTGAGCTGCACTTTTGNACCTGACATCAAC 251
Db 213 CAGCTGGGAACATTGGGGAGATGGAATCTGAGCTGCACTTTTGNACCTGACATCAAC 272
Qy 252 TTTCTGATATCGTGATACATAGCGCTGAGAGAAAGTGTTTTAGCGTTGCTCATGAGTTCA 311
Db 273 TTTCTGATATCGTGATACATAGCGCTGAGAGAAAGTGTTTTAGCGTTGCTCATGAGTTCA 332
Qy 312 AAGAAAGGCAAAATAGAGCTGGGAGCAGGATGAAATGTTCAAGGCCGGAGACAGAGTGT 371
Db 333 AAGAAAGGCAAAATAGAGCTGGGAGCAGGATGAAATGTTCAAGGCCGGAGACAGAGTGT 392
Qy 372 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAAAAACGTCAACTCACAG 431
Db 393 TTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAAAAACGTCAACTCACAG 452
Qy 432 ATGCTGGACCTTCAAAATGTTATATCATCTTCTTAAAGGCAAGGGGAAATGCTAACCTTG 491
Db 453 ATGCTGGACCTTCAAAATGTTATATCATCTTCTTAAAGGCAAGGGGAAATGCTAACCTTG 512
Qy 492 AGTATATTAACCTGGAGCTTCAGATGCCGGAAAGTGAATGATATATATGCAAGTCAAG 551
Db 513 AGTATATTAACCTGGAGCTTCAGATGCCGGAAAGTGAATGATATATATGCAAGTCAAG 572
Qy 552 AGACCTTGGCGGTGTGAGGCTCCCGCATGGTTCCCGCAGCCCAAGTGTCTGGGCAATCCC 611
Db 573 AGACCTTGGCGGTGTGAGGCTCCCGCATGGTTCCCGCAGCCCAAGTGTCTGGGCAATCCC 632
Qy 612 AAGTTGACCAAGGAGGCAACTTCTGCGAAGTCTCCAAATACAGCTTTGAGCTGAACTCTG 671
Db 633 AAGTTGACCAAGGAGGCAACTTCTGCGAAGTCTCCAAATACAGCTTTGAGCTGAACTCTG 692
Qy 672 AAGAAATGACCAATGAAGGTTGTGTGTCTGTACAAATGTTGATGATCAACATCACTAT 731
Db 693 AAGAAATGACCAATGAAGGTTGTGTGTCTGTACAAATGTTGATGATCAACATCACTAT 752
Qy 732 CCTGTATGATTGAAATGACATTTGCCAAAGCAACAGGGGATATCAAAAGTGAAGATCCG 791
Db 753 CCTGTATGATTGAAATGACATTTGCCAAAGCAACAGGGGATATCAAAAGTGAAGATCCG 812
Qy 792 AGATCAAAAGGGGAGTCACTTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTCTT 851
Db 813 AGATCAAAAGGGGAGTCACTTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTCTT 872
Qy 852 CTTTCTTTGGCAATGAGCTGGGCACTTCTGCTCTGAGCCCTTACCGGATGCTAAATAT 911
Db 873 CTTTCTTTGGCAATGAGCTGGGCACTTCTGCTCTGAGCCCTTACCGGATGCTAAATAT 932
Qy 912 GTGCTCTGGGCACAAAAAAGCATGCAAGTCAATTTGTTACAAGAGGATCTACAGACTAT 971
Db 933 GTGCTCTGGGCACAAAAAAGCATGCAAGTCAATTTGTTACAAGAGGATCTACAGACTAT 992
Qy 972 TTTACCAACAAGATATGACCTAAGTTTATATTTCTGGAGGAAATGATTCATATCTAGAA 1031
Db 993 TTTACCAACAAGATATGACCTAAGTTTATATTTCTGGAGGAAATGATTCATATCTAGAA 1052
Qy 1032 GTCTGAGTGAGCAAAACAAGAGCAAGAAACAAAAAAGCAAAAGCAAGAGGCTCCAT 1091
Db 1053 GTCTGAGTGAGCAAAACAAGAGCAAGAAACAAAAAAGCAAAAGCAAGAGGCTCCAT 1112
Qy 1092 ATGAACAAGATTAATCTATCTTCAAGACATATTTAGAAGTTGGGAAATATATTCATGTGA 1151
Db 1113 ATGAACAAGATTAATCTATCTTCAAGACATATTTAGAAGTTGGGAAATATATTCATGTGA 1172
Qy 1152 ACTAAGCAAGTGTATTAAGATGATTAAGTAAATGCAAGCTGAGACAAAGTCAATCCGAG 1211

Db 1173 ACTAAGCAAGTGTATTAAGATGATTAAGTAAATGCAAGCTGAGCAAAAGTCAATCCGAG 1232
Qy 1212 ATCTCAAGGACCTCCCTGCTGTCACCTGGGAGTGAAGAGACAGGATAGTGCATGTT 1271
Db 1233 ATCTCAAGGACCTCCCTGCTGTCACCTGGGAGTGAAGAGACAGGATAGTGCATGTT 1292
Qy 1272 CTTTGTCTGTGAATTTTATGTTATATGTGCTGTAAATGTTGCTCTGAGAGAGCCCTGGAA 1331
Db 1293 CTTTGTCTGTGAATTTTATGTTATATGTGCTGTAAATGTTGCTCTGAGAGAGCCCTGGAA 1352
Qy 1332 AGCTATATCCCAACATATCCATCTTAATTCACAAATTAAGCTATGATATGATCCCTA 1391
Db 1353 AGCTATATCCCAACATATCAATCTTAATTCACAAATTAAGCTATGATATGATCCCTA 1412
Qy 1392 AGACGCTGCTAATGACCTGCACATTCGCACTCAGAGGGCGGCTGCATTTTATATAGGGT 1451
Db 1413 AGACGCTGCTAATGACCTGCACATTCGCACTCAGAGGGCGGCTGCATTTTATATAGGGT 1472
Qy 1452 CAATGATTCACCTTTTATGATGCTTCCAAAGTGTGCTTGGCTTCTTCCCACTGACA 1511
Db 1473 CAATGATTCACCTTTTATGATGCTTCCAAAGTGTGCTTGGCTTCTTCCCACTGACA 1532
Qy 1512 AATGCAAAAGTTGAGAAAAATGATCATATTTTATGATTAACAGAGCAGTGGGAGAC 1571
Db 1533 AATGCAAAAGTTGAGAAAAATGATCATATTTTATGATTAACAGAGCAGTGGGAGAC 1592
Qy 1572 GATTTTATTAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1631
Db 1593 GATTTTATTAATTAACCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1652
Qy 1632 GATGATGTTCAATCCGTGAATGCTCCAGGAGAGACCTTTCACCTTGACTATATGGCATTA 1691
Db 1653 GATGATGTTCAATCCGTGAATGCTCCAGGAGAGAGACCTTTCACCTTGACTATATGGCATTA 1712
Qy 1692 TGTGATTCACAGGCTCTGAGGCTTCTCTTCCATCTGCGGGGAGCAGCTAAGACCTCAGT 1751
Db 1713 TGTGATTCACAGGCTCTGAGGCTTCTCTTCCATCTGCGGGGAGCAGCTAAGACCTCAGT 1772
Qy 1752 TTTCAATAGCAATCTGAGACAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCATCTCCGGG 1811
Db 1773 TTTCAATAGCAATCTGAGACAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCATCTCCGGG 1832
Qy 1812 GGAATGCTGAAGCAATTTTGTGTTACTCAATGAGGAGTGAAGAGATACAGTGTCTA 1871
Db 1833 GGAATGCTGAAGCAATTTTGTGTTACTCAATGAGGAGTGAAGAGATACAGTGTCTA 1892
Qy 1872 CTACCAACTAGTGAATAAGGCGAAGGATGTGCTCAACTCTCACTATGTACAGAGAGT 1931
Db 1893 CTACCAACTAGTGAATAAGGCGAAGGATGTGCTCAACTCTCACTATGTACAGAGAGT 1952
Qy 1932 CTCCCCATTTAACAATCCCAATCCGAAGTGTCAACTGTGTGAGGACTAAGAAACCTTGGT 1991
Db 1953 CTCCCCATTTAACAATCCCAATCCGAAGTGTCAACTGTGTGAGGACTAAGAAACCTTGGT 2012
Qy 1992 TTTGAGTGAAGAAAGGCTCTGGAAGAGGAGAGCCAAATCTGTCTCTT-CTCACATT 2050
Db 2013 TTTGAGTGAAGAAAGGCTCTGGAAGAGGAGAGCCAAATCTGTCTCTTCTTCTCACATT 2072
Qy 2051 AGTCAATGGCAATTAAGGATCTGTCTTTTGGCGTGGCTCCAGACAGAGAGCAGAA 2110
Db 2073 AGTCAATGGCAATTAAGGATCTGTCTTTTGGCGTGGCTCCAGACAGAGAGCAGAA 2132
Qy 2111 CTCTATCGGGCACAGATTAACATCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAA 2170
Db 2133 CTCTATCGGGCACAGATTAACATCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAA 2192
Qy 2171 TGCCTGATGGGATTAATCTTCAAGCTTTGAGCTTCAAGTTTCTTTCCCTTCAATTTACC 2230
Db 2193 TGCCTGATGGGATTAATCTTCAAGCTTTGAGCTTCAAGTTTCTTTCCCTTCAATTTACC 2252
Qy 2231 CTGCAAGCCAAAGTTCTGTGAAGAGAAATGCCGTAAGTTCAAGCTCAAGTTTCTTACTGGA 2290
Db 2253 CTGCAAGCCAAAGTTCTGTGAAGAGAAATGCCGTAAGTTCTAAGTTTCTTACTGGA 2312

Qy 2291 ATTAGATCTCCAGACCCCTTCTGGCCCAATTCATTAAGGCAAGAAACATFACCTT 2350
|||||
Db 2313 ATTAGATCTCCAGACCCCTTCTGGCCCAATTCATTAAGGCAAGAAACATFACCTT 2372
|||||
Qy 2351 CCATGAAGCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTGAGGCTTG 2410
|||||
Db 2373 CCATGAAGCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTGAGGCTTG 2432
|||||
Qy 2411 AGGATGAGCTTTGAAGAAAGAAATACCTTTTCCAGCCCCCTTCCACACTCTTCA 2470
|||||
Db 2433 AGGATGAGCTTTGAAGAAAGAAATACCTTTTCCAGCCCCCTTCCACACTCTTCA 2492
|||||
Qy 2471 TGTGTTAACACAGCTCCCTCCGACCTTGAAGCCAGCGTACCTTATTAAGTGTGTAT 2530
|||||
Db 2493 TGTGTTAACACAGCTCCCTCCGACCTTGAAGCCAGCGTACCTTATTAAGTGTGTAT 2552
|||||
Qy 2531 AGAAACTGATTTAGAGTTCTGATCGTTCAGAGATGATTAATATACCTTCT 2587
|||||
Db 2553 AGAAACTGATTTAGAGTTCTGATCGTTCAGAGATGATTAATATACCTTCT 2609
|||||

RESULT 2

US-09-910-689-207
; Sequence 207, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yujin
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910.689
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-689-207

Query Match 99.1%; Score 2565; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCCACTAGCCAGTACCAGATAGCGTGGAACTTCCCGACGATGGCTTCCC 71
|||||
Db 33 GGCAGCTCCACTAGCCAGTACCAGATAGCGTGGAACTTCCCGACGATGGCTTCCC 92
|||||
Qy 72 TGGGGCAGATCTCTTCTTGAGCATTAATAGCATCATCATTTATCTGGCTGAGCAATTG 131
|||||
Db 93 TGGGGCAGATCTCTTCTTGAGCATTAATAGCATCATCATTTATCTGGCTGAGCAATTG 152
|||||
Qy 132 CACTCATCATTTGGCTTGTGATTTTCAAGGAGACCTCATCAAGTACATGCTGGCT 191
|||||
Db 153 CACTCATCATTTGGCTTGTGATTTTCAAGGAGACCTCATCAAGTACATGCTGGCT 212
|||||
Qy 192 CAGCTGGAACTTTGGGAGATGGAATCTGAGCTCACTTTGAACTGACATCAAC 251
|||||
Db 213 CAGCTGGAACTTTGGGAGATGGAATCTGAGCTCACTTTGAACTGACATCAAC 272
|||||
Qy 252 TTTCTGATTCGTGATTCATATGCTGTAAGGAAGGTGTTTGAAGCTGGTCCATGATTC 311
|||||
Db 273 TTTCTGATTCGTGATTCATATGCTGTAAGGAAGGTGTTTGAAGCTGGTCCATGATTC 332
|||||
Qy 312 AAGAAGCAAAAGATGAGCTGTGGAGCAAGATGAAAATGTTCAAGAGCGCGGACAGCATGT 371
|||||

Db 333 AAGAAGCAAAAGATGAGCTGTGGAGCAAGATGAAAATGTTCAAGCGCCGACAGCATGT 392
|||||
Qy 372 TTTCTGATTCGTGATTCATATGCTGTAAGGAAGGTGTTTGAAGCTGGTCCATGATTC 431
|||||
Db 393 TTTCTGATTCGTGATTCATATGCTGTAAGGAAGGTGTTTGAAGCTGGTCCATGATTC 452
|||||
Qy 432 ATGCTGGCACTTCAAAATGTTATATCATCATCTTCAAGGCAAGGGAAGTCAACCTTG 491
|||||
Db 453 ATGCTGGCACTTCAAAATGTTATATCATCATCTTCAAGGCAAGGGAAGTCAACCTTG 512
|||||
Qy 492 AGTATAAACTGAGAGCTTCAAGATGCGGAAATGATGACTATTAATGCCAGCTCAG 551
|||||
Db 513 AGTATAAACTGAGAGCTTCAAGATGCGGAAATGATGACTATTAATGCCAGCTCAG 572
|||||
Qy 552 AGACCTTGGGTGAGAGCTCCCGATGTTCCCGACGCCACAGTGTCTGGCATCC 611
|||||
Db 573 AGACCTTGGGTGAGAGCTCCCGATGTTCCCGACGCCACAGTGTCTGGCATCC 632
|||||
Qy 612 AAGTTGACCGGAGCACTTCTCGGAAGTCTCCAAATACACCTTGAAGCTGAACCTTG 671
|||||
Db 633 AAGTTGACCGGAGCACTTCTCGGAAGTCTCCAAATACACCTTGAAGCTGAACCTTG 692
|||||
Qy 672 AGATGAGACCATGAAGGTGTGTCTGTCTACATGTTACGATCAACACACATCT 731
|||||
Db 693 AGATGAGACCATGAAGGTGTGTCTGTCTACATGTTACGATCAACACACATCT 752
|||||
Qy 732 CCTGTATGATTTGAAAATGACATTTGCCAAGCAACAGGGATATCAAGTACAGAAATCG 791
|||||
Db 753 CCTGTATGATTTGAAAATGACATTTGCCAAGCAACAGGGATATCAAGTACAGAAATCG 812
|||||
Qy 792 AGATCAAAAGGCGGAGTCACTTACAGTGTAACTCAAGGCTTCTGTGTCTCTT 851
|||||
Db 813 AGATCAAAAGGCGGAGTCACTTACAGTGTAACTCAAGGCTTCTGTGTGTCTCTT 872
|||||
Qy 852 CTTTCTTTGGCATCAGGTGGGCACTTCTGCTCTCAGACCTTACCTGATCTAAATAT 911
|||||
Db 873 CTTTCTTTGGCATCAGGTGGGCACTTCTGCTCTCAGACCTTACCTGATCTAAATAT 932
|||||
Qy 912 GTGCTTTGGCCACAAAAAAGCATGCAAGTCAATGTTTACCAAGGATCTACAGAACTAT 971
|||||
Db 933 GTGCTTTGGCCACAAAAAAGCATGCAAGTCAATGTTTACCAAGGATCTACAGAACTAT 992
|||||
Qy 972 TTTACCAACCAATATGATCCTAGTTTATATTTCTGGAGGAATGAAATTCATCTAGAA 1031
|||||
Db 993 TTTACCAACCAATATGATCCTAGTTTATATTTCTGGAGGAATGAAATTCATCTAGAA 1052
|||||
Qy 1032 GTCTGAGTGAAGCAACAGAGCAAGAAACAAAGAGCCAAAGCAAGAGGCTCCAT 1091
|||||
Db 1053 GTCTGAGTGAAGCAACAGAGCAAGAAACAAAGAGCCAAAGCAAGAGGCTCCAT 1112
|||||
Qy 1092 ATGAACAGATTAATCTATCTTCAAGACATATTAAGAGTTGGAAATTAATTCATGTGA 1151
|||||
Db 1113 ATGAACAGATTAATCTATCTTCAAGACATATTAAGAGTTGGAAATTAATTCATGTGA 1172
|||||
Qy 1152 ACTAGACAGTGTGTTAAGAGTATAGTAAATGACAGTGGAGCAAGTGCATCCCCAG 1211
|||||
Db 1173 ACTAGACAGTGTGTTAAGAGTATAGTAAATGACAGTGGAGCAAGTGCATCCCCAG 1232
|||||
Qy 1212 ATCTCAGGAGCTCCCCCTGCTGTCAACCTGGGAGTGAAGAGACAGATATGTCATGTT 1271
|||||
Db 1233 ATCTCAGGAGCTCCCCCTGCTGTCAACCTGGGAGTGAAGAGACAGATATGTCATGTT 1292
|||||
Qy 1272 CTTTGTCTCTGAATTTTATGTTATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAA 1331
|||||
Db 1293 CTTTGTCTCTGAATTTTATGTTATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAA 1352
|||||
Qy 1332 AGTCTATCCCAATATATCCATCTTATATTCACAAATTAAGCTGTAGATTAACCTTA 1391
|||||
Db 1353 AGTCTATCCCAATATATCCATCTTATATTCACAAATTAAGCTGTAGATTAACCTTA 1412
|||||
Qy 1392 AGAGCTGCTAAATTTGACTGCACTTGCACAACTCAGGGGCGGCTGCAATTTAGTAATGGT 1451
|||||

Db 1413 AGACCTGCTAATGACCTCCACTTCGCAACTCAGGGCGGCTGCATTTTAAATGAGGT 1472
Qy 1453 CAAATGATTCATTTTATGATGCTCCAAAGTGCTTGCGTCTTCCCACTGACA 1511
Db 1473 CAAATGATTCATTTTATGATGCTCCAAAGTGCTTGCGTCTTCCCACTGACA 1532
Qy 1512 AATGCCAAAGTGAAGAAAATGATCATATTTTAACTAAACAGACAGCTCGGCACAC 1571
Db 1533 AATGCCAAAGTGAAGAAAATGATCATATTTTAACTAAACAGACAGCTCGGCACAC 1592
Qy 1572 GATTTTATTAATTAATCTGACACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCA 1631
Db 1593 GATTTTATTAATTAATCTGACACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCA 1652
Qy 1632 GATGATGTCATCCGGAATGATCCAGGAGAGACCTTCACTTGACTATATGAGATTA 1691
Db 1653 GATGATGTCATCCGGAATGATCCAGGAGAGACCTTCACTTGACTATATGAGATTA 1712
Qy 1692 TGTCAATCAACAGCTGAGGCTTCTCTTTCATCTCGTGAGACAGCTAAGACCTCACT 1751
Db 1713 TGTCAATCAACAGCTGAGGCTTCTCTTTCATCTCGTGAGACAGCTAAGACCTCACT 1772
Qy 1752 TTTCAATGATCTAGAGCAGTGAGACTGAGCTGGGATATTTCCGCCCTTCCGGG 1811
Db 1773 TTTCAATGATCTAGAGCAGTGAGACTGAGCTGGGATATTTCCGCCCTTCCGGG 1832
Qy 1812 GGAATGCTGAAGACAAATTTTGGTTACCTCAATGAGGAGTGAAGAGGATACAGTCTA 1871
Db 1833 GGAATGCTGAAGACAAATTTTGGTTACCTCAATGAGGAGTGAAGAGGATACAGTCTA 1892
Qy 1872 CTACCAACTAGTGTGATTAAGGCGCAGGAGTGTCTCAACCTCTACATGTACAGAGCT 1931
Db 1893 CTACCAACTAGTGTGATTAAGGCGCAGGAGTGTCTCAACCTCTACATGTACAGAGCT 1952
Qy 1932 CTCCCATTTTCAACTACCAATCCCAAGTGTCACTGTGTCAAGACTAAGAAACCTGGT 1991
Db 1953 CTCCCATTTTCAACTACCAATCCCAAGTGTCACTGTGTCAAGACTAAGAAACCTGGT 2012
Qy 1992 TTTGATGATAAAGGCGCTGAAAGAGGAGGACCAACAAATCGTGTGCTT-CTACACT 2050
Db 2013 TTTGATGATAAAGGCGCTGAAAGAGGAGGACCAACAAATCGTGTGCTTCTCAACT 2072
Qy 2051 AGTCATTTGCAATTAAGCAATTTCTTCTGCTGCTGCTCCTCAGACAGAGGCGACAA 2110
Db 2073 AGTCATTTGCAATTAAGCAATTTCTTCTGCTGCTGCTCCTCAGACAGAGGCGACAA 2132
Qy 2111 CTCTATCGGCGCACAGGATTAACCTCTCTAGTGAACAGAGTTGACAAGGCTCTATGGGAA 2170
Db 2133 CTCTATCGGCGCACAGGATTAACCTCTCTAGTGAACAGAGTTGACAAGGCTCTATGGGAA 2192
Qy 2171 TGCCTGATGGATTAATCTTCAAGCTTGTGAGCTTAAGTTTCTTCCCTCATTTCTAC 2230
Db 2193 TGCCTGATGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTCATTTCTAC 2252
Qy 2231 CTGCAAGCCAGTCTGTAAAGAAATGCTGAGTTCTAAGCTCAAGTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAGTCTGTAAAGAAATGCTGAGTTCTAAGCTCAAGTTTCTTACTCTGA 2312
Qy 2291 ATTTAGATCTCAGACCTTCTCTGCGCAAAATTTAAGGCAACAAACATATACCTT 2350
Db 2313 ATTTAGATCTCAGACCTTCTCTGCGCAAAATTTAAGGCAACAAACATATACCTT 2372
Qy 2351 CCATGAGGACACACAGACTTTTGAAGAGAGACAAATGAGCTTGAATTAAGGCTTG 2410
Db 2373 CCATGAGGACACACAGACTTTTGAAGAGAGACAAATGAGCTTGAATTAAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAGAAATATCTTTGTTTCAGCCCTTCCCAACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAGAAATATCTTTGTTTCAGCCCTTCCCAACTCTTCA 2492
Qy 2471 TGTGTTAACTGCTCTTCTGAGCCTTGGAGCAGGAGTGTATTAATGATTTGTTAT 2530
Db 2493 TGTGTTAACTGCTCTTCTGAGCCTTGGAGCAGGAGTGTATTAATGATTTGTTAT 2552

Qy 2531 AGAAACTGATTTTGAAGTTCGATCTGTTCAAGAGAAATGATTAATATATTTCT 2587
Db 2553 AGAAACTGATTTTGAAGTTCGATCTGTTCAAGAGAAATGATTAATATATTTCT 2609
RESULT 3
US-09-884-441-391
; Sequence 391, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884.441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-441-391
Query Match 99.1%; Score 2565; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 12 GGCAGCTTCACTCAGCCAGTACCCAGATACGCTGGGAACTTTCCAGCCATGCTTCC 71
Db 33 GGCAGCTTCACTCAGCCAGTACCCAGATACGCTGGGAACTTTCCAGCCATGCTTCC 92
Qy 72 TGGGGCAATCTCTTCTGAGCAATTAATGATCATATTTCTGCTGGAGCAATTG 131
Db 93 TGGGGCAATCTCTTCTGAGCAATTAATGATCATATTTCTGCTGGAGCAATTG 152
Qy 132 CACTCATATTTGGCTTGTGATTTTCAAGGAGACACTCCATGACAGTCACTGTGCT 191
Db 133 CACTCATATTTGGCTTGTGATTTTCAAGGAGACACTCCATGACAGTCACTGTGCT 212
Qy 192 CAGCTGGGAACTTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACAAAC 251
Db 213 CAGCTGGGAACTTGGGAGAGATGGAATCTGAGCTGCACTTTGAACCTGACAAAC 272
Qy 252 TTTCTGATATGATTAATAATGCTGAGAGAAAGGTTTAAAGGCTTGGCTCATGAGTTCA 311
Db 273 TTTCTGATATGATTAATAATGCTGAGAGAAAGGTTTAAAGGCTTGGCTCATGAGTTCA 332
Qy 312 AAGAAGCAAGATGAGCTGTGAGCAGATGGAATGTTCAAGGCGGAGCAGCAGTGT 371
Db 333 AAGAAGCAAGATGAGCTGTGAGCAGATGGAATGTTCAAGGCGGAGCAGCAGTGT 392
Qy 372 TTTGCTGATCAAGTATGATTTGCAATGCTCTTTGCGGCTGAATAAGCTGCACTCAG 431
Db 393 TTTGCTGATCAAGTATGATTTGCAATGCTCTTTGCGGCTGAATAAGCTGCACTCAG 452
Qy 432 ATGCTGGGACCTTCAAAATGTTATATCATCACTTCTAAAGGCAAGGGAATGTAACCTTG 491
Db 453 ATGCTGGGACCTTCAAAATGTTATATCATCACTTCTAAAGGCAAGGGAATGTAACCTTG 512
Qy 492 AGTATAAATGAGCCTTTCAGACATGCGGAGAGTGAATGTAATGATTAATGACAGTCA 551
Db 513 AGTATAAATGAGCCTTTCAGACATGCGGAGAGTGAATGTAATGATTAATGACAGTCA 572
Qy 552 AGACCTTGGGTGAGGCTTCCCGATGTTTCCCGACCCACAGTGTCTGGGATCTCC 611
Db 573 AGACCTTGGGTGAGGCTTCCCGATGTTTCCCGACCCACAGTGTCTGGGATCTCC 632
Qy 612 AAGTTGAACAGGAGCCCACTTCTCGGAAGTCCCAATACAGCTTTGAGCTGAACCTG 671
Db 633 AAGTTGAACAGGAGCCCACTTCTCGGAAGTCCCAATACAGCTTTGAGCTGAACCTG 692

QY 672 AGAATGACCATGAAGTTGTGTCGTGCTCTACAAATGTTAGATGCAACAACATACT 731
DB 693 AGAATGACCATGAAGTTGTGTCGTGCTCTACAAATGTTAGATGCAACAACATACT 752
QY 732 CCTGTATGATTTGAATAATGACATTGCAAGCAACAGGGGATATCAAAATGACAGATCGG 791
DB 753 CCTGTATGATTTGAATAATGACATTGCAAGCAACAGGGGATATCAAAATGACAGATCGG 812
QY 792 AGATCAAAAGGCGGAGTCACTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTT 851
DB 813 AGATCAAAAGGCGGAGTCACTACAGCTGCTAACTCAAAAGGCTTCTGTGTGTCTT 872
QY 852 CTTTCTTTGCGCATGAGCTGGGCACTTGCGCTCTCAGCCCTTACCTGATGCTAAATAT 911
DB 873 CTTTCTTTGCGCATGAGCTGGGCACTTGCGCTCTCAGCCCTTACCTGATGCTAAATAT 932
QY 912 GTGCTTGGGCAACAAAAGATGCAAGTCTGTTACAAACAGGATCTACAGAACTAT 971
DB 933 GTGCTTGGGCAACAAAAGATGCAAGTCTGTTACAAACAGGATCTACAGAACTAT 992
QY 972 TTCAACCAAGATATGACCTGATTTATATTTCTGGAGAAATGAAATTCATATCTAGAA 1031
DB 993 TTCAACCAAGATATGACCTGATTTATATTTCTGGAGAAATGAAATTCATATCTAGAA 1052
QY 1032 GTCTTGAGTAGAGCAAAAGAGCAAGAAACAAAAGGCCAAAGAGAGGCTCCAAAT 1091
DB 1053 GTCTTGAGTAGAGCAAAAGAGCAAGAAACAAAAGGCCAAAGAGGCTCCAAAT 1112
QY 1092 ATGAACAAGATTAATCTATCTTCAAAAGACATATTAGAAGTTGGGAAATTAATCATGTGA 1151
DB 1113 ATGAACAAGATTAATCTATCTTCAAAAGACATATTAGAAGTTGGGAAATTAATCATGTGA 1172
QY 1152 ACTAGACAAGTGTGTTAAGAGTGAATGAATAATGACGTTGAGACAAGTGCAATCCCGAG 1211
DB 1173 ACTAGACAAGTGTGTTAAGAGTGAATGAATAATGACGTTGAGACAAGTGCAATCCCGAG 1232
QY 1212 ATCTGAGGGAACCTCCCGCTGCTGCACTGGGAGAGGAGAGACAAGATAGTGCAATGT 1271
DB 1233 ATCTGAGGGAACCTCCCGCTGCTGCACTGGGAGAGGAGAGACAAGATAGTGCAATGT 1292
QY 1272 CTTTGTCTCGAATTTTATGATGCTGATGCTGATGCTCTGAGGAAAGCCCTGGA 1331
DB 1293 CTTTGTCTCGAATTTTATGATGCTGATGCTGATGCTCTGAGGAAAGCCCTGGA 1352
QY 1332 AGTCTATCCCAACATATCAATCTTATATTCACAAATTAAGCTGATGATGATCCCTA 1391
DB 1353 AGTCTATCCCAACATATCAATCTTATATTCACAAATTAAGCTGATGATGATCCCTA 1412
QY 1392 AGAGCGCTGCTAATTTGACGCACTTGCACTGAGGCGGCGCTGCAATTTAGTAAGGT 1451
DB 1413 AGAGCGCTGCTAATTTGACGCACTTGCACTGAGGCGGCGCTGCAATTTAGTAAGGT 1472
QY 1452 CAATGATGACCTTTTATGATGCTTCCAAAGGCTGCTGCTCTTCCCAACTGACA 1511
DB 1473 CAATGATGACCTTTTATGATGCTTCCAAAGGCTGCTGCTCTTCCCAACTGACA 1532
QY 1512 AATGCCAAAGTTGAGAAAATGATCATATTTTATGATTAACAGAGACGTCGGGACACC 1571
DB 1533 AATGCCAAAGTTGAGAAAATGATCATATTTTATGATTAACAGAGACGTCGGGACACC 1592
QY 1572 GATTTTATTAATAAAGTGAAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
DB 1593 GATTTTATTAATAAAGTGAAGACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1652
QY 1632 GATGATGTTGATCCGTAATGATGCTCAAGGAAAGACCTTTGACCTGATGATGATGCACTTA 1691
DB 1653 GATGATGTTGATCCGTAATGATGCTCAAGGAAAGACCTTTGACCTGATGATGATGCACTTA 1712
QY 1692 TGTGATCAACAAGCTCTGAGGCTTCTCTTTTCATCTGCTGGAACAGCTAAGACCTCAGT 1751
DB 1713 TGTGATCAACAAGCTCTGAGGCTTCTCTTTTCATCTGCTGGAACAGCTAAGACCTCAGT 1772

QY 1752 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTCCGCCCCCATCTCCGGG 1811
DB 1773 TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTCCGCCCCCATCTCCGGG 1832
QY 1812 GGAATGCTGGAACAATTTTGGTTACTTCAATGAAGGAGTGAAGAGATGATGACTA 1871
DB 1833 GGAATGCTGGAACAATTTTGGTTACTTCAATGAAGGAGTGAAGAGATGATGACTA 1892
QY 1872 CTACCAACTGATGATTAAGGCGCAGAGGATGCTCTCACTCTTACATGATGAGAGCT 1931
DB 1893 CTACCAACTGATGATTAAGGCGCAGAGGATGCTCTCACTCTTACATGATGAGAGCT 1952
QY 1932 CTCGCCATTAACACTACCCCAATCCGAAGTGTCAACTGTGACAGACTAAGAAACCCGCT 1991
DB 1953 CTCGCCATTAACACTACCCCAATCCGAAGTGTCAACTGTGACAGACTAAGAAACCCGCT 2012
QY 1992 TTTGAGTAGAAAAGGCGCTGGAAGAAGGAGGCAACAACTGTCTGCTT-CTCACTT 2050
DB 2013 TTTGAGTAGAAAAGGCGCTGGAAGAAGGAGGCAACAACTGTGTCTGCTTCTCACTT 2072
QY 2051 AGTCAATGGCAATTAAGCATTTCTGTCTCTTTGGCTGTGCTCAACAGAGGCCAGAA 2110
DB 2073 AGTCAATGGCAATTAAGCATTTCTGTCTCTTTGGCTGTGCTCAACAGAGGCCAGAA 2132
QY 2111 CTCTATCGGCGACAGGATTAACATCTCTGATGAGACAGATGTAACAAGGCTTATGGGAAA 2170
DB 2133 CTCTATCGGCGACAGGATTAACATCTCTGATGAGACAGATGTAACAAGGCTTATGGGAAA 2192
QY 2171 TGCCGTAGTGGAATTTCTCAGCTGTGAGCTTCTTAAGTTCTTTCCCTTCAATTCACC 2230
DB 2193 TGCCGTAGTGGAATTTCTCAGCTGTGAGCTTCTTAAGTTCTTTCCCTTCAATTCACC 2252
QY 2231 CTGCAAGCCCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTAGGTTTCTTACTGTA 2290
DB 2253 CTGCAAGCCCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTAGGTTTCTTACTGTA 2312
QY 2291 ATTTAGATCTCGAGACCTTCTCGGCAACAATTAAGGCAACAAATATATACCTT 2350
DB 2313 ATTTAGATCTCGAGACCTTCTCGGCAACAATTAAGGCAACAAATATATACCTT 2372
QY 2351 CCATGAAGCAACACAGACTTTTGAAGAAGACATGACTGTTGAATTTGAGGCTTG 2410
DB 2373 CCATGAAGCAACACAGACTTTTGAAGAAGACATGACTGTTGAATTTGAGGCTTG 2432
QY 2411 AGGAATGAAGCTTTGAAGAAGAAATACTTTGTTCCAGCCCTTCCCACTCTTCA 2470
DB 2433 AGGAATGAAGCTTTGAAGAAGAAATACTTTGTTCCAGCCCTTCCCACTCTTCA 2492
QY 2471 TGTGTTAACCACTGCTTCTGGAAGCTTGAAGCAGGATGATGATGATGATGAT 2530
DB 2493 TGTGTTAACCACTGCTTCTGGAAGCTTGAAGCAGGATGATGATGATGATGAT 2552
QY 2531 AGAAAACGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATATCATTTCT 2587
DB 2553 AGAAAACGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATATCATTTCT 2609

RESULT 4
US-09-969-391
; Sequence 391, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Ranger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C8
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 391
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-969-391

Query Match 99.1%; Score 2565; DB 10; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 12 GGCAGCTCAGTCAAGCAGTACCCAGATACGCTGGAACTTCCCGACCATGCTTCCC 71
DB 33 GGCAGCTCAGTCAAGCAGTACCCAGATACGCTGGAACTTCCCGACCATGCTTCCC 92
QY 72 TGGGGCAGATCCTCTTCTGAGCATTAATGATCATCTTAATCTGCTGAGGCAATTG 131
DB 93 TGGGGCAGATCCTCTTCTGAGCATTAATGATCATCTTAATCTGCTGAGGCAATTG 152
QY 132 CACTCATCTTGGCTTGGTATTTTCAGGAGACACTCCATCAAGTCACTACTGCTGCT 191
DB 153 CACTCATCTTGGCTTGGTATTTTCAGGAGACACTCCATCAAGTCACTACTGCTGCT 212
QY 192 CAGCTGGGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTTGAACTGACATCAAC 251
DB 213 CAGCTGGGAACATTGGGAGAGATGGAATCTGAGCTGCACTTTTGAACTGACATCAAC 272
QY 252 TTTCTGATTCGTGATACATAGCTGGAAGGAAGTCTTTAGCTTGGTGCATGAGTTCA 311
DB 273 TTTCTGATTCGTGATACATAGCTGGAAGGAAGTCTTTAGCTTGGTGCATGAGTTCA 332
QY 312 AAGAAGGCAAAAGTAGCTGTGCGAGCAGATGAATAATGTTCAAGGCGCGAGCAGTGT 371
DB 333 AAGAAGGCAAAAGTAGCTGTGCGAGCAGATGAATAATGTTCAAGGCGCGAGCAGTGT 392
QY 372 TTGCTGATCAAGTATGATTGGCAATGCTCTTTGGGCTGAATAAAGTGCATCTCAG 431
DB 393 TTGCTGATCAAGTATGATTGGCAATGCTCTTTGGGCTGAATAAAGTGCATCTCAG 452
QY 432 ATGCTGGCACTACAAATGTTAATGATCACTTCTAAGGCAAGGGGAATGCTAACCTTG 491
DB 453 ATGCTGGCACTACAAATGTTAATGATCACTTCTAAGGCAAGGGGAATGCTAACCTTG 512
QY 492 AGTATAAACTGGAGCTTCAGCATCCCGAAAGTGAATGGAATGACTTAATGCAAGCTCAG 551
DB 513 AGTATAAACTGGAGCTTCAGCATCCCGAAAGTGAATGGAATGACTTAATGCAAGCTCAG 572
QY 552 AGAAGCTTGGGTGTGAGGCTCCCGAGTGTTCGCCAGCCCAAGTGTCTGGGCAATCCC 611
DB 573 AGAAGCTTGGGTGTGAGGCTCCCGAGTGTTCGCCAGCCCAAGTGTCTGGGCAATCCC 632
QY 612 AAGTTGACCAAGGAGCACTTCTGGAAGTCTCCCAATACAGCTTTGAGCTGAATCTTG 671
DB 633 AAGTTGACCAAGGAGCACTTCTGGAAGTCTCCCAATACAGCTTTGAGCTGAATCTTG 692
QY 672 AGAATGACCAAGGAGCTTCTGCTCTCAATGATGATGATCAACAACATCACTACT 731
DB 693 AGAATGACCAAGGAGCTTCTGCTCTCAATGATGATGATCAACAACATCACTACT 752
QY 732 CCTGTATGATTGAAAATGACATTTGCCAAAGCAACAGGGGATATCAAAATGACAGAAATCG 791
DB 753 CCTGTATGATTGAAAATGACATTTGCCAAAGCAACAGGGGATATCAAAATGACAGAAATCG 812
QY 792 AGATCAAAAGGCGGAGTCACTACAGCTGTAACTCAAAAGGCTTCTGTGTGTCTTT 851
DB 813 AGATCAAAAGGCGGAGTCACTACAGCTGTAACTCAAAAGGCTTCTGTGTGTCTTT 872

QY 852 CTTTCTTTCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATATAT 911
DB 873 CTTTCTTTCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATATAT 932
QY 912 GTGCTTGGCCCAAAAAAGCATGCAAGTATTTTACCAACAGGATCTCAGAACTAT 971
DB 933 GTGCTTGGCCCAAAAAAGCATGCAAGTATTTTACCAACAGGATCTCAGAACTAT 992
QY 972 TTACCAACCAATATGACCTAGTTTATTTCTGGAGGAATGATTCATCTAGAA 1031
DB 993 TTACCAACCAATATGACCTAGTTTATTTCTGGAGGAATGATTCATCTAGAA 1052
QY 1032 GTCTGAGTGAACAAACAGAGCAAAACAAAGAACCCAAAGCAGAAAGCTCCAT 1091
DB 1053 GTCTGAGTGAACAAACAGAGCAAAACAAAGAACCCAAAGCAGAAAGCTCCAT 1112
QY 1092 ATGAACCAATATATCTTCTTCAAGCATATTAAGATTTGGGAAATATTCATGTA 1151
DB 1113 ATGAACCAATATATCTTCTTCAAGCATATTAAGATTTGGGAAATATTCATGTA 1172
QY 1152 ACTAGACAAGTGTGTTAAGATGATTAAGTAAATGCAAGTGAAGCAAGTCAATCCCAG 1211
DB 1173 ACTAGACAAGTGTGTTAAGATGATTAAGTAAATGCAAGTGAAGCAAGTCAATCCCAG 1232
QY 1212 ATCTCAGGACCTCCCTGCTGTCACTGGGAGTGAAGACAGATATGTCATTT 1271
DB 1233 ATCTCAGGACCTCCCTGCTGTCACTGGGAGTGAAGACAGATATGTCATTT 1292
QY 1272 CTTTGTCTCTGAATTTTATGATTAATGTCGTATATGTTGCTGAGGAAGCCCTGAA 1331
DB 1293 CTTTGTCTCTGAATTTTATGATTAATGTCGTATATGTTGCTGAGGAAGCCCTGAA 1352
QY 1332 AGCTATCCCAACATATCAATCTTATATTCACAAATTAAGCTGATGATGATCCTTA 1391
DB 1353 AGCTATCCCAACATATCAATCTTATATTCACAAATTAAGCTGATGATGATCCTTA 1412
QY 1392 AGACGCTCTAATTTGACTGCACTTTCGCACTCAGGGGCGCTGCTTTTATGATGCGT 1451
DB 1413 AGACGCTCTAATTTGACTGCACTTTCGCACTCAGGGGCGCTGCTTTTATGATGCGT 1472
QY 1452 CAATGATTTCACTTTTATGATGCTTCCAAAGGCGCTTGTCTCTTCCCACTGACA 1511
DB 1473 CAATGATTTCACTTTTATGATGCTTCCAAAGGCGCTTGTCTCTTCCCACTGACA 1532
QY 1512 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAACAGAGCAGTGGGACACC 1571
DB 1533 AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAACAGAGCAGTGGGACACC 1592
QY 1572 GATTTTATTAATTAACCTAGACACTTCTTTTAAACAAACAAATGCGGCTTATTTCTCA 1631
DB 1593 GATTTTATTAATTAACCTAGACACTTCTTTTAAACAAACAAATGCGGCTTATTTCTCA 1652
QY 1632 GATGATGTTCAATCCGTAATGCTTCCAGGGAAGGACCTTCACTTATATGACATTA 1691
DB 1653 GATGATGTTCAATCCGTAATGCTTCCAGGGAAGGACCTTCACTTATATGACATTA 1712
QY 1692 TGTCACTCAAGAGCTTGAAGCTTCTCTTTCATCTCTGCTGACAGCTAAGACCTCAGT 1751
DB 1713 TGTCACTCAAGAGCTTGAAGCTTCTCTTTCATCTCTGCTGACAGCTAAGACCTCAGT 1772
QY 1752 TTTCAATATGATCTAGACAGATGGAACCTGAGGAGTGTTCGCCCCCATCTCCGG 1811
DB 1773 TTTCAATATGATCTAGACAGATGGAACCTGAGGAGTGTTCGCCCCCATCTCCGG 1832
QY 1812 GGAATGTCTGAAGACAAATTTTGTGTTAACTCAATGAGGAGTGAAGAGATACAGTGTCTA 1871
DB 1833 GGAATGTCTGAAGACAAATTTTGTGTTAACTCAATGAGGAGTGAAGAGATACAGTGTCTA 1892
QY 1872 CTACCAACTAATGATTAAGGCAAGGATGCTGCTCAACTCTTCACTGATACAGAGAGT 1931
DB 1893 CTACCAACTAATGATTAAGGCAAGGATGCTGCTCAACTCTTCACTGATACAGAGAGT 1952
QY 1932 CTCCCATTTACAACTAACCAATCCGAGAGTGTCAACTGTGTCAAGATCTAAGAAACCTGAT 1991

|||||
Db 1953 CTCCCATTCACATACCCATCCGAAGTCACTGTGACAGACTTAAGAAACCTGTG 2012
Qy 1992 TTGAGTAAAGAAAGGGCTGGAAAGAGGGAGCCAAAGAAATCTGTCTGCTT-CTCAAT 2050
Db 2013 TTGAGTAAAGAAAGGGCTGGAAAGAGGGAGCCAAAGAAATCTGTCTGCTTCTCAAT 2072
Qy 2051 AGTCAATGGCAAAATTAACATCTGTCTGTGTGCTGCTGCTGAGCAAGAGAGCCAGAA 2110
Db 2073 AGTCAATGGCAAAATTAACATCTGTCTGTGTGCTGCTGCTGAGCAAGAGAGCCAGAA 2132
Qy 2111 CTCTATGGGCAACAGAGATTAACATCTGTGTGAGTGAACAGAGTTGCAAGGCTTATGGAAA 2170
Db 2133 CTCTATGGGCAACAGAGATTAACATCTGTGTGAGTGAACAGAGTTGCAAGGCTTATGGAAA 2192
Qy 2171 TGCTGTATGGGATTAATCTGTGTGAGTGTGTGAGTGTCTTAAGTTCTTCTTCCATCTTACC 2230
Db 2193 TGCTGTATGGGATTAATCTGTGTGAGTGTGTGAGTGTCTTAAGTTCTTCTTCCATCTTACC 2252
Qy 2231 CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGATTCTAGCTCAGTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGATTCTAGCTCAGTTTCTTACTCTGA 2312
Qy 2291 ATTATGATGTCAGACCTTCTGTGCAATTCCTGCAATTCCTGCAATTCCTGCAATTCCTG 2350
Db 2313 ATTATGATGTCAGACCTTCTGTGCAATTCCTGCAATTCCTGCAATTCCTGCAATTCCTG 2372
Qy 2351 CCATGAAGCAACACACATTTTGAAGCAAGCAATGACTGTTGAATTTGAGGCTTG 2410
Db 2373 CCATGAAGCAACACACATTTTGAAGCAAGCAATGACTGTTGAATTTGAGGCTTG 2432
Qy 2411 AGAATGAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCCCTCCACACTCTTCA 2470
Db 2433 AGAATGAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCCCTCCACACTCTTCA 2492
Qy 2471 TGTGTAAACCACTGCTTCTGTGACCTTGTGAGCCAGCAGTGTATATTAATGTTTAT 2530
Db 2493 TGTGTAAACCACTGCTTCTGTGAGCTTGTGAGCCAGCAGTGTATATTAATGTTTAT 2552
Qy 2531 AGAAACTGATTTTGAAGTTCTGTGCTTCAAGAGATGATTAATATTAATTTCTT 2587
Db 2553 AGAAACTGATTTTGAAGTTCTGTGCTTCAAGAGATGATTAATATTAATTTCTT 2609

RESULT 5
US-09-827-271-391
; Sequence 391, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ. ID NOS: 461
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ. ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-271-391

Query Match 99.1%; Score 2565; DB 10; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGGAGCTCCACTAGCCAGTACCAAGTACGCTGGGAACCTTCCCGCATGGCTTCCC 71
Db 33 GGGAGCTCCACTAGCCAGTACCAAGTACGCTGGGAACCTTCCCGCATGGCTTCCC 92
Qy 72 TGGGAGAGATCTCTTCTGAGCATATATGATCATCATTTATTTGCTGAGCAATTG 131

|||||
Db 93 TGGGAGAGATCTCTTCTGAGCATATATGATCATCATTTATTTGCTGAGCAATTG 152
Qy 132 CACTCATCATTTGGCTTTGTATTTTCAGGAGACATCTCATCAAGTCACTAGTGGCT 191
Db 153 CACTCATCATTTGGCTTTGTATTTTCAGGAGACATCTCATCAAGTCACTAGTGGCT 212
Qy 192 CAGCTGGGAACATTTGGGAGAGATGGAATCTGTAGCTGCACTTTTGAACCTGATCAAC 251
Db 213 CAGCTGGGAACATTTGGGAGAGATGGAATCTGTAGCTGCACTTTTGAACCTGATCAAC 272
Qy 252 TTTCTGATTCGTATACAAATGCTGAAAGAGAGTGTATTTAGCTTGTTCATGAGTTCA 311
Db 273 TTTCTGATTCGTATACAAATGCTGAAAGAGAGTGTATTTAGCTTGTTCATGAGTTCA 332
Qy 312 AAGAAGCAAAAGTATGAGCTGTGGAGACAGATGAATTTTCAAGGCGGACAGCACTGT 371
Db 333 AAGAAGCAAAAGTATGAGCTGTGGAGACAGATGAATTTTCAAGGCGGACAGCACTGT 392
Qy 372 TTGCTGATCAAGATATGTTGGCAATGCTTGTGGGCTGAAAAAAGTCACTGACAG 431
Db 393 TTGCTGATCAAGATATGTTGGCAATGCTTGTGGGCTGAAAAAAGTCACTGACAG 452
Qy 432 ATGCTGGCACTTCAATGTTATATCATCATTTCTAAAGCAAGGGAATGCTAACCTTG 491
Db 453 ATGCTGGCACTTCAATGTTATATCATCATTTCTAAAGCAAGGGAATGCTAACCTTG 512
Qy 492 AGTATTAAGTGAAGCTTCTGAGCATGCGGAAGTGAATGTGAATTTATGCACTGAG 551
Db 513 AGTATTAAGTGAAGCTTCTGAGCATGCGGAAGTGAATGTGAATTTATGCACTGAG 572
Qy 552 AGACCTTGGGAGTGAAGGCTCCCGAGTGTCCCGGCAAGGAGTGTGGGCAATCCC 611
Db 573 AGACCTTGGGAGTGAAGGCTCCCGAGTGTCCCGGCAAGGAGTGTGGGCAATCCC 632
Qy 612 AAGTTGACAGGAGGCAACTTCTCGGAAGTCTCAATACAGACTTTGAGCTGAACTTG 671
Db 633 AAGTTGACAGGAGGCAACTTCTCGGAAGTCTCAATACAGACTTTGAGCTGAACTTG 692
Qy 672 AGAATGTACATGAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 731
Db 693 AGAATGTACATGAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 752
Qy 732 CCTGTATGATGTAATATGATTTGCAAGCAACAGGGATATCAAGTGAAGCAATGCG 791
Db 753 CCTGTATGATGTAATATGATTTGCAAGCAACAGGGATATCAAGTGAAGCAATGCG 812
Qy 792 AGATCAAAAGGCGAGTCACTACAGCTGCTAACTCAAGGCTTCTGTGTGTCTT 851
Db 813 AGATCAAAAGGCGAGTCACTACAGCTGCTAACTCAAGGCTTCTGTGTGTCTT 872
Qy 852 CTTTCTTGGCATGAGCTGGGCACTTCTGCTCTGAGCCCTTACCTGATGCTAAATAT 911
Db 873 CTTTCTTGGCATGAGCTGGGCACTTCTGCTCTGAGCCCTTACCTGATGCTAAATAT 932
Qy 912 GTGCTTGGGCAAAAGGATGCAATGCTATTTTAAACAGGATCTACAGAACTAT 971
Db 933 GTGCTTGGGCAAAAGGATGCAATGCTATTTTAAACAGGATCTACAGAACTAT 992
Qy 972 TTCAACACAGATATGATGCTTATTTTCTGAGGAGAAATGATTAATCATATAGAA 1031
Db 993 TTCAACACAGATATGATGCTTATTTTCTGAGGAGAAATGATTAATCATATAGAA 1052
Qy 1032 GTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAGCAGAGGCTCAAT 1091
Db 1053 GTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAGCAGAGGCTCAAT 1112
Qy 1092 ATGAACAAGATTAATTTATCTTCAAGACATTTTGAATTTGGGAAAAATTCATGTA 1151
Db 1113 ATGAACAAGATTAATTTATCTTCAAGACATTTTGAATTTGGGAAAAATTCATGTA 1172
Qy 1152 ACTAGACAAGTGTATTAAGATGATTAATTAATGACGTGAGCAAGTGCATCCCGAG 1211

```
Db 1173 ACTAGACAAGTGTGTTAAGATGATTAAGTAAATGACAGCTGGAGACAAGATGATCCGAG 1232
QY 1212 ATCTGAGGAGACCTCCCGCTGCTGACCTGAGGAGTGAAGAGAGATAGTGATGTT 1271
Db 1233 ATCTGAGGAGACCTCCCGCTGCTGACCTGAGGAGTGAAGAGAGATAGTGATGTT 1292
QY 1272 CTTTGTCTCTGAATTTTATAGTTATATAGTCTGTTAAATGTTGCTCTGAGAGAGCCCTGGAA 1331
Db 1293 CTTTGTCTCTGAATTTTATAGTTATATAGTCTGTTAAATGTTGCTCTGAGAGAGCCCTGGAA 1352
QY 1332 AGTCTATCCCAATATCCACATCTTATATTCACAATTAAGCTGTAGTATGTAACCTTA 1391
Db 1353 AGTCTATCCCAATATCCACATCTTATATTCACAATTAAGCTGTAGTATGTAACCTTA 1412
QY 1392 AGAGCTGTCTAATGATGCTGCGACCTTGCAAGCTCAGGGGGGGCTGCAATTTAGTAAATGGGT 1451
Db 1413 AGAGCTGTCTAATGATGCTGCGACCTTGCAAGCTCAGGGGGGGCTGCAATTTAGTAAATGGGT 1472
QY 1452 CAATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTGCTCTTCCCACTGACA 1511
Db 1473 CAATGATTCACCTTTTATGATGCTTCCAAAGTGCCTTGCTCTTCCCACTGACA 1532
QY 1512 AATGCCAAAGTTGAGAAAAATATATATATTTAGATTAACAAGACAGTGGCGACAC 1571
Db 1533 AATGCCAAAGTTGAGAAAAATATATATATTTAGATTAACAAGACAGTGGCGACAC 1592
QY 1572 GATTTTATTAATAAATGAGACACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1631
Db 1593 GATTTTATTAATAAATGAGACACCTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA 1652
QY 1632 GATGATGTTTCATCCGTGAATGGTCCAGGGAGAGACCTTTCACCTTGATATATGACATTA 1691
Db 1653 GATGATGTTTCATCCGTGAATGGTCCAGGGAGAGACCTTTCACCTTGATATATGACATTA 1712
QY 1692 TGTCATTCACAGACTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGCTTAACACTCACT 1751
Db 1713 TGTCATTCACAGACTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGCTTAACACTCACT 1772
QY 1752 TTTCAATGAGCATCTAGAGAGTGGAGCTCAGCTGGGGGTGATTTGCGCCCCCATCTCCGGG 1811
Db 1773 TTTCAATGAGCATCTAGAGAGTGGAGCTCAGCTGGGGGTGATTTGCGCCCCCATCTCCGGG 1832
QY 1812 GGAATGTCGAAAGCAATTTTGGTTAACCCTCAATGAAGGAGTGAAGAGATACAGTGTCTA 1871
Db 1833 GGAATGTCGAAAGCAATTTTGGTTAACCCTCAATGAAGGAGTGAAGAGATACAGTGTCTA 1892
QY 1872 CTACCAACTAGTGAATAAAGGCGCAGGAGTGTCTCAACCTCTCAACATGTAACAGAGCT 1931
Db 1893 CTACCAACTAGTGAATAAAGGCGCAGGAGTGTCTCAACCTCTCAACATGTAACAGAGCT 1952
QY 1932 CTCCCATTTACCAACTACCAATCCGAAGTGTCAACCTGTGTGAGACTAAGAAACCTGTGT 1991
Db 1953 CTCCCATTTACCAACTACCAATCCGAAGTGTCAACCTGTGTGAGACTAAGAAACCTGTGT 2012
QY 1992 TTTGAGTGAAGAAAGGCGCTGAAAGAGGGGAGCCAAACAAATCTGTCTGTCTT-CTCACAT 2050
Db 2013 TTTGAGTGAAGAAAGGCGCTGAAAGAGGGGAGCCAAACAAATCTGTCTGTCTTCTCACAT 2072
QY 2051 AGTCAATGAGCAATTAAGCAATCTGTCTCTTTGGCTGTCTGCTCAGACACAGAGAGCAAGA 2110
Db 2073 AGTCAATGAGCAATTAAGCAATCTGTCTCTTTGGCTGTCTGCTCAGACACAGAGAGCAAGA 2132
QY 2111 CTCTATCGGGGACACAGATTAACATCTCTCAGTGAACAGATGTAAGAGGCTATGGGAAA 2170
Db 2133 CTCTATCGGGGACACAGATTAACATCTCTCAGTGAACAGATGTAAGAGGCTATGGGAAA 2192
QY 2171 TGCTGATGAGATTAATCTTCACTTGTGAGCTTGAAGTTCTTCCCTTCAATCTAAC 2230
Db 2193 TGCTGATGAGATTAATCTTCACTTGTGAGCTTGAAGTTCTTCCCTTCAATCTAAC 2252
QY 2231 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
```

```
QY 2291 ATTAGATCTCCAGACCTTCTGCGCACATTCATAATTAAGGCAACAATATACCTT 2350
Db 2313 ATTTAGATCTCCAGACCTTCTGCGCACATTCATAATTAAGGCAACAATATACCTT 2372
QY 2351 CCATGAGCACACACAGACTTTTGAAGCAAGACCAATGACTGCTTGAATGAGGCTTG 2410
Db 2373 CCATGAGCACACACAGACTTTTGAAGCAAGACCAATGACTGCTTGAATGAGGCTTG 2432
QY 2411 AGGAATGAAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCCCTTCCACACTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAAAGAAATATCTTGTTCAGGCCCCCTTCCACACTTCA 2492
QY 2471 TGCTTAAACCACTGCTTCTCTGACCTTGAAGCAAGGCTGATGATTAATGTTGTTAT 2530
Db 2493 TGCTTAAACCACTGCTTCTCTGACCTTGAAGCAAGGCTGATGATTAATGTTGTTAT 2552
QY 2531 AGAAAACTGATTTTGAAGTCTGATCGTTCAAGAAATGATTAATATCAATTTCT 2587
Db 2553 AGAAAACTGATTTTGAAGTCTGATCGTTCAAGAAATGATTAATATCAATTTCT 2609

RESULT 6
US-10-010-742-207
; Sequence 207, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jlang, Yungli
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retzer, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010.742
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-742-207

Query Match 99.1%; Score 2565; DB 13; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Db 273 TTTCTGATATCGTATACAAATGGCTGAAGAGAGGTGTTTAAAGGTTGTCATGATGCTCA 332
Qy 312 AAGAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGGCCGGAACAGACTGT 371
Db 333 AAGAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGGCCGGAACAGACTGT 392
Qy 372 TTGCTGATCAAGATAGTGTGGCAATGCCCTTTGGCGGCTGMAAAAGCTGCACTCAG 431
Db 393 TTGCTGATCAAGATAGTGTGGCAATGCCCTTTGGCGGCTGMAAAAGCTGCACTCAG 452
Qy 432 ATGCTGGACCTTCAAAATGTTATATCATCACTTTAAAGGCAAGGGAGATGCTAACCTTG 491
Db 453 ATGCTGGACCTTCAAAATGTTATATCATCACTTTAAAGGCAAGGGAGATGCTAACCTTG 512
Qy 492 AGTATAAACTGAGCTTCAAGATGCGGAGAGTGAATGTGACTATATATGCCAGCTCAG 551
Db 513 AGTATAAACTGAGCTTCAAGATGCGGAGAGTGAATGTGACTATATATGCCAGCTCAG 572
Qy 552 AGACCTTGGGCTGTGAGAGCTCCCGAATGTTCCCGGACCCCAAGTGTCTGGGCAATCCC 611
Db 573 AGACCTTGGGCTGTGAGAGCTCCCGAATGTTCCCGGACCCCAAGTGTCTGGGCAATCCC 632
Qy 612 AAGTTGACAGAGGAGCAACTTCTCGGAAGTCTCAATACAGGCTTTGAGCTGAACCTTG 671
Db 633 AAGTTGACAGAGGAGCAACTTCTCGGAAGTCTCAATACAGGCTTTGAGCTGAACCTTG 692
Qy 672 AGAATGTGACATGAGAGGTTGTGTCTGTGCTCTTCAATGTTACGATCAACAACATACT 731
Db 693 AGAATGTGACATGAGAGGTTGTGTCTGTGCTCTTCAATGTTACGATCAACAACATACT 752
Qy 732 CCGTATGATTTGAAAATGAGATTGGCCAAAGCAAGGGGATATCAAGTGAACGAATCGG 791
Db 753 CCGTATGATTTGAAAATGAGATTGGCCAAAGCAAGGGGATATCAAGTGAACGAATCGG 812
Qy 792 AGATCAAAAGGCGGAGTCACTTCAAGCTGTAAACTCAAAAGCTTCTGTGTGTCTCT 851
Db 813 AGATCAAAAGGCGGAGTCACTTCAAGCTGTGTAAACTCAAAAGCTTCTGTGTGTCTCT 872
Qy 852 CTTTCTTTGGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATCTAAATATAT 911
Db 873 CTTTCTTTGGCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATCTAAATATAT 932
Qy 912 GTGCCCTTGGCCACAAAAGCAATGCAAAAGTCAATTTGTTACAAAGGATCTACGAATAT 971
Db 933 GTGCCCTTGGCCACAAAAGCAATGCAAAAGTCAATTTGTTACAAAGGATCTACGAATAT 992
Qy 972 TTGACCAACAGATATGACTAGTATTATTTCTGGGAGAAATGAATTCATATCTTGAA 1031
Db 993 TTGACCAACAGATATGACTAGTATTATTTCTGGGAGAAATGAATTCATATCTTGAA 1052
Qy 1032 GTCTGAGTGAAGCAAAACAGAGCAAGAAACAAAAGAGCCAAAAGCAGAAAGGCTCCAT 1091
Db 1053 GTCTGAGTGAAGCAAAACAGAGCAAGAAACAAAAGAGCCAAAAGCAGAAAGGCTCCAT 1112
Qy 1092 ATGAAACAAGTAAATCTATCTTCAAGAATATTTAAGAAAGTTGGAAAAATATTCATGTGA 1151
Db 1113 ATGAAACAAGTAAATCTATCTTCAAGAATATTTAAGAAAGTTGGAAAAATATTCATGTGA 1172
Qy 1152 ACTAGACAAGTGTTAAGAGTATAAGTAAATAATGACGTGAGAGCAAGTGCATCCCGAG 1211
Db 1173 ACTAGACAAGTGTTAAGAGTATAAGTAAATAATGACGTGAGAGCAAGTGCATCCCGAG 1232
Qy 1212 ATCTCAGGAGCTTCCCTGCTGTCACTGGGGAGTGAAGAGACAGATATGTCATGTT 1271
Db 1233 ATCTCAGGAGCTTCCCTGCTGTCACTGGGGAGTGAAGAGACAGATATGTCATGTT 1292
Qy 1272 CTTTGTCTCGAATTTTAAATTAATGTGTGTTAATGTTTCTGAGGAAAGCCCTCGGAA 1331
Db 1293 CTTTGTCTCGAATTTTAAATTAATGTGTGTTAATGTTTCTGAGGAAAGCCCTCGGAA 1352
Qy 1332 AGTCTATCCCAATATCCACATCTTATATTTCCAAATTAAGCTGATGATGACCTTA 1391
Db 1353 AGTCTATCCCAATATCCACATCTTATATTTCCAAATTAAGCTGATGATGACCTTA 1412
Qy 1392 AGACGCTGCTAATTTGACTGCTGCACTTGGCAACTAGGGGGGCGCTGCATTTTAAATGGGT 1451
Db 1413 AGACGCTGCTAATTTGACTGCTGCACTTGGCAACTAGGGGGGCGCTGCATTTTAAATGGGT 1472
Qy 1452 CAATGATTCACCTTTTAAATTAATGATGCTTCAAAAGGTGCTTGGGCTTCTTCCCAACTGACA 1511
Db 1473 CAATGATTCACCTTTTAAATTAATGATGCTTCAAAAGGTGCTTGGGCTTCTTCCCAACTGACA 1532
Qy 1512 AATGCCAAAGTTGAGAAAAATGATCATTAATTTTAAAGATAAAGAGAGTGGCGACACC 1571
Db 1533 AATGCCAAAGTTGAGAAAAATGATCATTAATTTTAAAGATAAAGAGAGTGGCGACACC 1592
Qy 1572 GATTTTAAATTAATCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1631
Db 1593 GATTTTAAATTAATCTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCA 1652
Qy 1632 GATGATGTTCAATCCGGAATGATCCAGGGAGGACCTTTCACTGACTATATGGCACTTA 1691
Db 1653 GATGATGTTCAATCCGGAATGATCCAGGGAGGACCTTTCACTGACTATATGGCACTTA 1712
Qy 1692 TGTCTATCAAGAGCTTGAAGGCTTCTCTTTCCATCCCTGGGTGAGACAGTAAAGACTCAGT 1751
Db 1713 TGTCTATCAAGAGCTTGAAGGCTTCTCTTTCCATCCCTGGGTGAGACAGTAAAGACTCAGT 1772
Qy 1752 TTTCAATAGCATTAAGAGAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGG 1811
Db 1773 TTTCAATAGCATCTAAGAGAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGG 1832
Qy 1812 GGAATGTCTGAAGACAAATTTTGGTTACTCAATGAAGGAGTGGAGAGGATACAGTGCTA 1871
Db 1833 GGAATGTCTGAAGACAAATTTTGGTTACTCAATGAAGGAGTGGAGAGGATACAGTGCTA 1892
Qy 1872 CTACCAACTAGTGAATAAAGGCGCAGAGATGCTGCTCAACTCCTCAATGATACAGGACGT 1931
Db 1893 CTACCAACTAGTGAATAAAGGCGCAGAGATGCTGCTCAACTCCTCAATGATACAGGACGT 1952
Qy 1932 CTGCCCATTAACAATACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGGT 1991
Db 1953 CTGCCCATTAACAATACCAATCCGAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGGT 2012
Qy 1992 TTTGATGAGAAAAGGCGCTGGAAGGAGGAGCAACAAATGCTGTGCTT-CTCACTT 2050
Db 2013 TTTGATGAGAAAAGGCGCTGGAAGGAGGAGCAACAAATGCTGTGCTTCTTCACTT 2072
Qy 2051 AGTCATTTGCAATAATAGCAATTTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2110
Db 2073 AGTCATTTGCAATAATAGCAATTTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAA 2132
Qy 2111 CTCTATCGGCAACAGAGATPAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGAGAAA 2170
Db 2133 CTCTATCGGCAACAGAGATPAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGAGAAA 2192
Qy 2171 TGCCTGATGGGANTTACTTCAAGCTGTGAGCTTCAAGTTTCTTCCCTCACTTAC 2230
Db 2193 TGCCTGATGGGANTTACTTCAAGCTGTGAGCTTCAAGTTTCTTCCCTCACTTAC 2252
Qy 2231 CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGA 2290
Db 2253 CTGCAAGCCAAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTTCTTACTCTGA 2312
Qy 2291 ATTTAGATCTCCAGAGCTTCTGCTGCGCACAATTCAAATTAAGGCAACAAACATATCTT 2350
Db 2313 ATTTAGATCTCCAGAGCTTCTGCTGCGCACAATTCAAATTAAGGCAACAAACATATCTT 2372
Qy 2351 CCAATGAAGACACAGACTTTTGAAGAGAAAGATGACTGCTGAATTAAGGCTTG 2410
Db 2373 CCAATGAAGACACAGACTTTTGAAGAGAAAGATGACTGCTGAATTAAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAGAAAGATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAGAAAGATATCTTTGTTTCCAGCCCTTCCCAACTCTTCA 2492
```

```

RESULT 7
US-10-198-053-391
; Sequence 391, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 2627
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-391

```

Db	573	AGACCTTGCGGTGTGAGGCTCTCCCGATGTTCCCCAGCCCAAGTGTGTCTGGGCACTCC	632
Qy*	612	AAGTTGACCAAGGAGCCCACTTCTCGAAGCTTCCAAATACAGCTTTGAGCTGAACCTG	671
Db	633	AAGTTGACCAAGGAGCCCACTTCTCGGAAAGTCTCAATACAGCTTTGAGCTGAACCTG	692
Qy	672	AGAAATGACCATGAAGGTTGTGTGTGCTGTACAAATGTTACATCAACAACATCACT	731
Db	693	AGAAATGACCATGAAGGTTGTGTGTGCTGTACAAATGTTACATCAACAACATCACT	752
Qy	732	CCTGATATGATGAATAATGACATTGSCCAAGCAACAGGGAGATATCAAGTGAACAGATCG	791
Db	753	CCTGATATGATGAATAATGACATTGSCCAAGCAACAGGGAGATATCAAGTGAACAGATCG	812
Qy	792	AGATCAAAAGCGGAGTCACTTCAGAGTGTAACTCAAAAGGCTTCTGTGTGTCTCTT	851
Db	813	AGATCAAAAGCGGAGTCACTTCAGAGTGTAACTCAAAAGGCTTCTGTGTGTCTCTT	872
Qy	852	CTTTCTTTTGCATGAGCTGGGCACTTGTGCTCTCAGCCTTACCTGATGTCAATAATAT	911
Db	873	CTTTCTTTTGCATGAGCTGGGCACTTGTGCTCTCAGCCTTACCTGATGTCAATAATAT	932
Qy	912	GTGCTTGGGCAAAAAGATGCAAGTCAATGTTACAAACGGAGATCTACAGAACTAT	971
Db	933	GTGCTTGGGCAAAAAGATGCAAGTCAATGTTACAAACGGAGATCTACAGAACTAT	992
Qy	972	TTCAACACCAATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA	1031
Db	993	TTCAACACCAATATGACCTAGTTTATATTTCTGGAGGAAATGAATTCATATCTAGAA	1052
Qy	1032	GTCGTGAGTAGCAAAACAGACAAAGAAACAAAAGAACCCAAAGCAAGAGCTCCAAAT	1091
Db	1053	GTCGTGAGTAGCAAAACAGACAAAGAAACAAAAGAACCCAAAGCAAGAGCTCCAAAT	1112
Qy	1092	ATGAACAAGATTAATCTATCTTCAACACATATAGAAAGTTGGGAAATTAATTCATGTGA	1151
Db	1113	ATGAACAAGATTAATCTATCTTCAACACATATAGAAAGTTGGGAAATTAATTCATGTGA	1172
Qy	1152	ACTAGACAAGTGTAAAGTGTAAAGTAAATATGACGTGAGACAAAGTGCATCCCCAG	1211
Db	1173	ACTAGACAAGTGTAAAGTGTAAAGTAAATATGACGTGAGACAAAGTGCATCCCCAG	1232
Qy	1212	ATCTCAGGAGCTCTCCCTGCTGTCACTGSGGAGTGAAGAGACAGAGATATGTCATGTT	1271
Db	1233	ATCTCAGGAGCTCTCCCTGCTGTCACTGSGGAGTGAAGAGACAGAGATATGTCATGTT	1292
Qy	1272	CTTTGTGTCTGTGAATTTTAAAGTAAATATGTCGTGAATGTGTCTGAGAGAACCCCTGAA	1331
Db	1293	CTTTGTGTCTGTGAATTTTAAAGTAAATATGTCGTGAATGTGTCTGAGAGAACCCCTGAA	1352
Qy	1332	AGTCATCCCAACATATCACAATCTTAAATCCCAAAATTAAGCTGTATGATGACCTTA	1391
Db	1353	AGTCATCCCAACATATCACAATCTTAAATCCCAAAATTAAGCTGTATGATGACCTTA	1412
Qy	1392	AGAGCGTGCTAATGACCTGCCACTTTCGCACTCAGGGGCGGCTGCATTTTAAGTAATGGT	1451
Db	1413	AGAGCGTGCTAATGACCTGCCACTTTCGCACTCAGGGGCGGCTGCATTTTAAGTAATGGT	1472
Qy	1452	CAATGATTCACCTTTTATGATGCTTCCAAAGGTGCTTGCTTCTTCCCACTGACA	1511
Db	1473	CAATGATTCACCTTTTATGATGCTTCCAAAGGTGCTTGCTTCTTCCCACTGACA	1532
Qy	1512	AATGCAAAAGTGAAGAAAATGATCATATTTTGAATTAACAAGAGAGTGGGAGACACC	1571
Db	1533	AATGCAAAAGTGAAGAAAATGATCATATTTTGAATTAACAAGAGAGTGGGAGACACC	1592
Qy	1572	GATTTTAATAATAAATGAGCACTTCTTTTAAACAACAACAATGCGGGTTTATTTCTCA	1631
Db	1593	GATTTTAATAATAAATGAGCACTTCTTTTAAACAACAACAATGCGGGTTTATTTCTCA	1652
Qy	1632	GATGATGTTCAATCCGTGAATGTGCAGAGGAAGACCTTTCACTTGAACATATATGGCATTA	1691


```
Db 1653 GATGATGTCATCCGTGAATGATGTCAGGAGGAGCACTTTCACCTTGACATATATGACATTA 1712
Qy 1692 TGTGATACCAAGCTCTGAGGCTTCTCTTTCATCTCCGTGAGACACTTAAGACTTAAGT 1751
Db 1713 TGTGATACCAAGCTCTGAGGCTTCTCTTTCATCTCCGTGAGACACTTAAGACTTAAGT 1772
Qy 1752 TTTCAATAGACTCTAGAGAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCATCTCCGGG 1811
Db 1773 TTTCAATAGACTCTAGAGAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCATCTCCGGG 1832
Qy 1812 GGAATGTCTGAAGACAAATTTTGTGTACCTCAATGAGGAGTGAAGAGATACAGTGTCTA 1871
Db 1833 GGAATGTCTGAAGACAAATTTTGTGTACCTCAATGAGGAGTGAAGAGATACAGTGTCTA 1892
Qy 1872 CTACCAACTGATGATTAAGGCGCAGGAGTGTCTGTCACTCTCCATCACTGATACAGAGCT 1931
Db 1893 CTACCAACTGATGATTAAGGCGCAGGAGTGTCTGTCACTCTCCATCACTGATACAGAGCT 1952
Qy 1932 CTCCCATTTACAACTACCCCAATCCGAAGTGTCAACTGTCTCAGGACTTAAGAAACCTGGT 1991
Db 1953 CTCCCATTTACAACTACCCCAATCCGAAGTGTCAACTGTCTCAGGACTTAAGAAACCTGGT 2012
Qy 1992 TTTGAGTAGAAAAGGCGCTGAAAAGAGGGAGCCCAAAATCTGTCTGCTT-CTCACATT 2050
Db 2013 TTTGAGTAGAAAAGGCGCTGAAAAGAGGGAGCCCAAAATCTGTCTGCTTCTCCATCATT 2072
Qy 2051 AGTCATTTGGCAATTAAGCATTTCTGTCTCTTTTGGTGTGCTCTCAGCAAGAGAGCCGAA 2110
Db 2073 AGTCATTTGGCAATTAAGCATTTCTGTCTCTTTTGGTGTGCTCTCAGCAAGAGAGCCGAA 2132
Qy 2111 CTCTATCGGGCACAGGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTAAGGAAA 2170
Db 2133 CTCTATCGGGCACAGGATTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTAAGGAAA 2192
Qy 2171 TGCCTGATGGGATTAATCTTCAGCTGTGTGAAGCTTCTAAGTTTCTTCCCTTCAATTCAC 2230
Db 2193 TGCCTGATGGGATTAATCTTCAGCTGTGTGAAGCTTCTTCCCTTCAATTCAC 2252
Qy 2231 CTGCAAGCCCAAGTTCTGTGAAGAAATGCTGAGTTTCTACTCAGGTTTCTTAATCTGA 2290
Db 2253 CTGCAAGCCCAAGTTCTGTGAAGAAATGCTGAGTTTCTACTCAGGTTTCTTAATCTGA 2312
Qy 2291 ATTAGTCTCCAGACCTTCTCTGSCCAATTCCTTAAGCAACAATTAATACCTT 2350
Db 2313 ATTAGTCTCCAGACCTTCTCTGSCCAATTCCTTAAGCAACAATTAATACCTT 2372
Qy 2351 CCATGAAGCACACAGACTTTTGAAGCAAGAGCAATGACTGCTTGAATTTGAAGGCTTG 2410
Db 2373 CCATGAAGCACACAGACTTTTGAAGCAAGAGCAATGACTGCTTGAATTTGAAGGCTTG 2432
Qy 2411 AGGAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCCCTTCCCACTCTTCA 2470
Db 2433 AGGAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCCCTTCCCACTCTTCA 2492
Qy 2471 TGTGTTAAACCACTGCTCTCTGAGCTTTGAGGCAAGGAGTGAATTAATCATGTTGTTAT 2530
Db 2493 TGTGTTAAACCACTGCTCTCTGAGCTTTGAGGCAAGGAGTGAATTAATCATGTTGTTAT 2552
Qy 2531 AGAAAACTGATTTTGAAGTTCTGATGCTTCAAGAGAAATGAATTAATACATTTCTT 2587
Db 2553 AGAAAACTGATTTTGAAGTTCTGATGCTTCAAGAGAAATGAATTAATACATTTCTT 2609
```

RESULT 8
US-10-714-389-207
; Sequence 207, Application US/10714389
; Publication No. US20040101899A1

; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Jang, Yung H.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer

```
; APPLICANT: Wang, Tongtong  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.491D1  
; CURRENT APPLICATION NUMBER: US/10/714,389  
; CURRENT FILING DATE: 2003-11-14  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 207  
; LENGTH: 2627  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-714-389-207
```

Query Match 99.1%; Score 2565; DB 18; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy 12 GGCAGCTCCACTGAGCCAGTACCCAGATAGCTGGGAACTTCCCGACGATGGCTTCCC 71
Db 33 GGCAGCTCCACTGAGCCAGTACCCAGATAGCTGGGAACTTCCCGACGATGGCTTCCC 92
Qy 72 TGGGGCAGATCTCTCTGAGAGCATTAATGACATCATTAATTTCTGGCTGAGCAATTG 131
Db 93 TGGGGCAGATCTCTCTGAGAGCATTAATGACATCATTAATTTCTGGCTGAGCAATTG 152
Qy 132 CACTCATATTGGCTTTGATTTTCAAGGAGACATCTCATACAGTCACTGCTGCTT 191
Db 153 CACTCATATTGGCTTTGATTTTCAAGGAGACATCTCATACAGTCACTGCTGCTT 212
Qy 192 CAGCTGGGAACATTTGGGGAGATGGAATCTGAGCTGCATTTTGAACCTGACATCAAC 251
Db 213 CAGCTGGGAACATTTGGGGAGATGGAATCTGAGCTGCATTTTGAACCTGACATCAAC 272
Qy 252 TTTCTGATATCGATATACATAGCTGAAGAAAGTGTGTTTGAAGCTTGCATGATTTCA 311
Db 273 TTTCTGATATCGATATACATAGCTGAAGAAAGTGTGTTTGAAGCTTGCATGATTTCA 332
Qy 312 AAGAGGCAAAAGATGAGCTGTGAGAGCAGAGATGAATGTTTCAGAGGCCGAGCAGAGT 371
Db 333 AAGAGGCAAAAGATGAGCTGTGAGAGCAGAGATGAATGTTTCAGAGGCCGAGCAGAGT 392
Qy 372 TTGCTGATCAAGATGATTTGGCAATGCTCTTTGGGGCTGAAGAAAGTGAATCTACAG 431
Db 393 TTGCTGATCAAGATGATTTGGCAATGCTCTTTGGGGCTGAAGAAAGTGAATCTACAG 452
Qy 432 ATGCTGGCACTTCAATATGTTATATCATCTTCTAAGGCAAGGGAATGCTAACCTTG 491
Db 453 ATGCTGGCACTTCAATATGTTATATCATCTTCTAAGGCAAGGGAATGCTAACCTTG 512
Qy 492 AGTATTAACCTGAGGCTTTCAGATGCGGAAAGTGAATGATCTATTAATGCAAGCTCAG 551
Db 513 AGTATTAACCTGAGGCTTTCAGATGCGGAAAGTGAATGATCTATTAATGCAAGCTCAG 572
Qy 552 AGACCTTTGGGAGTGAAGCTTCCCGATGTTTCCCGACAGGAGCTGGGCAATCCC 611
Db 573 AGACCTTTGGGAGTGAAGCTTCCCGATGTTTCCCGACAGGAGCTGGGCAATCCC 632
Qy 612 AAGTTGACAGGAGGCACTTCTCGAAGTCTCAATATCAAGCTTTGAGAGTGAAGCTCTG 671
Db 633 AAGTTGACAGGAGGCACTTCTCGAAGTCTCAATATCAAGCTTTGAGAGTGAAGCTCTG 692
Qy 672 AGAATGTGACATGAAGGTTGTGTCTGTCTCTCAATGTTTACATCAACAACATTAAT 731
Db 693 AGAATGTGACATGAAGGTTGTGTCTGTCTCTCAATGTTTACATCAACAACATTAAT 752
Qy 732 CCTGATGATTAAGAAATGACATTTGCCAAGCAAGGGGATTAATCAAGGAGCAGATCGG 791
Db 753 CCTGATGATTAAGAAATGACATTTGCCAAGCAAGGGGATTAATCAAGGAGCAGATCGG 812
Qy 792 AGATCAAAAGGGGAGTCACTTACAGCTCTAAAGCTCAAGGCTTCTGTGTCTCTT 851
```

Db 813 AGATCAAAAAGCGAGTCACTACAGCTGCTAAACTCAAAAGGCTTCTGCTGCTCTT 872
Qy 852 CTTTCTTTGGCCATCAGCTGGGCACTTTCGCCCTCAGACCCCTTACCTGATGCTAAATAT 911
Db 873 CTTTCTTTGGCCATCAGCTGGGCACTTTCGCCCTCAGACCCCTTACCTGATGCTAAATAT 932
Qy 912 GTGCCCTGGCCCAAAAAGCATGCAAAAGTCATTGTTCAACAGGGATCTACAGAACTAT 971
Db 933 GTGCCCTGGCCCAAAAAGCATGCAAAAGTCATTGTTCAACAGGGATCTACAGAACTAT 992
Qy 972 TTCAACCAAGATATGACCTAGTTTATATTTCTGGAGAGAAATGATATCATATCTAGAA 1031
Db 993 TTCAACCAAGATATGACCTAGTTTATATTTCTGGAGAGAAATGATATCATATCTAGAA 1052
Qy 1032 GTCTGAGTGAACCAAAAGAGCAAAAGAAACAAAAGACCAAAAGCGAAGGCTCCAT 1091
Db 1053 GTCTGAGTGAACCAAAAGAGCAAAAGAAACAAAAGACCAAAAGCGCTCCAT 1112
Qy 1092 ATGAACAAGATATCTATCTTCAAAAGATATTAAGATTTGGAATAATTAATTCATGTA 1151
Db 1113 ATGAACAAGATATATCTATCTTCAAAAGATATTAAGATTTGGAATAATTAATTCATGTA 1172
Qy 1152 ACTGAACAAGTGTATAGAGATATGTAATGAATGACGCTGAGACAGATGATCCGAG 1211
Db 1173 ACTGAACAAGTGTATAGAGATATGTAATGAATGACGCTGAGACAGATGATCCGAG 1232
Qy 1212 ATCTAGAGGACCTCCCGCTGCTACCTGGGAGTGAAGAGACAGATGATGATGTT 1271
Db 1233 ATCTAGAGGACCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
Qy 1272 CTTTGTCTGTAATTTTATGTAATATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCT 1331
Db 1293 CTTTGTCTGTAATTTTATGTAATATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCT 1352
Qy 1332 AGTCTATCCCAACATATCCCAACATCTTATATCCCAACATATGCTGTAATGCTGTAAT 1391
Db 1353 AGTCTATCCCAACATATCCCAACATCTTATATCCCAACATATGCTGTAATGCTGTAAT 1412
Qy 1392 AAGAGCTGTAATGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1451
Db 1413 AAGAGCTGTAATGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1472
Qy 1452 CAATGATTCACCTTTTATGATGCTTCAAAAGTGGCTTGGCTTCTTCCCACTGCA 1511
Db 1473 CAATGATTCACCTTTTATGATGCTTCAAAAGTGGCTTGGCTTCTTCCCACTGCA 1532
Qy 1512 AATGCCAAGTTGAGAAAAATGATCAATTTTATGATCAACAGCACTGCGGCACTC 1571
Db 1533 AATGCCAAGTTGAGAAAAATGATCAATTTTATGATCAACAGCACTGCGGCACTC 1592
Qy 1572 GATTTTATTAATAAATGAGCACTTCTTTTAAACAAATGCGGGTTTATTTCTCA 1631
Db 1593 GATTTTATTAATAAATGAGCACTTCTTTTAAACAAATGCGGGTTTATTTCTCA 1652
Qy 1632 GATGATGTTTATCCGTAATGCTCAGGAGAGACCTTTTACCTGATATATGAGATTA 1691
Db 1653 GATGATGTTTATCCGTAATGCTCAGGAGAGACCTTTTACCTGATATATGAGATTA 1712
Qy 1692 TGTATCACAAGCTGAGGCTTCTCTTTTCAATCTGCTGAGCAAGCTTCAAGCTCAGT 1751
Db 1713 TGTATCACAAGCTGAGGCTTCTCTTTTCAATCTGCTGAGCAAGCTTCAAGCTCAGT 1772
Qy 1752 TTTGATATGATCTGAGAGAGTGGAGCTGAGCTGGGGGTATTTGCGCCCACTCCGGG 1811
Db 1773 TTTGATATGATCTGAGAGAGTGGAGCTGAGCTGGGGGTATTTGCGCCCACTCCGGG 1832
Qy 1812 GGAATGCTGAAGACAAATTTGGTTACTCAATGAAGGAGTGGAGAGGATACAGTCTCA 1871
Db 1833 GGAATGCTGAAGACAAATTTGGTTACTCAATGAAGGAGTGGAGAGGATACAGTCTCA 1892
Qy 1872 CTACCAACTAGTGTAAAGGCGAGGAGTGTCTCAACCTTCTTACATATACAGAGCT 1931
Db 1893 CTACCAACTAGTGTAAAGGCGAGGAGTGTCTCAACCTTCTTACATATACAGAGCT 1952

Qy 1932 CTCCCATTTAACAATACCAATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGGT 1991
Db 1953 CTCCCATTTAACAATACCAATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGGT 2012
Qy 1992 TTTGATGAAAAAGGCGCTGGAAAAAGAGGAGCCCAACATCTGTCTGCTT-CTCACTT 2050
Db 2013 TTTGATGAAAAAGGCGCTGGAAAAAGAGGAGCCCAACATCTGTCTGCTTCTCACTT 2072
Qy 2051 AGTCATTTGGCAATTAAGATCTGTCTTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2110
Db 2073 AGTCATTTGGCAATTAAGATCTGTCTTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2132
Qy 2111 CTCTATCGGAGCAGAGTAACATCTCTCACTGTAACAGATTTGACAAAGGCTTATGGAAA 2170
Db 2133 CTCTATCGGAGCAGAGTAACATCTCTCACTGTAACAGATTTGACAAAGGCTTATGGAAA 2192
Qy 2171 TGCTGATGGATTAATCTTCAAGCTTTGAGCTTTGAGCTTTTCTTCTTCTTCTTCTTCTT 2230
Db 2193 TGCTGATGGATTAATCTTCAAGCTTTGAGCTTTGAGCTTTTCTTCTTCTTCTTCTTCTT 2252
Qy 2231 CTGCAAGCAGATCTGTAAGAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2290
Db 2253 CTGCAAGCAGATCTGTAAGAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2312
Qy 2291 ATTTAGATCTCCAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2350
Db 2313 ATTTAGATCTCCAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2372
Qy 2351 CCATGAGCAGACACAGACCTTTTGAAGAGAGACATATGATCTGCTGTAATGAGGCTTGG 2410
Db 2373 CCATGAGCAGACACAGACCTTTTGAAGAGAGACATATGATCTGCTGTAATGAGGCTTGG 2432
Qy 2411 AGGATGAGAGCTTTGAAGAGAAAGATATCTTGTGTTCCAGGCCCCCTTCCCACTCTTCA 2470
Db 2433 AGGATGAGAGCTTTGAAGAGAAAGATATCTTGTGTTCCAGGCCCCCTTCCCACTCTTCA 2492
Qy 2471 TGTGTTAAACAAGCTGCTTCTGAGACCTTGAAGCAGCGTGAATGATTAATGTTGTTAT 2530
Db 2493 TGTGTTAAACAAGCTGCTTCTGAGACCTTGAAGCAGCGTGAATGATTAATGTTGTTAT 2552
Qy 2531 AGAAAACTGATTTTGAATGATCTGATCTTCAAGAGATGATTAATATACATTTCTT 2587
Db 2553 AGAAAACTGATTTTGAATGATCTGATCTTCAAGAGATGATTAATATACATTTCTT 2609

RESULT 9
US-10-717-296-207
; Sequence 207, Application US/10717296
; Publication No. US20040142361A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Davin C.
; APPLICANT: Jilang, Yuhui
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C8
; CURRENT APPLICATION NUMBER: US/10/717,296
; CURRENT FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FASTSEQ For Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-296-207

Query Match 99.1%; Score 2565; DB 18; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCAGCTCAGGAGTACCAAGTACGCTGGGAACTTTCCCAAGCAATGGCTTCC 71
Db 33 GGCAGCTCAGCTCAGGAGTACCAAGTACGCTGGGAACTTTCCCAAGCAATGGCTTCC 92

QY	72	TGGGGCAGATCTCTTCTCGAGCATAAATTAGCATCATTAATTCTGGCTGGAGCATTG	131
Db	93	TGGGGCAGATCTCTTCTCGAGCATAAATTAGCATCATTAATTCTGGCTGGAGCAATTG	152
QY	132	CACATCATGTTGGCTTTGGTATTTTCAAGGAGACACTCCATCAAGTCATCTATCGGCT	191
Db	153	CACATCATGTTGGCTTTGGTATTTTCAAGGAGACACTCCATCAAGTCATCTATCGGCT	212
QY	192	CAGCTGGAACTTGGGGAGATGGAATCTGAGCTGACCTTTTGAACCTGACATCAAC	251
Db	213	CAGCTGGAACTTGGGGAGATGGAATCTGAGCTGACCTTTTGAACCTGACATCAAC	272
QY	252	TTTCTGATATCGTGATACATGCGTGAAGAAAGTTTAAAGCTGGTCCATAGTTCA	311
Db	273	TTTCTGATATCGTGATACATGCGTGAAGAAAGTTTAAAGCTGGTCCATAGTTCA	332
QY	312	AAGAAGCAAGATAGCTGTGCGAGCAGATGAATTTGAGAGCGCGGACAGAGTG	371
Db	333	AAGAAGCAAGATAGCTGTGCGAGCAGATGAATTTGAGAGCGCGGACAGAGTG	392
QY	372	TTGCTGATCAAGTATAGTTGGCAATGCTCTTTTGGCTGAATAAGTCACTCACG	431
Db	393	TTGCTGATCAAGTATAGTTGGCAATGCTCTTTTGGCTGAATAAGTCACTCACG	452
QY	432	ATGCTGGACACCTACAAATGTTATATCATCATCTTCAAAAGGCAAGGGAAATCTTAACCTG	491
Db	453	ATGCTGGACACCTACAAATGTTATATCATCATCTTCAAAAGGCAAGGGAAATCTTAACCTTG	512
QY	492	AGTATAAACTGAGACCTTCAGCATGCCGGAAGTGAATGTGACTATTAATCCAGCTCAG	551
Db	513	AGTATAAACTGAGACCTTCAGCATGCCGGAAGTGAATGTGACTATTAATCCAGCTCAG	572
QY	552	AGACCTTGCGGTGAGAGCTCCCGGATGGTTCCCGACCGCACAGTGGTCTGGGCATGCC	611
Db	573	AGACCTTGCGGTGAGAGCTCCCGGATGGTTCCCGACCGCACAGTGGTCTGGGCATGCC	632
QY	612	AAGTTGACCAAGGAGCCCAACTCTCTGGAAAGTCTCCCAATACCAGCTTTGAGCTGAACCTG	671
Db	633	AAGTTGACCAAGGAGCCCAACTCTCTGGAAAGTCTCCCAATACCAGCTTTGAGCTGAACCTG	692
QY	672	AGATATGTGACCATGAAGTTGTGTCTGTGCTCTACATGTTACGATCAACAACATATCT	731
Db	693	AGATATGTGACCATGAAGTTGTGTCTGTGCTCTACATGTTACGATCAACAACATATCT	752
QY	732	CCTGATGATTTGAAAAATGACATGTGCCAAGCAACAGGGGATATCAAGATGACAGAAATCGG	791
Db	753	CCTGATGATTTGAAAAATGACATGTGCCAAGCAACAGGGGATATCAAGATGACAGAAATCGG	812
QY	792	AGATCAAAAGGCGAGTCACTTACAGCTTAACTCAAAAGGCTTCTGTGTGTCTCTT	851
Db	813	AGATCAAAAGGCGAGTCACTTACAGCTTAACTCAAAAGGCTTCTGTGTGTCTCTT	872
QY	852	CTTTTCTTTGCCATCAGCTGGGCACTTCTGCGCTCTCAGCGCTTACTGTATGCTAAATAT	911
Db	873	CTTTTCTTTGCCATCAGCTGGGCACTTCTGCGCTCTCAGCGCTTACTGTATGCTAAATAT	932
QY	912	GTCGCTTGGCCACAAAAAGCATGCAAAAGTCAATGTTTCAACAGGGATCTACAGAACTAT	971
Db	933	GTCGCTTGGCCACAAAAAGCATGCAAAAGTCAATGTTTCAACAGGGATCTACAGAACTAT	992
QY	972	TTTACCAACCAATATGACCTTACTGTTTATATTTCTGGGAGAAATGAATTCATATCTAGAA	1031
Db	993	TTTACCAACCAATATGACCTTACTGTTTATATTTCTGGGAGAAATGAATTCATATCTAGAA	1052
QY	1032	GTCGTGAGTGAACAACAAGACAAGAAACAAAAAGGCCAAAGCGCAAGCTCCCAAT	1091
Db	1053	GTCGTGAGTGAACAACAAGACAAGAAACAAAAAGGCCAAAGCGCTCCCAAT	1112
QY	1092	ATGAACAAGATTAATCTATCTTCAAAAGCATATTGAAAGTTGGGAAAAATTAATCATGTGA	1151
Db	1113	ATGAACAAGATTAATCTATCTTCAAAAGCATATTGAAAGTTGGGAAAAATTAATCATGTGA	1172

QY	1152	ACTAGACAAAGTGTGTAAAGTGTAAAGTAAATAGCAACTGCGAGACAAGTGCATCCCGAG	1211
Db	1173	ACTGACAAAGTGTGTAAAGTGTAAAGTAAATAGCAAGTGGAGACAAGTGCATCCCGAG	1232
QY	1212	ATCTCAGGAGCCTCCCCCTGCTCTCACTCTGGGAGTGAAGAGACAGATATAGTCACTGTT	1271
Db	1233	ATCTCAGGAGCCTCCCCCTGCTCTCACTCTGGGAGTGAAGAGACAGATATAGTCACTGTT	1292
QY	1272	CTTGTCTCTGAATTTTGTAGTATATATGCTGTATGTGCTCTGAGAAAGCCCTGGAA	1331
Db	1293	CTTGTGTCTGAATTTTGTAGTATATATGCTGTATGTGCTCTGAGAAAGCCCTGGAA	1352
QY	1332	AGTCTATCTCCAACTATCCACTCTTATATTCCAAATTAAGCTGTATGTATACCTTA	1391
Db	1353	AGTCTATCTCCAACTATCCACTCTTATATTCCAAATTAAGCTGTATGTATACCTTA	1412
QY	1392	AGAGCGTCTAATTGACCTGCGCACTTGGCACTGAGGGGGCGGCTGCATTTTATGTATGGGT	1451
Db	1413	AGAGCGTCTAATTGACCTGCGCACTTGGCACTGAGGGGGCGGCTGCATTTTATGTATGGGT	1472
QY	1452	CAAAATGATTCACCTTTTATGATGCTGCCAAAGTGCTTGCTCTCTCCCACTGACA	1511
Db	1473	CAAAATGATTCACCTTTTATGATGCTGCCAAAGTGCTTGCTCTCTCCCACTGACA	1532
QY	1512	AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAACATTAACAGAGCATGTCGCGACACC	1571
Db	1533	AATGCCAAAGTTGAGAAAAATGATCATATTTTATGATTAACATTAACAGAGCATGTCGCGACACC	1592
QY	1572	GATTTTATTAATTAATCACTGAGCATCTTCTTTTAAACAACAAATGCGGGTTTATTTCTCA	1631
Db	1593	GATTTTATTAATTAATCACTGAGCATCTTCTTTTAAACAACAAATGCGGGTTTATTTCTCA	1652
QY	1632	GATGATGTTCACTCCGTGTAATGTGTCAGGGAAGAGACCTTTCACCTTGACTATATGCACTTA	1691
Db	1653	GATGATGTTCACTCCGTGTAATGTGTCAGGGAAGAGACCTTTCACCTTGACTATATGCACTTA	1712
QY	1692	TGTCAATCAAGAGCTCTGAGGCTTCTCCTTTCATCTGTGCTGACAGCTAAGACTCTCAGT	1751
Db	1713	TGTCAATCAAGAGCTCTGAGGCTTCTCCTTTCATCTGTGCTGACAGCTAAGACTCTCAGT	1772
QY	1752	TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTTGGGGTGAATTTGGCCCCCATCTCCGGG	1811
Db	1773	TTTCAATAGCATCTAGAGCAGTGGGACTCAGCTTGGGGTGAATTTGGCCCCCATCTCCGGG	1832
QY	1812	GGAATGTCTGAAGCAATTTTGTGTAACTCTCAATAGGGAAGTGAAGAGATACAGTCTCTA	1871
Db	1833	GGAATGTCTGAAGCAATTTTGTGTAACTCTCAATAGGGAAGTGAAGAGATACAGTCTCTA	1892
QY	1872	CTACCAACTAGTGTGATTAAGGCGCAGGGATGTGCTCAACCTCTTACCATGTACAGAGCGT	1931
Db	1893	CTACCAACTAGTGTGATTAAGGCGCAGGGATGTGCTCAACCTCTTACCATGTACAGAGCGT	1952
QY	1932	CTCCCATTTACACTACCCCAATCCGAAGTGTCAACTGTGTACAGACTTAAGAAACCTTGCT	1991
Db	1953	CTCCCATTTACACTACCCCAATCCGAAGTGTCAACTGTGTACAGACTTAAGAAACCTTGCT	2012
QY	1992	TTTGAAGTGAAGAAAGGCGCTGGAAAGAGGGAGGCCAACAATCTGTCTGCTTT-CTCACATT	2050
Db	2013	TTTGAAGTGAAGAAAGGCGCTGGAAAGAGGGAGGCCAACAATCTGTCTGTCTTCTTCACATT	2072
QY	2051	AGTCATTGGCAAAATTAAGCATTTCTGTCTCTTGTGGCTGTGCTCTCAGCACAGAGAGCCAGAA	2110
Db	2073	AGTCATTGGCAAAATTAAGCATTTCTGTCTCTTGTGGCTGTGCTCTCAGCACAGAGAGCCAGAA	2132
QY	2111	CTCTATGGGGCAACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAA	2170
Db	2133	CTCTATGGGGCAACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAA	2192
QY	2171	TGCGCGAAGGGATTAATCTTCAGCTTGTGTGAGCTCTTAAGTTTCTTCCCTTCAATCTTACC	2230
Db	2193	TGCGCGAAGGGATTAATCTTCAGCTTGTGTGAGCTCTTAAGTTTCTTCCCTTCAATCTTACC	2252
QY	2231	CTGCAGACCAAGTTCTGTATAGAGAAATGCGCTGAAGTTCTAGCTCAGGTTTCTTACTCTGA	2290

Db 2253 CTGCAAGCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGA 2312
Qy 2291 ATTGTGATCTCCAGACCCCTTCTGGCCCAATTTCAATTAAGGCAACAACATTAACCTT 2350
Db 2233 ATTGTGATCTCCAGACCCCTTCTGGCCCAATTTCAATTAAGGCAACAACATTAACCTT 2372
Qy 2351 CCATAGAGCACAACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGG 2410
Db 2373 CCATAGAGCACAACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTAAGGCTTGG 2432
Qy 2411 AGAAATGAAGCTTTGAAGGAAAAAGAAATCTTTGTTTCCAGCCCCCTTCCCACTCTTCA 2470
Db 2433 AGAAATGAAGCTTTGAAGGAAAAAGAAATCTTTGTTTCCAGCCCCCTTCCCACTCTTCA 2492
Qy 2471 TGTGTTAAACCACTGCTTCTTGGACCTTGGACCCAGGAGTGTATTAATGTTGTTAT 2530
Db 2493 TGTGTTAAACCACTGCTTCTTGGACCTTGGACCCAGGAGTGTATTAATGTTGTTAT 2552
Qy 2531 AGAAATGAAGCTTTGAAGTGTGATGCTTCAAGAGATGATTAATATCATTTTCT 2587
Db 2553 AGAAATGAAGCTTTGAAGTGTGATGCTTCAAGAGATGATTAATATCATTTTCT 2609

RESULT 10
US-10-860-790-391
; Sequence 391, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-860-790-391

Query Match 99.1%; Score 2565; DB 19; Length 2627;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 12 GGCAGCTCCAGCTCAGCCAGTACCCAGATAGCGTGGGAACCTTCCCAGCCATGGCTTCCC 71
Db 33 GGCAGCTCCAGCTCAGCCAGTACCCAGATAGCGTGGGAACCTTCCCAGCCATGGCTTCCC 92
Qy 72 TGGGGGAGATCCCTCTTCTGAGGATTAATTAGATCATCTATTCTGGCTGGAGCAATTG 131
Db 93 TGGGGGAGATCCCTCTTCTGAGGATTAATTAGATCATCTATTCTGGCTGGAGCAATTG 152
Qy 132 CACTATCATTTGGCTTTGGTATTTCAGGAGACACTCATCAAGTCACTACTGTGCGCT 191
Db 153 CACTATCATTTGGCTTTGGTATTTCAGGAGACACTCATCAAGTCACTACTGTGCGCT 212
Qy 192 CAGCTGGGAACTTTGGGGAGGATGGAATCTGAGCTGCACTTTGAACTGACATCAAAC 251
Db 213 CAGCTGGGAACTTTGGGGAGGATGGAATCTGAGCTGCACTTTGAACTGACATCAAAC 272
Qy 252 TTTTGTATTCGTGATACATAGGCTGTAAGAGAGTGTGTTAGGCTTGTCTCAATGATTCA 311
Db 273 TTTTGTATTCGTGATACATAGGCTGTAAGAGAGTGTGTTAGGCTTGTCTCAATGATTCA 332
Qy 312 AAGAAAGCAAGATGAGCTGTGGAGCAGAGATGAATGTTCAAGAGCCGGAACAGAGTGT 371
Db 333 AAGAAAGCAAGATGAGCTGTGGAGCAGAGATGAATGTTCAAGAGCCGGAACAGAGTGT 392

Qy 372 TTGCTGATCAAGTATAGTTGGCAATGCTCTTTGCGGCTGAAAAAGCTGCACTCAAG 431
Db 393 TTGCTGATCAAGTATAGTTGGCAATGCTCTTTGCGGCTGAAAAAGCTGCACTCAAG 452
Qy 432 ATGCTGGACCTTCAAAATGTTATATCATCACTTTTAAAGGCAAGGGATGCTTAACCTTG 491
Db 453 ATGCTGGACCTTCAAAATGTTATATCATCACTTTTAAAGGCAAGGGATGCTTAACCTTG 512
Qy 492 AGTATTAACCTGGAGCTTGCAGATGCGGGAAGTGAATGTTGATTAATGATGCTGAG 551
Db 513 AGTATTAACCTGGAGCTTGCAGATGCGGGAAGTGAATGTTGATTAATGATGCTGAG 572
Qy 552 AGACCTTGGCTGTGAGGCTCCCGATGTTCCCGAGCCCAAGTGTCTGGCATGCC 611
Db 573 AGACCTTGGCTGTGAGGCTCCCGATGTTCCCGAGCCCAAGTGTCTGGCATGCC 632
Qy 612 AAGTTGACAGGAGGCCAATCTTCTGGAAATGTTCCAAATCCAGCTTTGAGCTGAATCTG 671
Db 633 AAGTTGACAGGAGGCCAATCTTCTGGAAATGTTCCAAATCCAGCTTTGAGCTGAATCTG 692
Qy 672 AGAATGACATGAAGGTTGTGTGCTGTCTCAATGTTAGATCAACAACATCACT 731
Db 693 AGAATGACATGAAGGTTGTGTGCTGTCTCAATGTTAGATCAACAACATCACT 752
Qy 732 CCTGTATGATTAATAATGACATTCGCAAGCAAGGAGATATCAAGTGAACAGATCGG 791
Db 753 CCTGTATGATTAATAATGACATTCGCAAGCAAGGAGATATCAAGTGAACAGATCGG 812
Qy 792 AGATCAAAAAGCGGAGTCACTCAAGCTGCTTAACTCAAAAGCTTCTGTGTCTCTT 851
Db 813 AGATCAAAAAGCGGAGTCACTCAAGCTGCTTAACTCAAAAGCTTCTGTGTCTCTT 872
Qy 852 CTTTCTTTGCAATGAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATAT 911
Db 873 CTTTCTTTGCAATGAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTAAATAT 932
Qy 912 GTGCTTGGCCCAAAAAAGCATGCAAAATGTTTCAACAAGGATCTACAGAACTAT 971
Db 933 GTGCTTGGCCCAAAAAAGCATGCAAAATGTTTCAACAAGGATCTACAGAACTAT 992
Qy 972 TTCACCAACAGATATGACTTATGTTTATTTCTGGAGGAAATGATTCATATCTGAA 1031
Db 993 TTCACCAACAGATATGACTTATGTTTATTTCTGGAGGAAATGATTCATATCTGAA 1052
Qy 1032 GTCTGGAGTGAACAACAAGCAAGCAAAAAAGAACCCAAAGCAGAGGCTCCAT 1091
Db 1053 GTCTGGAGTGAACAACAAGCAAGCAAAAAAGAACCCAAAGCAGAGGCTCCAT 1112
Qy 1092 ATGAACAAGATTAATCTATCTTCAAAAGCATATTAAGATTTGGGAAATTAATTCATGTA 1151
Db 1113 ATGAACAAGATTAATCTATCTTCAAAAGCATATTAAGATTTGGGAAATTAATTCATGTA 1172
Qy 1152 ACTAGACAAGTGTGTTAAGATGATTAATAATGCAAGCTGGAACAAGTCAATCCAG 1211
Db 1173 ACTAGACAAGTGTGTTAAGATGATTAATAATGCAAGCTGGAACAAGTCAATCCAG 1232
Qy 1212 ATCTAGAGGACCTCCCTGCTGTCACTGAGGAGTGAAGAGCAGGATAGTGCATGTT 1271
Db 1233 ATCTAGAGGACCTCCCTGCTGTCACTGAGGAGTGAAGAGCAGGATAGTGCATGTT 1292
Qy 1272 CTTTGTCTCTGAATTTTATGTTATGCTGTATATGTTGCTCTGAGGAAGCCCTGGAA 1331
Db 1293 CTTTGTCTCTGAATTTTATGTTATATGCTGTATATGTTGCTCTGAGGAAGCCCTGGAA 1352
Qy 1332 AGTCTATCCCAACATATCAATCTTATATTCACAAATTAAGCTGTATGTAACCTTA 1391
Db 1353 AGTCTATCCCAACATATCAATCTTATATTCACAAATTAAGCTGTATGTAACCTTA 1412
Qy 1392 AGAGCTGCTAATTAAGCTGCACTTGGCAATCGAGGGGCGCTGATTTGTAATGGGT 1451
Db 1413 AGAGCTGCTAATTAAGCTGCACTTGGCAATCGAGGGGCGCTGATTTGTAATGGGT 1472

Db 969 AAGTGGACGAGGGAGCAACTTCTCGGAAGTCTCCAAATACAGAGCTTGGAGCTGACTCG 1028
Qy 672 AGAATGTACCATGAAAGGTGTGTGCTGTCTACAAATGTTACGATGCAACAATCAATCT 731
Db 1029 AGAAATGTACCATGAAAGGTGTGTGCTGTCTACAAATGTTACGATGCAACAATCAATCT 1088
Qy 732 CCTGTATGATGAAATGACATTTGGCAAGCAAGGGATATCAAGTGAAGAAATGG 791
Db 1089 CCTGTATGATGAAATGACATTTGGCAAGCAAGGGATATCAAGTGAAGAAATGG 1148
Qy 792 AGATCAAAAGCGGAGTCACTTACAGCTGCTAACTCAAGGCTTCTGTGTCTCTT 851
Db 1149 AGATCAAAAGCGGAGTCACTTACAGCTGCTAACTCAAGGCTTCTGTGTCTCTT 1208
Qy 852 CTTTCTTTGGCCATCAGCTGCGGAGCTTCTGCTCTCAGGCTTACCTGATGCTAAATAT 911
Db 1209 CTTTCTTTGGCCATCAGCTGCGGAGCTTCTGCTCTCAGGCTTACCTGATGCTAAATAT 1268
Qy 912 GTGCCCTGGCCACAAAGAAAGCATGCAAGTCAATGTTCAACAGGGATCTACAGAACTAT 971
Db 1269 GTGCCCTGGCCACAAAGAAAGCATGCAAGTCAATGTTCAACAGGGATCTACAGAACTAT 1328
Qy 972 TTACCCACCAATATGACCTTAAATTTATTTCTGGAGGAAATGAAATTCATATCTAGAA 1031
Db 1329 TTACCCACCAATATGACCTTAAATTTATTTCTGGAGGAAATGAAATTCATATCTAGAA 1388
Qy 1032 GTCTGAGTGAAGCAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1091
Db 1389 GTCTGAGTGAAGCAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1448
Qy 1092 ATGAACAAAGATTAATCTATCTTCAAGACATATTAAGAGTTGGGAAATTAATTCATGTA 1151
Db 1449 ATGAACAAAGATTAATCTATCTTCAAGACATATTAAGAGTTGGGAAATTAATTCATGTA 1508
Qy 1152 ACTAGCAAGTGTGTAGAGTGAATTAATGCAAGTGAAGCAAGTGAAGTCCAG 1211
Db 1509 ACTAGCAAGTGTGTAGAGTGAATTAATGCAAGTGAAGCAAGTGAAGTCCAG 1568
Qy 1212 ATCTCAGGAGACCTCCCTGCTGTCACTGGGAGTGAAGAGCAAGTGAAGT 1271
Db 1569 ATCTCAGGAGACCTCCCTGCTGTCACTGGGAGTGAAGAGCAAGTGAAGT 1628
Qy 1272 CTTTGTCTCTGAATTTTATGTTATATGCTGTAAATGTTCTCTGAGGAAGCCCTGGA 1331
Db 1629 CTTTGTCTCTGAATTTTATGTTATATGCTGTAAATGTTCTCTGAGGAAGCCCTGGA 1688
Qy 1332 AGTCTATCCCAATATCCCAATCTTATATTCACAAATTAAGCTGTAGTATGTAACCTTA 1391
Db 1689 AGTCTATCCCAATATCCCAATCTTATATTCACAAATTAAGCTGTAGTATGTAACCTTA 1748
Qy 1392 AGACGCTGTATATGACCTGCACTTGGCACTCAGGGGAGGCTGCAATTTTATTAATGGGT 1451
Db 1749 AGACGCTGTATATGACCTGCACTTGGCACTCAGGGGAGGCTGCAATTTTATTAATGGGT 1808
Qy 1452 CAATATGATCACTTTTATGATGCTTCCAAAGTGTGCTGCTCTTCCCACTGACA 1511
Db 1809 CAATATGATCACTTTTATGATGCTTCCAAAGTGTGCTGCTCTTCCCACTGACA 1868
Qy 1512 AATGCCAAAGTTGAGAAAATGATCAATATTTAGCATTAACAGAGCACTGCGCACTC 1571
Db 1869 AATGCCAAAGTTGAGAAAATGATCAATATTTAGCATTAACAGAGCACTGCGCACTC 1928
Qy 1572 GATTTTATTAATTAACCTGACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCA 1631
Db 1929 GATTTTATTAATTAACCTGACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCA 1988
Qy 1632 GATGATGTTTCATCCGTGAATGTGTCCAGGAGAGCACTTCACTTGAATATGACATTA 1691
Db 1989 GATGATGTTTCATCCGTGAATGTGTCCAGGAGAGCACTTCACTTGAATATGACATTA 2048
Qy 1692 TGTCATCAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGTAAAGCTCACT 1751

Db 2049 TGTCATCAAGCTCTGAGGCTTCTCTTTCATCTCTGCTGAGACAGTAAAGCACTCACT 2108
Qy 1752 TTTCAATAGCATCTAGAGCACTGAGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGG 1811
Db 2109 TTTCAATAGCATCTAGAGCACTGAGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGG 2168
Qy 1812 GGAATGTGGAAGCAATTTTGTGTTACTCTCAATGAGGAGTGAAGAGATACAGTGTCTA 1871
Db 2169 GGAATGTGGAAGCAATTTTGTGTTACTCTCAATGAGGAGTGAAGAGATACAGTGTCTA 2228
Qy 1872 CTACCAACTAGTGAATTAAGGCGCAGGAGTGTGTCTCAACCTCCACATGATACAGGAGCT 1931
Db 2229 CTACCAACTAGTGAATTAAGGCGCAGGAGTGTGTCTCAACCTCCACATGATACAGGAGCT 2288
Qy 1932 CTCCCATTTACACTACCCCATCCGAAGTGTCAACTGTGTCTGAGGACTTAAGAAACCTGTGT 1991
Db 2289 CTCCCATTTACACTACCCCATCCGAAGTGTCAACTGTGTCTGAGGACTTAAGAAACCTGTGT 2348
Qy 1992 TTTGATGAAAAGGGCTGTGAAAAGAGGGAGCCCAAAATCTGTCTGCTTCTCACATTT 2050
Db 2349 TTTGATGAAAAGGGCTGTGAAAAGAGGGAGCCCAAAATCTGTCTGCTTCTCACATTT 2408
Qy 2051 AGTCAATGGGCAATTAAGATCTGTCTTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2110
Db 2409 AGTCAATGGGCAATTAAGATCTGTCTTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2468
Qy 2111 CTCTATCGGGGCAAGATTAACATCTCTCAGTGAACAGATGTGAACAAGGCTTATGGGAAA 2170
Db 2469 CTCTATCGGGGCAAGATTAACATCTCTCAGTGAACAGATGTGAACAAGGCTTATGGGAAA 2528
Qy 2171 TGCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCCCTTCAATTTACC 2230
Db 2529 TGCTGATGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCCCTTCAATTTACC 2588
Qy 2231 CTGCAAGGCAAGTCTGTGAAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2290
Db 2589 CTGCAAGGCAAGTCTGTGAAGAAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2648
Qy 2291 ATTTAGATCTCAGACCTTCTCTGAGCAATTTAGGCAACAATTAAGGCAACAATTAACCTT 2350
Db 2649 ATTTAGATCTCAGACCTTCTCTGAGCAATTTAGGCAACAATTAAGGCAACAATTAACCTT 2708
Qy 2351 CCATGAGCAACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTGG 2410
Db 2709 CCATGAGCAACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTGG 2768
Qy 2411 AGGAATGAAGCTTTGAAGAAAGAAATTAATTTTCCAGCCCTTCCCACTCTTCA 2470
Db 2769 AGGAATGAAGCTTTGAAGAAAGAAATTAATTTTCCAGCCCTTCCCACTCTTCA 2828
Qy 2471 TGTGTTAACCACTGCTTCTGCACTTGGAGCCAGGCTGACTGATTAATCAATGTTGTTAT 2530
Db 2829 TGTGTTAACCACTGCTTCTGCACTTGGAGCCAGGCTGACTGATTAATCAATGTTGTTAT 2888
Qy 2531 AGAAAAGTGAATTTTGAAGTCTGATCTTCAAGAGATGATTAATTAATTAATTTCTT 2587
Db 2889 AGAAAAGTGAATTTTGAAGTCTGATCTTCAAGAGATGATTAATTAATTAATTTCTT 2945

RESULT 12
US-09-896-738-1
; Sequence 1, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; PRIOR FILING DATE: 2000-06-30


```
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (53)..(901)
US-09-896-738-1

Query Match      99.1%; Score 2563; DB 9; Length 2603;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2574; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      12  GGCAGCTCCACTGACCCAGATACCGATAGCGTGGAACTTCCCGCCAGCTGCTTCC
DB      3   GGCAGCTCCACTGACCCAGATACCGATAGCGTGGAACTTCCCGCCAGCTGCTTCC
QY      72  TGGGGCAGATCCTCTCTGAGGCAATATTAGCATCATATTCTGGCTGGAGCAATTG
DB      63  TGGGGCAGATCCTCTCTGAGGCAATATTAGCATCATATTCTGGCTGGAGCAATTG
QY      132  CACTCATATTGCTTTGTAATTTCAAGAGACACTCCATCAAGTCACTACTGCTGCT
DB      123  CACTCATATTGCTTTGTAATTTCAAGAGACACTCCATCAAGTCACTACTGCTGCT
QY      192  CAGCTGGAACTTTGGGAGAGATGAAATCTGAGCTGCACTTTTGAACCTGACATCAAC
DB      183  CAGCTGGAACTTTGGGAGAGATGAAATCTGAGCTGCACTTTTGAACCTGACATCAAC
QY      252  TTTCTGATCGTATCAATAGCTGTAAGAGAGTGTTTTAGAGTTGCTCATGAGTTCA
DB      243  TTTCTGATCGTATCAATAGCTGTAAGAGAGTGTTTTAGAGTTGCTCATGAGTTCA
QY      312  AAGAGCAAAAGATGAGCTGTCCGAGCAGATGAATGTTCAAGAGCCGAGCAGAGTGT
DB      303  AAGAGCAAAAGATGAGCTGTCCGAGCAGATGAATGTTCAAGAGCCGAGCAGAGTGT
QY      372  TTGCTGATCAAGTATGTTGGCAATGCTTTTGGCGCTGAAAACCTGCAACTCAG
DB      363  TTGCTGATCAAGTATGTTGGCAATGCTTTTGGCGCTGAAAACCTGCAACTCAG
QY      432  ATGCTGCACCTCAAAATGTTATTCATCACTTCTTAAGGCAAGGGAAATGCTAACTTG
DB      423  ATGCTGCACCTCAAAATGTTATTCATCACTTCTTAAGGCAAGGGAAATGCTAACTTG
QY      492  AGTATAAACTGAGCTTCAGCATGCGGAAAGTGAATGAGACTATATATGCCAGTCA
DB      483  AGTATAAACTGAGCTTCAGCATGCGGAAAGTGAATGAGACTATATATGCCAGTCA
QY      552  AGACCTTGGCGGTGAGAGCTTCCCGATGTTCCCGCCAGCCCAAGTGGTCTGGAGTCC
DB      543  AGACCTTGGCGGTGAGAGCTTCCCGATGTTCCCGCCAGCCCAAGTGGTCTGGAGTCC
QY      612  AAGTTGACGAGGAGCCAACTTCTCGGAAGTCCCAATACCAAGTTTGAAGTCAACTTG
DB      603  AAGTTGACGAGGAGCCAACTTCTCGGAAGTCCCAATACCAAGTTTGAAGTCAACTTG
QY      672  AGAATGACCATGAAGGTTGTGCTGTGCTTACATGTTACATGAACAACATACT
DB      663  AGAATGACCATGAAGGTTGTGCTGTGCTTACATGTTACATGAACAACATACT
QY      732  CCTGTATGATTAATAATGACATTTGCCAAGCAACAGGGGATATCAAGATCGG
DB      723  CCTGTATGATTAATAATGACATTTGCCAAGCAACAGGGGATATCAAGATCGG
QY      792  AGATCAAAAGGCGAGTCACTCAAGTGTCTAACTCAAGGCTTCTGTGTGCTCTT
DB      783  AGATCAAAAGGCGAGTCACTCAAGTGTCTAACTCAAGGCTTCTGTGTGCTCTT
QY      852  CTTTCTTTGCTCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATCTAAATAT
DB      911  CTTTCTTTGCTCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATCTAAATAT
```

```
DB      843  CTTTCTTTGCTCATGAGCTGGGCACTTCTGCTCTCAGCCCTTACCTGATCTAAATAT
QY      912  GTGCTTTGGCCAAACCAAGATGCAAGTCAATTTGTTACCAAGGATCTACGAATAT
DB      903  GTGCTTTGGCCAAACCAAGATGCAAGTCAATTTGTTACCAAGGATCTACGAATAT
QY      972  TTCAACCAAGATGAGTCAAGTATTTTCTGGAGGAAATGATTCATTCAGAA
DB      963  TTCAACCAAGATGAGTCAAGTATTTTCTGGAGGAAATGATTCATTCAGAA
QY      1032  GTCTGAGTGAAGCAACAGAGCAAGAAACAAAGAGCCAAAGCAGAGCTCCAT
DB      1023  GTCTGAGTGAAGCAACAGAGCAAGAAACAAAGAGCCAAAGCAGAGCTCCAT
QY      1092  ATGAACAAGTAAATCTATCTTCAAGACATATTAGAAGTTGGGAAATTAATCATGTA
DB      1083  ATGAACAAGTAAATCTATCTTCAAGACATATTAGAAGTTGGGAAATTAATCATGTA
QY      1152  ACTAGAACAAGTGTATTAAGTGTAAATGCAACGAGAGCAAGTCCAG
DB      1143  ACTAGAACAAGTGTATTAAGTGTAAATGCAACGAGAGCAAGTCCAG
QY      1212  ATCTCAGGAGCTTCCCTGCTGCTGCACTGGGAGTGAAGAGCAGATAGTCAATGTT
DB      1203  ATCTCAGGAGCTTCCCTGCTGCTGCACTGGGAGTGAAGAGCAGATAGTCAATGTT
QY      1272  CTTTGTCTGAAATTTTATGATTAATGCTGTAAATGTTGCTTGAAGAACCCCTGAA
DB      1263  CTTTGTCTGAAATTTTATGATTAATGCTGTAAATGTTGCTTGAAGAACCCCTGAA
QY      1332  AGTCTATCCCAATATCCACATCTATATTCACAAATTAAGCTGATGATGACCTTA
DB      1323  AGTCTATCCCAATATTCACATCTTATTTCCAAATTAAGCTGATGATGATGACCTTA
QY      1392  AGACGCTGTAAATGATGCTGCACTGCACTGAGGCGGCTGCAATTTAGTATGCT
DB      1383  AGACGCTGTAAATGATGCTGCACTGCACTGAGGCGGCTGCAATTTAGTATGCT
QY      1452  CAAATGATTCATTTTATGATGCTTCCAAAGTGTGCTTCTTCCCACTGACA
DB      1443  CAAATGATTCATTTTATGATGCTTCCAAAGTGTGCTTCTTCCCACTGACA
QY      1512  AATGCCAAAGTTGAGAAATATGATCATATTTTAAAGATTAACAGACAGTGGCGACCC
DB      1503  AATGCCAAAGTTGAGAAATATGATCATATTTTAAAGATTAACAGACAGTGGCGACCC
QY      1572  GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA
DB      1563  GATTTTATTAATTAACCTGAGCACTTCTTTTAAACAAACAAATGCGGGTTATTTCTCA
QY      1632  GATGATGTTCAATCGTGAATGCTCCAGGAGAGGACCTTTCACTTGAATATGCAATTA
DB      1623  GATGATGTTCAATCGTGAATGCTCCAGGAGAGGACCTTTCACTTGAATATGCAATTA
QY      1692  TGTGATCAACAAGCTGAGAGCTTCTCTTTCATCTGCTGAGAGCAAGCTTAAGCTCAGT
DB      1683  TGTGATCAACAAGCTGAGAGCTTCTCTTTCATCTGCTGAGAGCAAGCTTCAAGCTCAGT
QY      1752  TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGATATTTCCGCCCATCTCCGAG
DB      1743  TTTCAATAGCATCTAGAGAGTGGAGCTCAGCTGGGATATTTCCGCCCATCTCCGAG
QY      1812  GGAATGCTGAAGACAAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTGTCTA
DB      1803  GGAATGCTGAAGACAAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTGTCTA
QY      1872  CTACCAACTAGTGAATTAAGGCGCAGGGAGTCTCAACCTCTCAATCATGTACAGGACGT
DB      1863  CTACCAACTAGTGAATTAAGGCGCAGGGAGTCTCAACCTCTCAATCATGTACAGGACGT
QY      1932  CTCGCCATTACAACCTAACCTGCAAGTGTCAACTGTGTCAAGGACTAAGAAACCTGTGT
DB      1923  CTCGCCATTACAACCTAACCTGCAAGTGTCAACTGTGTCAAGGACTAAGAAACCTGTGT
```



```

RESULT 13
US-09-850-178-23
Sequence 23, Application US/09850178
Patent No. US2002003479A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colipits, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Russell, John C.
APPLICANT: Gramados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Stroupe, Stephen D.
APPLICANT: Gordon, Julian
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
FILE REFERENCE: 6251 US pt
CURRENT APPLICATION NUMBER: US/09/850,178
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Fastseq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 2591
TYPE: DNA
ORGANISM: Homo sapiens

```

QY	12	GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCCAGCCATGGCTTCC	71
Db	11	GGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCCAGCCATGGCTTCC	70
QY	72	TGGGGCAGATCCTCTTCTGAGCATATTAGCATCATATTATTTGCGCTGGAGCAATTG	131
Db	71	TGGGGCAGATCCTCTTCTGAGCATATTAGCATCATATTATTTGCGCTGGAGCAATTG	130
QY	132	CAGTCATATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGAGTCACTACTGTGCGCT	191
Db	131	CAGTCATATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGAGTCACTACTGTGCGCT	190
QY	192	CAGCTGGGAACATTGGGGAGATGGAAATCTGAGCTGCACCTTTTGAACCTGCATCAAAAC	251
Db	191	CAGCTGGGAACATTGGGGAGATGGAAATCTGAGCTGCACCTTTTGAACCTGCATCAAAAC	250
QY	252	TTTCTGATATTCGTATATCAATAGCGTGAAGAAAGTTTATAGGCGTTGGTCCATGATCTCA	311
Db	251	TTTCTGATATTCGTATATCAATAGCGTGAAGAAAGTTTATAGGCGTTGGTCCATGATCTCA	310
QY	312	AAGAAGCAAAAGATAGCTGTTCGAGCAGATGAAATGTTTCAGAGGCCGGAACAGCAGTGT	371
Db	311	AAGAAGCAAAAGATAGCTGTTCGAGCAGATGAAATGTTTCAGAGGCCGGAACAGCAGTGT	370
QY	372	TTTGCTGATCAAGTATAGTTAGTTGGCAATGCGCTCTTTTGGCGCTGAAAAAGTGCACATCCACAG	431
Db	371	TTTGCTGATCAAGTATAGTTAGTTGGCAATGCGCTCTTTTGGCGCTGAAAAAGTGCACATCCACAG	430
QY	432	ATGCTGGCACCCTCAAAATGTTATATCATCATCTTCTTAAAGGCAAGGGAGATGTAACCTTG	491
Db	431	ATGCTGGCACCCTCAAAATGTTATATCATCATCTTCTTAAAGGCAAGGGAGATGTAACCTTG	490
QY	492	AGTATAAACTGAGACCTTTCAGCATGCCGGAATGGAATGTGGACTATATATGCACTCAG	551
Db	491	AGTATAAACTGAGACCTTTCAGCATGCCGGAATGGAATGTGGACTATATATGCACTCAG	550
QY	552	AGACCTTGGGATGAGAGGCTCCCGATGTTCCCCAGCCCAAGTGGCTGCGGCATCCC	611
Db	551	AGACCTTGGGATGAGAGGCTCCCGATGTTCCCCAGCCCAAGTGGCTGCGGCATCCC	610
QY	612	AAAGTTGACAGGAGACCAACTTCTTGGAAAGTCTCCAAATACAGACTTTGAGCTGAACTCTG	671
Db	611	AAAGTTGACAGGAGACCAACTTCTTGGAAAGTCTCCAAATACAGACTTTGAGCTGAACTCTG	670
QY	672	AGAAATGACCATGAAAGTTGTGTGTGCTGTCAATATGTTACGATTCAAACAAACATATCT	731
Db	671	AGAAATGACCATGAAAGTTGTGTGTGCTGTCAATATGTTACGATTCAAACAAACATATCT	730
QY	732	CCTGATGATTGAAATATGACATTGGCCAAAGCAACAGGGATATCAAAATGACAGAAATCGG	791
Db	731	CCTGATGATTGAAATATGACATTGGCCAAAGCAACAGGGATATCAAAATGACAGAAATCGG	790
QY	792	AGATCAAAAAGGGGAGTCACTTACAGCTGTCTAACTCAAAGGCTTCTCTGTGTGTCTCTT	851
Db	791	AGATCAAAAAGGGGAGTCACTTACAGCTGTCTAACTCAAAGGCTTCTCTGTGTGTCTCTT	850
QY	852	CTTTCCTTGGCATAGCTGGGGCACTTTCGCGCTCTCAGGCCCTTACCTGATGCTTAAATATAT	911
Db	851	CTTTCCTTGGCATAGCTGGGGCACTTTCGCGCTCTCAGGCCCTTACCTGATGCTTAAATATAT	910
QY	912	GTGCTTGGCCACAACAAAAAGCATGCAAAAGTCAATTTGTTACAACAGGAGTCTACAGAACTAT	971
Db	911	GTGCTTGGCCACAACAAAAAGCATGCAAAAGTCAATTTGTTACAACAGGAGTCTACAGAACTAT	970
QY	972	TTTCAACACCAATATGACTAGTTTATATTTCTGGGAGGAATGAAATTCATATCTTAAGA	1033
Db	971	TTTCAACACCAATATGACTAGTTTATATTTCTGGGAGGAATGAAATTCATATCTTAAGA	1033

Db 71 TGGGGAGATCCTCTTCTGGAGCATTAATGACATCATTAATTCTGCTGGAGCAATTG 130
Qy 132 CACTCATCTTGGCTTTGGTATTTTCAGGGAGACATCCCATCAAGCATCTACTGCGCT 191
Db 131 CACTCATCTTGGCTTTGGTATTTTCAGGGAGACATCCCATCAAGCATCTACTGCGCT 190
Qy 192 CAGCTGGGAACATTTGGGGAGAGATGGAATCTGAGCTGCATCTTTTGAACCTGACATCAAC 251
Db 191 CAGCTGGGAACATTTGGGGAGAGATGGAATCTGAGCTGCATCTTTTGAACCTGACATCAAC 250
Qy 252 TTTTCGATATCGTGATACATGCGCTGAGAGAAAGTGTTTTAAAGCTTGGTTCATGAGTTCA 311
Db 251 TTTTCGATATCGTGATACATGCGCTGAGAGAAAGTGTGTTTTAAAGCTTGGTTCATGAGTTCA 310
Qy 312 AAGAAAGGCAAAATGAGCTGCGGAGCAGAGATGAATGTTCAGAGGCGGAGCAGAGTGT 371
Db 311 AAGAAAGGCAAAATGAGCTGCGGAGCAGAGATGAATGTTCAGAGGCGGAGCAGAGTGT 370
Qy 372 TTTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAATAAAGCTGCAACTCAG 431
Db 371 TTTGCTGATCAAGTATGATTTGGCAATGCTCTTTTGGCGCTGAATAAAGCTGCAACTCAG 430
Qy 432 ATGCTGGCACTTCAAAATGTTATATCATCTTAAAGGCAAGGGAAATGCTAACCTTG 491
Db 431 ATGCTGGCACTTCAAAATGTTATATCATCTTAAAGGCAAGGGAAATGCTAACCTTG 490
Qy 492 AGATATAAAGTGGAGCTCAGCATGCGGAAGTGAATGGAGCTATATGCAAGCTGAG 551
Db 491 AGATATAAAGTGGAGCTCAGCATGCGGAAGTGAATGGAGCTATATGCAAGCTGAG 550
Qy 552 AGACCTTGGCGTGTGAGGCTCCCGAGTGGTCCCGGAGCCCAAGTGTCTGGGCAATGCC 611
Db 551 AGACCTTGGCGTGTGAGGCTCCCGAGTGGTCCCGGAGCCCAAGTGTCTGGGCAATGCC 610
Qy 612 AAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATACAGCTTTGAGCTGAAGCTG 671
Db 611 AAGTTGACCAAGGAGCCAACTTCTGGAAAGTCTCCAAATACAGCTTTGAGCTGAAGCTG 670
Qy 672 AAGAAATGACCATGAAGGTTGTGTCTGTCTCAAAATGTTAAGATCAACAACATCT 731
Db 671 AAGAAATGACCATGAAGGTTGTGTCTGTCTCAAAATGTTAAGATCAACAACATCT 730
Qy 732 CCTGTATGATTTGAAATGACATTTGCCAAAGCAACAGGGAGTATCAAAAGTACAGAAATCG 791
Db 731 CCTGTATGATTTGAAATGACATTTGCCAAAGCAACAGGGAGTATCAAAAGTACAGAAATCG 790
Qy 792 AGATCAAAAGGCGGAGTCACTTACAGCTGTAAATCAAAAGCTTCTGTGTGTCTCT 851
Db 791 AGATCAAAAGGCGGAGTCACTTACAGCTGTAAATCAAAAGCTTCTGTGTGTCTCT 850
Qy 852 CTTTCTTTGCAATCAGCTGGGCACTCTGTCTCTGAGCCCTTACCTGATGCTAAATAT 911
Db 851 CTTTCTTTGCAATCAGCTGGGCACTCTGTCTCTGAGCCCTTACCTGATGCTAAATAT 910
Qy 912 GTGCCCTTGGCCAC-AAAAAGCATGCAAGTCAATTGTTCAACAGGAGTCTACAGAACTA 970
Db 911 GTGCCCTTGGCCACAAAAAAGCATGCAAGTCAATTGTTCAACAGGAGTCTACAGAACTA 970
Qy 971 TTTTCAACCAAGATATGACCTATGTTTAAATTTCTGGGAGAAATCAATTCATATCAAA 1030
Db 971 TTTTCAACCAAGATATGACCTATGTTTAAATTTCTGGGAGAAATCAATTCATATCAAA 1030
Qy 1031 AGTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAAGCAGAAAGGCTCCAA 1090
Db 1031 AGTCTGAGTGAAGCAAAAGAGCAAGAAACAAAAGAGCCAAAAGCAGAAAGGCTCCAA 1090
Qy 1091 TATGAAACAAGATTAATCTATCTTCAAAAGCATATTTGAAGTTGGGAAAATTAATTCATG 1150
Db 1091 TATGAAACAAGATTAATCTATCTTCAAAAGCATATTTGAAGTTGGGAAAATTAATTCATG 1150
Qy 1151 AACTAGACAAGTGTGTTAAAGTATGATTAAGTAAATCAAGTGAAGCAAGTGTATCCCA 1210
Db 1151 AACTAGACAAGTGTGTTAAAGTATGATTAAGTAAATCAAGTGAAGCAAGTGTATCCCA 1210
Qy 1210 AACTAGACAAGTGTGTTAAAGTATGATTAAGTAAATCAAGTGAAGCAAGTGTATCCCA 1209
Db 1210 AACTAGACAAGTGTGTTAAAGTATGATTAAGTAAATCAAGTGAAGCAAGTGTATCCCA 1209

Qy 1211 GATCTCAGGAGACCTCCCTGCTGTCACTTGGGAGTGAAGAGACAGAAATGTCATGT 1270
Db 1210 GATCTCAGGAGACCTCCCTGCTGTCACTTGGGAGTGAAGAGACAGAAATGTCATGT 1269
Qy 1271 TCTTTGTCTGAAATTTTATGATATGCTGTATATGTTGCTGTGAGAAAGCCCTGGA 1330
Db 1270 TCTTTGTCTGAAATTTTATGATATGCTGTATATGCTGTGAGAAAGCCCTGGA 1329
Qy 1331 AAGCTATCCCAACATATCCATCTATATTTCCCAAAATTAAGCTATGATATGACCT 1390
Db 1330 AAGCTATCCCAACATATCCATCTATATTTCCCAAAATTAAGCTATGATATGACCT 1389
Qy 1391 AAGAGCTCTAATTTAGCTGCCACTTCCCACTCAGGGGCGGCTGCAATTTTAAATGAG 1450
Db 1390 AAGAGCTCTAATTTAGCTGCCACTTCCCACTCAGGGGCGGCTGCAATTTTAAATGAG 1449
Qy 1451 TCAAAATGATCACTTTTATGATGCTTCCAAAGTGTGCTTGTCTTCCCACTGAC 1510
Db 1450 TCAAAATGATCACTTTTATGATGCTTCCAAAGTGTGCTTGTCTTCCCACTGAC 1509
Qy 1511 AAATGCCAAAGTGAAGAAAAATGATCATTAATTTTGAACAAACAGAGAGTGGGCAAC 1570
Db 1510 AAATGCCAAAGTGAAGAAAAATGATCATTAATTTTGAACAAACAGAGAGTGGGCAAC 1569
Qy 1571 CGATTTTAAATTAATTAAGTGAACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTC 1630
Db 1570 CGATTTTAAATTAATTAAGTGAACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTC 1629
Qy 1631 AGATGATGTTCACTCCGTGATATGCTCAGGAAAGACCTTTTCACTTGAATATGAGCAAT 1690
Db 1630 AGATGATGTTCACTCCGTGATATGCTCAGGAAAGACCTTTTCACTTGAATATGAGCAAT 1689
Qy 1691 ATGTATACCAAGCTCTGAGGCTTCCCTTCCATCTGCGGAGCAGCTAAGACCTGAG 1750
Db 1690 ATGTATACCAAGCTCTGAGGCTTCCCTTCCATCTGCGGAGCAGCTAAGACCTGAG 1749
Qy 1751 TTTTCAATAGCATCTAGAGCAAGTGGAGTCAAGCTGGGAGTGAATTTGGCCCCCATCTCGG 1810
Db 1750 TTTTCAATAGCATCTAGAGCAAGTGGAGTCAAGCTGGGAGTGAATTTGGCCCCCATCTCGG 1809
Qy 1811 GGGAAATGCTGAAGCAATTTTGTACTCTCAATAGAGGAGTGAAGATACAGTGT 1870
Db 1810 GGGAAATGCTGAAGCAATTTTGTACTCTCAATAGAGGAGTGAAGATACAGTGT 1869
Qy 1871 ACTACCAATAGTGAATTAAGGCGAGGAGTGTCTCAACCTCTAACCATGTAACGAGAG 1930
Db 1870 ACTACCAATAGTGAATTAAGGCGAGGAGTGTCTCAACCTCTAACCATGTAACGAGAG 1929
Qy 1931 TCTCCCAATTAACATCAACCAATCCGAAGTGTCAACTGTGTGAGGACTAAGAAACCTTGG 1990
Db 1930 TCTCCCAATTAACATCAACCAATCCGAAGTGTCAACTGTGTGAGGACTAAGAAACCTTGG 1989
Qy 1991 TTTTGAATGAAAGAGGCTGGAAGAGGGAGCCCAAAATCTGTCTGCTT-CTCACAT 2049
Db 1990 TTTTGAATGAAAGAGGCTGGAAGAGGGAGCCCAAAATCTGTCTGCTTCTCTCACAT 2049
Qy 2050 TAGCATTTGGCAAAATAGCATTTCTCTTTTGGCTGTGCTCTGAGCAGAGAGCCAGA 2109
Db 2050 TAGCATTTGGCAAAATAGCATTTCTCTTTTGGCTGTGCTCTGAGCAGAGAGCCAGA 2109
Qy 2110 ACTCTATCGGAGCAGAGATTAACATCTCTCACTGAACAGAGTTGAACAAGGCTATGGGA 2169
Db 2110 ACTCTATCGGAGCAGAGATTAACATCTCTCACTGAACAGAGTTGAACAAGGCTATGGGA 2169
Qy 2170 ATGCTGATGGGATTAATCTTCACTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCAC 2229
Db 2170 ATGCTGATGGGATTAATCTTCACTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCAC 2229
Qy 2230 CCGTGAAGCAAGTCTGTGAAGAAAGCCGAGTGTAGCTCAGGTTTCTTACTCTG 2289
Db 2230 CCGTGAAGCAAGTCTGTGAAGAAAGCCGAGTGTAGCTCAGGTTTCTTACTCTG 2289

QY 2290 AATTAGATCTCCAGACCCCTCTGCGCACAATTCAATTAAAGGCAACAATATATCT 2349
|
|
Db 2290 AATTAGATCTCCAGACCCCTCTGCGCACAATTCAATTAAAGGCAACAATATATCT 2349
QY 2350 TCCATGAAAGCAGACAGACTTTTGAAGCAAGACAATGACTCTTGAATTGAGGCTT 2409
|
|
Db 2350 TCCATGAAAGCAGACAGACTTTTGAAGCAAGACAATGACTCTTGAATTGAGGCTT 2409
QY 2410 GAGGAATGAAGCTTTGAAGGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTC 2469
|
|
Db 2410 GAGGAATGAAGCTTTGAAGGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTC 2469
QY 2470 ATGTGTTAACCACTGCTTCTGAGACCTTGAGCCACGCTGACTGTAATTACATGTTGTA 2529
|
|
Db 2470 ATGTGTTAACCACTGCTTCTGAGACCTTGAGCCACGCTGACTGTAATTACATGTTGTA 2529
QY 2530 TAGAAAATGATTTTGAAGTTCTGATCTGTTCAAGAGAATGATTAATATACATTTCTT 2587
|
|
Db 2530 TAGAAAATGATTTTGAAGTTCTGATCTGTTCAAGAGAATGATTAATATACATTTCTT 2587

RESULT 15

US-10-023-339-9
; Sequence 9, Application US/10023339
; Publication No. US20030208058A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: B7-Like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P1124P1
; CURRENT APPLICATION NUMBER: US/10/023,339
; PCT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/20917
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-339-9

Query Match 93.6%; Score 2421.8; DB 17; Length 2626;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2535; Conservative 0; Mismatches 7; Indels 11; Gaps 11;

QY 45 GGGAACTTCCCGCAGCATGGCTTCCCTGGGGGAGATCCTCTTGGAGCATTA-TTACG 103
|
|
Db 57 GGAACCTTCCCGCAGCATGGCTTCCCTGGGGGAGATCCTCTTGGAGCATTAATTAGC 116
QY 104 ATCATCATTTATTCGTGCTGAGCAATTGCACTCATCATTTGGTATTTTCAGGAGA 163
|
|
Db 117 ATCATCATTTATTCGTGCTGAGCAATTGCACTCATCATTTGGTATTTTCAGGAGA 176
QY 164 CACTTCATCAAGTCACTACTGCTGCTCAGCTGGGAACTTGGGAGAGATGATCTTG 223
|
|
Db 177 CACTTCATCAAGTCACTACTGCTGCTCAGCTGGGAACTTGGGAGAGATGATCTTG 236
QY 224 AGCTGCATTTTGAACCTGACATCAAACTTTCTGATATTCGTAATCAATGGCTGAAGAA 283
|
|
Db 237 AGCTGCATTTTGAACCTGACATCAAACTTTCTGATATTCGTAATCAATGGCTGAAGAA 296
QY 284 GGTGTTTAAAGCTTGTCTCAAGTTCAGAAAGG-CAAGATGAGCTGTGAGAGAGA 342
|
|
Db 297 GGTGTTTAAAGCTTGTCTCAAGTTCAGAAAGG-CAAGATGAGCTGTGAGAGAGA 356
QY 343 TGAATGTTCAAGAGCC-GGACAGCAGTGTGTTGCTGATCAAGTATGTTGGCAATGCTT 401
|
|
Db 357 TGAATGTTCAAGAGCCGGGAGCAGCAGTGTGTTGCTGATCAAGTATGTTGGCAATGCTT 416

QY 402 C-TTGGCGGTGAAAAAGTGCACACTCAGATGCTGGACCTTACAAATGTTATATATC 460
|
|
Db 417 CTTTGGCGGTGAAAAAGTGCACACTCAGATGCTGGACCTTACAAATGTTATATATC 476
QY 461 ACTTCAAAAGCAAGGGAAATGCTAACTTTGATATTAATCTGAGCTTTCAGATGCG 520
|
|
Db 477 ACTTCAAAAGCAAGGGAAATGCTAACTTTGATATTAATCTGAGCTTTCAGATGCG 536
QY 521 GAAATGAAATGGAATTAATGCGAGTCAAGACCTTGGGAGTGAAGCTTCCCGCATG 580
|
|
Db 537 GAAATGAAATGGAATTAATGCGAGTCAAGACCTTGGGAGTGAAGCTTCCCGCATG 596
QY 581 TTCCCGCAGCCACAGTGTCTGGGACATCCCAAGTTGACCAAGGAGCAACTTCTCGAA 640
|
|
Db 597 TTCCCGCAGCCACAGTGTCTGGGACATCCCAAGTTGACCAAGGAGCAACTTCTCGAA 656
QY 641 GTCTCAATACAGCTTTGAGCTGAATCTGAGAAATGACATGAAGGTTGTCTGTG 700
|
|
Db 657 GTCTCAATACAGCTTTGAGCTGAATCTGAGAAATGACATGAAGGTTGTGTCTGTG 716
QY 701 CTCTCAATGTTACGATCAACACATATCTCTGTAATGATTGAAAATGACATTGCCAA 760
|
|
Db 717 CTCTCAATGTTACGATCAACACATATCTCTGTAATGATTGAAAATGACATTGCCAA 776
QY 761 GCAACAGGGGATATCAAGTGAAGAAATGGAGATCAAAAGGCGAGTCACTACAGCTG 820
|
|
Db 777 GCAACAGGGGATATCAAGTGAAGAAATGGAGATCAAAAGGCGAGTCACTACAGCTG 836
QY 821 CTAAACTCAAGGCTTCTGTGTGTCTCTTCTTCTTTCATCAGCTGGGACCTTCTG 880
|
|
Db 837 CTAAACTCAAGGCTTCTGTGTGTCTCTTCTTCTTTCATCAGCTGGGACCTTCTG 896
QY 881 CCTCTCAGCCCTTACCTGATGCTAAATTAATGTGCTTGGCCACAAAAAGCATGCAAG 940
|
|
Db 897 CCTCTCAGCCCTTACCTGATGCTAAATTAATGTGCTTGGCCACAAAAAGCATGCAAG 956
QY 941 TCATTTGTTAACAGGGATATACAGAACTATTCACACAGATATGACCTAGTTTATA 1000
|
|
Db 957 TCATTTGTTAACAGGGATATACAGAACTATTCACACAGATATGACCTAGTTTATA 1016
QY 1001 TTTCTGGAGAAATGATTCATATCTGAAAGTCTGGAGTGAACAAAGCAAGCAAGAA 1060
|
|
Db 1017 TTTCTGGAGAAATGATTCATATCTGAAAGTCTGGAGTGAACAAAGCAAGCAAGAA 1076
QY 1061 CAAAAAGAGCCAAAGCAGAAAGCTTCAATATGAACAGATTAATCTATCTTCAAGAC 1120
|
|
Db 1077 CAAAAAGAGCCAAAGCAGAAAGCTTCAATATGAACAGATTAATCTATCTTCAAGAC 1136
QY 1121 ATATTGAAGTTGGGAAATTAATTCATGTGAACATGACAGATGTTTAAAGTATAGT 1180
|
|
Db 1137 ATATTGAAGTTGGGAAATTAATTCATGTGAACATGACAGATGTTTAAAGTATAGT 1196
QY 1181 AAAATGACCTGAGAGCAAGTGCATCCCGATCTCAGGAGCTCCCTGCTGTACCC 1240
|
|
Db 1197 AAAATGACCTGAGAGCAAGTGCATCCCGATCTCAGGAGCTCCCTGCTGTACCC 1256
QY 1241 TGGGAGTGAAGAGCAGATATGTCATGTTCTTTGTCTGTGAATTTTATATATGTG 1300
|
|
Db 1257 TGGGAG-TGAGAGAGCAGATATGTCATGTTCTTTGTCTGTGAATTTTATATATGTG 1315
QY 1301 CTGTAATGTTGCTGTGAGGAAGCCCTGGAAGATCTATCCCAATATCCACATCTTATA 1360
|
|
Db 1316 CTGTAATGTTGCTGTGAGGAAGCCCTGGAAGATCTATCCCAATATCCACATCTTATA 1375
QY 1361 TTCCCAAAATTAAGCTGATATGATACCTTAAGACCTGCTAATTAAGCTGCCA 1420
|
|
Db 1376 TTCCCAAAATTAAGCTGATATGATACCTTAAGACCTGCTAATTAAGCTGCCA 1435
QY 1421 ACTCAGGGGCGGCTGCACTTTTATGTAATGGTCAATATGATCACTTTTATGATGCTTCCA 1480
|
|
Db 1436 ACTCAGGGGCGGCTGCACTTTTATGTAATGGTCAATATGATCACTTTTATGATGCTTCCA 1495
QY 1481 AAGGTGCTTGGGCTTCTTCCCACTGACAAATGCC-AAAGTTGAGAAAAATGATCATTA 1539

Db 1496 AAGTGCCTGGCTTCTCTCCCACTGACAAATGCGCAAAAGTGGAGAAAAATGATCANA 1555
QY 1540 ATTTTAGCATTAACAGAGC-AGTCCGCGCACCCGATTTTATTAATACTGAGCACCTTC 1598
Db 1556 ATTTTAGCATTAACAGAGCAGAGTGGCGACACGATTTTATTAATACTGAGCACCTTC 1615
QY 1599 TTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTTCAAT-CCGTGAATGGTCCA 1657
Db 1616 TTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTTCAATCCGTGAATGGTCCA 1675
QY 1658 GGGAGGACCTTTACCTTGACTATATGCGATTATGTCATCAACGCTCTGAGGCTTCTC 1717
Db 1676 GGGAGGACCTTTACCTTGACTATATGCGATTATGTCATCAACGCTCTGAGGCTTCTC 1735
QY 1718 CTTTCATCTCGGTGAGAGACTAAGACCTCAGTTTCAATAGCACTTAGAGCATGGGA 1777
Db 1736 CTTTCATCTCGGTGAGAGACTAAGACCTCAGTTTCAATAGCATCTAGAGCATGGGA 1795
QY 1778 CTCAGCTGGGGTGAATTTCCGCCCATCTCCGGGGGAATGTGAAGACAATTTTGGTTA 1837
Db 1796 CTCAGCTGGGGTGAATTTCCGCCCATCTCCGGGGGAATGTGAAGACAATTTTGGTTA 1855
QY 1838 CCTCAATGAGGAGTGGAGAGGATACAGTGTCTACTACCACTAGTGATTAAGGCCAGG 1897
Db 1856 CCTCAATGAGGAGTGGAGAGGATACAGTGTCTACTACCACTAGTGATTAAGGCCAGG 1915
QY 1898 GATGCTGCTCAA-CCTCCTACATGTACAGAGAGTCTCCCATTTACAATCAATCCG 1956
Db 1916 GATGCTGCTCAA-CCTCCTACATGTACAGAGAGTCTCCCATTTACAATCAATCCG 1975
QY 1957 AAGTGTG-AACTGTGTGAGGACTTAAGAAACCTGTGTTTGAAGTGAAGAGGCGCTGAAA 2015
Db 1976 AAGTGTCAACTGTGTGAGGACTTAAGAAACCTGTGTTTGAAGTGAAGAGGCGCTGAAA 2035
QY 2016 GAGGGAGGCCAACAAATCTGTCTGCTT-CTCATTATGCTATGGCAATTAAGCATTTG 2074
Db 2036 GAGGGAGGCCAACAAATCTGTCTGCTTCTCATTATGCTATGGCAATTAAGCATTTG 2095
QY 2075 TCTCTTGGCTGTGCTGCTGACGACAGAGGCCAGAACTCATGCGGACACGAGTAAACAT 2134
Db 2096 TCTCTTGGCTGTGCTGCTGACGACAGAGGCCAGAACTCATGCGGACACGAGTAAACAT 2155
QY 2135 CTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTGATGGGATTAATCTTCAGCT 2194
Db 2156 CTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTGATGGGATTAATCTTCAGCT 2215
QY 2195 TGTGAGCTTTAAGTTTCTTCCCTTCATTCTACCTGACAGCTTCTGTAAAGAA 2254
Db 2216 TGTGAGCTTTAAGTTTCTTCCCTTCATTCTACCTGACAGCTTCTGTAAAGAA 2275
QY 2255 AATGCTGAGTTCTACTCAGGTTTCTTACTGAAATTTAGATCTCCAGACCTTCCTG 2314
Db 2276 AATGCTGAGTTCTACTCAGGTTTCTTACTGAAATTTAGATCTCCAGACCTTCCTG 2335
QY 2315 GCCACAATTCAATTAAAGGCAACAACATTAATCACTTCAATGAAGACACACAGACTTTG 2374
Db 2336 GCCACAATTCAATTAAAGGCAACAACATTAATCACTTCAATGAAGACACACAGACTTTG 2395
QY 2375 AAAGCAAGACAAATGACTGCTTGAATTTGAGGCTTGAAGATGAAGCTTTGAAGGAAAAG 2434
Db 2396 AAAGCAAGACAAATGACTGCTTGAATTTGAGGCTTGAAGATGAAGCTTTGAAGGAAAAG 2455
QY 2435 AATACTTTGTTCCAGCCCCCTCCACACTCTTCATGTTTAAACCACTGCTTCGGA 2494
Db 2456 AATACTTTGTTCCAGCCCCCTCCACACTCTTCATGTTTAAACCACTGCTTCGGA 2515
QY 2495 CTTTGAGGCAACGAGTACTGATATTAATGATGTTGTTATGAAGAACTGATTTTGAAGTTCTGA 2554
Db 2516 CTTTGAGGCAACGAGTACTGATATTAATGATGTTGTTATGAAGAACTGATTTTGAAGTTCTGA 2575
QY 2555 TCGTTCAAGAGATGATTAATTAATTAATTTCTT 2587

Db 2576 TCGTTCAAGAGATGATTAATTAATTAATTTCTT 2608

Search completed: May 31, 2005, 10:07:34
Job time : 1781.97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:48:09 ; Search time 10061.7 Seconds

(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978B-1

Perfect score: 2587
Sequence: 1 ggaagcgagcgagcgagctcc.....tgatataatatacatcttcc 2587

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2393.4	92.5	2431	3	CR603772 full-length
2	849.4	32.8	939	5	BX371687 BX371687
3	831.4	32.1	1018	5	BX337228 BX337228
4	801.4	31.0	925	5	BX369964 BX369964
5	769	29.7	779	6	CA311913 UI-CF-FNO
6	740.6	28.6	751	5	BM981657 UI-CF-FNO
7	725	26.9	737	7	CN259810 170006001
8	696.8	26.9	767	5	BX358434 BX358434
9	694	26.8	737	6	CA313445 UI-CF-FNO
10	690	26.7	714	7	CN259813 170006000
11	676.6	26.2	698	7	CN259812 170006001
12	665.8	25.7	681	2	BE741325 BE741325
13	665	25.7	700	5	BU632767 UI-H-FBI-
14	661	25.6	691	6	CB241729 UI-CF-FNO
15	660	25.5	691	6	CA314865 UI-CF-FNO
16	656.2	25.4	691	5	BU608696 UI-CF-FNO
17	653.4	25.3	655	7	CN259811 170006000
18	625.8	24.2	660	6	CB852239 UI-CF-FNO
19	622.4	24.1	660	6	CA426580 UI-H-FBI-
20	620.2	24.0	679	6	CA312678 UI-CF-FNO
21	620	24.0	622	7	CN259814 170006001
22	605	23.4	610	7	CN259817 170006000
23	598.4	23.1	624	7	CN259815 170006000
24	587	22.7	595	5	BU680630 UI-CF-DUI

25	583	22.5	604	5	BX499180 BX499180
26	562.4	21.7	584	5	BP255229 BP255229
27	561	21.7	583	5	BP255264 BP255264
28	556	21.5	594	6	CA503188 UI-CF-FNO
29	551	21.3	563	1	AA404225 zt43h04.r
30	545.8	21.1	571	5	BP276199 BP276199
31	545.4	21.1	556	1	AI684143 cx79904.x
32	543.8	21.0	568	6	CD632169 56084071H
33	536.8	20.7	560	6	CD632170 56084071J
34	536.6	20.7	757	4	BI454643 603170538
35	529.2	20.5	557	5	BM982674 UI-CF-FNO
36	518	20.0	530	4	BI963964 i63c03.y
37	514.8	19.9	578	6	CD686218 EST2739.h
38	511	19.8	529	2	AM615203 hg78a06.x
39	507.4	19.6	553	5	BU742690 UI-E-B01-
40	501	19.4	849	9	AY405846 Homo sapi
41	494	19.1	524	1	AA171844 z098e08.8
42	493.6	19.1	598	1	AA075632 zm88h04.r
43	480.6	18.6	580	5	BP275659 BP275659
44	478.4	18.5	482	1	AI683712 tw53a09.x
45	478	18.5	481	2	AM470108 xr29h08.x

ALIGNMENTS

RESULT 1	CR603772	2431 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CS0D1039YG21 of Placenta Cot 25-normalized				
DEFINITION	CR603772	2431 bp	mrna	linear	HTC 21-JUL-2004
ACCESSION	CR603772	GI:50484579			
VERSION	CR603772.1	GI:50484579			
KEYWORDS	HTC; CNSLT_CDNA				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2431)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polyes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact: Peng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 2431)				
AUTHORS	Genoscope.				
TITLE	Direct Submision				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1. .2431 /organism="Homo sapiens" /mol_type="mrna" /db_xref="taxon:9606" /clone="CS0D1039YG21" /tissue_type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6"				
ORIGIN	Query Match 92.5%; Score 2393.4; DB 3; Length 2431; Best Local Similarity 99.3%; Pred. No. 0; Matches 2414; Conservative 0; Mismatches 16; Indels 1; Gaps 1;				
OY	131 GCACATCATTCGCTTGGTATTCAGGAGACACTCCATCAGTCACTACTGTCGCC 190				
Db	1 GCATTATCTTTCCTTCGAACTGCAGGAGACACTCCATCAGTCACTACTGTCGCC 60				

QY 191 TCAGCTGGAGACATTTGGGGAGATGGATCTGAGCTGACCTTTTGAACCTGACATCAAA 250
Db 61 TCAGCTGGAGACATTTGGGGAGATGGATCTGAGCTGACCTTTTGAACCTGACATCAAA 120
QY 251 CTTTCTGATATGCTGATATACATGGCTGAAGAAAGTGTTTTAGCGTTGCTGATGATGTC 310
Db 121 CTTTCTGATATGCTGATATACATGGCTGAAGAAAGTGTTTTAGCGTTGCTGATGATGTC 180
QY 311 AAAAGAGCAAGATGAGCTGTGCGAGCAGATGAAATGTTCAGAGGCCGAGACAGCATG 370
Db 181 AAAAGAGCAAGATGAGCTGTGCGAGCAGATGAAATGTTCAGAGGCCGAGACAGCATG 240
QY 371 TTTTGCATCAAGTGAATGATGTCGATGCTCTTTTGGCGGTGAAAAACGTGCACTCACA 430
Db 241 TTTTGCATCAAGTGAATGATGTCGATGCTCTTTTGGCGGTGAAAAACGTGCACTCACA 300
QY 431 GATGCTGGACCTTACAAATGTTATATCATCTTCTTAAAGCCAGGGGAATGCTAACCTT 490
Db 301 GATGCTGGACCTTACAAATGTTATATCATCTTCTTAAAGCCAGGGGAATGCTAACCTT 360
QY 491 GAGTATATAAATGAGCTTACAGATGCGGGAAGTGAATGTGATATATATGCTGACCTCA 550
Db 361 GAGTATATAAATGAGCTTACAGATGCGGGAAGTGAATGTGATATATGCTGACCTCA 420
QY 551 GAGACCTTGGCGGTGATGAGGCTCCCGATGGTTCCCGAGGCCACAGTGGCTGGGACATCC 610
Db 421 GAGACCTTGGCGGTGATGAGGCTCCCGATGGTTCCCGAGGCCACAGTGGCTGGGACATCC 480
QY 611 CAAGTTGACCAAGGAGCCAACTTCTCGAAGTCTCCAAATACAGCTTTGATGAACTCT 670
Db 481 CAAGTTGACCAAGGAGCCAACTTCTCGAAGTCTCCAAATACAGCTTTGATGAACTCT 540
QY 671 GAGATGTGACATGAAAGTGTGTCTGTCTTAATGTTTACATCAACAACAATAC 730
Db 541 GAGATGTGACATGAAAGTGTGTCTGTCTTAATGTTTACATCAACAACAATAC 600
QY 731 TCCCTGATGATTTGAAAAATGACATTTGCCAAAGCAACAGGGGATATCAAGATGACAGATG 790
Db 601 TCCCTGATGATTTGAAAAATGACATTTGCCAAAGCAACAGGGGATATCAAGATGACAGATG 660
QY 791 GAGATCAAAAAGCGGAGTCACTTACAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTCT 850
Db 661 GAGATCAAAAAGCGGAGTCACTTACAGCTGCTTAACTCAAAAGGCTTCTGTGTGTCTCT 720
QY 851 TCTTTTCTTTGCCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTTAAATTA 910
Db 721 TCTTTTCTTTGCCATCAGCTGGGCACTTGTGCTCTCAGCCCTTACCTGATGCTTAAATTA 780
QY 911 TGTGCTTGGGCCCAAAAAGACATGCAAAAGTCAATGTTTCAACAGGGATCTACAGAACTA 970
Db 781 TGTGCTTGGGCCCAAAAAGACATGCAAAAGTCAATGTTTCAACAGGGATCTACAGAACTA 840
QY 971 TTTTACCACCAAGATATGACCTAGTTTATATTTCTGGAGAAATGAATTCATATCTAGA 1030
Db 841 TTTTACCACCAAGATATGACCTAGTTTATATTTCTGGAGAAATGAATTCATATCTAGA 900
QY 1031 AGTCTGAGTGAACCAACAGAGACAGAAACAAAAGAGCCAAAGCAGAGAGGCTTCCA 1090
Db 901 AGTCTGAGTGAACCAACAGAGACAGAAACAAAAGAGCCAAAGCAGAGAGGCTTCCA 960
QY 1091 TATGAACAAGATTAATCTATCTTCAAAAGACATATTTGAAGTTGGGAAATTAATTCATG 1150
Db 961 TATGAACAAGATTAATCTATCTTCAAAAGACATATTTGAAGTTGGGAAATTAATTCATG 1020
QY 1151 AACTAGACAAGTGTGTTAAGATGATTAAGTAAAAATGACAGCTGGAGACAAGTGCATCCCA 1210
Db 1021 AACTAGACAAGTGTGTTAAGATGATTAAGTAAAAATGACAGCTGGAGACAAGTGCATCCCA 1080
QY 1211 GATCTCAGGAGACCTCCCTGCTGTCACTGGGAGTGAAGAGACAGATGATGATGT 1270
Db 1081 GATCTCAGGAGACCTCCCTGCTGTCACTGGGAGTGAAGAGACAGATGATGATGT 1140

QY 1271 TCTTGTCTCTGAATTTTTTAAGTATATGCTGTATATGTTGCTCTGAGAAAGCCCTTGA 1330
Db 1141 TCTTGTCTCTGAATTTTTTAAGTATATGCTGTATATGTTGCTCTGAGAAAGCCCTTGA 1200
QY 1331 AAGTATATCCCAACATATCCCATCTTATATTTCCAAATAAAGTGTATATGATACCT 1390
Db 1201 AAGTATATCCCAACATATCCCATCTTATATTTCCAAATAAAGTGTATATGATACCT 1260
QY 1391 AAGAGCTGTATATGACCTGCACTTCCCACTCAGAGGGCGGCTGCAATTTTATATGG 1450
Db 1261 AAGAGCTGTATATGACCTGCACTTCCCACTCAGAGGGCGGCTGCAATTTTATATGG 1320
QY 1451 TCAAAATGATCACTTTTATATGATGCTTCCAAAGTGCCTTGTGCTTCTTCCCACTGAC 1510
Db 1321 TCAAAATGATCACTTTTATATGATGCTTCCAAAGTGCCTTGTGCTTCTTCCCACTGAC 1380
QY 1511 AATGCCAAAGTTGAGAAAAATGATCAATTTTATAGCAATAACAGAGAGTCCGGGACAC 1570
Db 1381 AATGCCAAAGTTGAGAAAAATGATCAATTTTATAGCAATAACAGAGAGTCCGGGACAC 1440
QY 1571 CGATTTTATATAAATACTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTC 1630
Db 1441 CGATTTTATATAAATACTGAGACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTC 1500
QY 1631 AGATGATGTTCAATCCGTGAATGCTCAGGAGAGACCTTTTCACTTGAATATGCACTT 1690
Db 1501 AGATGATGTTCAATCCGTGAATGCTCAGGAGAGACCTTTTCACTTGAATATGCACTT 1560
QY 1691 ATGTATATCAAAAGCTTGAAGCTTCTCTTTCATCCGCGGTGACAGCTTAAAGCTGAG 1750
Db 1561 ATGTATATCAAAAGCTTGAAGCTTCTCTTTCATCCGCGGTGACAGCTTAAAGCTGAG 1620
QY 1751 TTTTCAATAGCATCTAGAGCAGTGGGACCTCAGCTGGGCTGATTTTGGCCCCATCTCCG 1810
Db 1621 TTTTCAATAGCATCTAGAGCAGTGGGACCTCAGCTGGGCTGATTTTGGCCCCATCTCCG 1680
QY 1811 GGGAAATGCTGTAAGAACAATTTTGTACTCAATAGAGGAGTGAAGAGATACAGTCT 1870
Db 1681 GGGAAATGCTGTAAGAACAATTTTGTACTCAATAGAGGAGTGAAGAGATACAGTCT 1740
QY 1871 ACTACCAATAGTGAATAAAGCCAGGAGTGTGCTCAACCTTCCATAGATACAGAGAG 1930
Db 1741 ACTACCAATAGTGAATAAAGCCAGGAGTGTGCTCAACCTTCCATAGATACAGAGAG 1800
QY 1931 TCTCCCATTTACAACTAACCCAAATCCGAAGTGTCAACTGTGTCAAGGACTTAAGAAACCTCG 1990
Db 1801 TCTCCCATTTACAACTAACCCAAATCCGAAGTGTCAACTGTGTCAAGGACTTAAGAAACCTCG 1860
QY 1991 TTTTGAATGAAAAAGGCTGGAAGAGGGAGCCAAACAATGTGTCTTCTTCTCAAT 2049
Db 1861 TTTTGAATGAAAAAGGCTGGAAGAGGGAGCCAAACAATGTGTCTTCTTCTCAAT 1920
QY 2049 TATGCTATGGCAATTAAGATCTGTCTTGTGGCTGGCTGAGCAGAGAGCCAGA 2109
Db 1921 TATGCTATGGCAATTAAGATCTGTCTTGTGGCTGGCTGAGCAGAGAGCCAGA 1980
QY 2110 ACTCTATGGGCAACAGATTAACATCTCAGTGAACAGAGTTTGAACAAGGCTTATGGGA 2169
Db 1981 ACTCTATGGGCAACAGATTAACATCTCAGTGAACAGAGTTTGAACAAGGCTTATGGGA 2040
QY 2170 ATGCTGATGGAGTATATCTTACGCTTGTGAGCTTCTTAAATGTTTCTTCTTCAATTTAC 2229
Db 2041 ATGCTGATGGAGTATATCTTACGCTTGTGAGCTTCTTAAATGTTTCTTCTTCAATTTAC 2100
QY 2230 CCGCAGGCAAGTCTGTGAAGAAATGCTGAGTGTCTAGCTCAGGTTTCTTACTCTCG 2289
Db 2101 CCGCAGGCAAGTCTGTGAAGAAATGCTGAGTGTCTAGCTCAGGTTTCTTACTCTCG 2160
QY 2290 AATTTAGATCTCAAGCCCTTCTGGGCACAATTCAAATTTAAGGCAACAACATATACCT 2349
Db 2161 AATTTAGATCTCAAGCCCTTCTGGGCACAATTCAAATTTAAGGCAACAACATATACCT 2220
QY 2350 TCCATGAACACACAGACTTTTGAAGCAAGCAATGACTGTGTAATTTAGGCTT 2409

Contact: Genoscope
Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
The first strand cDNA was primed with a NotI-oligo(dT) primer. Five primers
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMWSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.x
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSDBA10212B08_CS01978_1lc=742.x.

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/classuse_type="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end cloned, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

	32.8%; Similarity ; Conservative	Score 849.4; 96.7%; 0;	DB 5; Pred. No. 1.9e-23; 5;	Length 933; Indels 7; Gaps 7;
AAATCTATCTTCAAGACAT- TTAGAACTGGGAAATTA- TTCATGTGAACTAGACA				1166
AAATCTATCTTCAAGACAT- TTAGAACTGGGAAATTA- TTCATGTGAACTAGACA				880
G- TGTGTTAAGAGTAAAGTAAATGACGTGAGACAATGCATCCCGAGCTCAGG				1219
GATGTGTAAAGTAAAGTAAAGTAAATGACGTGAGACAATGCATCCCGAGCTCAGG				820
GA- CTTCCCTCCCTGCTTCACTCTGGGAGTAGAGACAGGATATGTGATTTCTTTCTC				1278

1279	TCGTAATTTT	AGTTATATATGCTGTAATGTTGCTCTGAGGAGCCCTCGAAAGTCTAT	1338
758	TCGTGAATTT	TAGTATATATGCTGTAAATGTTGCTCTGAGGAGCCCTCGAAAGTCTAT	700
1339	CCCAACATAT	CCATCTTATATTCACAAATTAAGCTGTACTATGTAACCTTAAGACGCT	1398
699	CCCAACATAT	CCATCTTATATTCACAAATTAAGCTGTACTATGTAACCTTAAGACGCT	640
1399	GCTAATTTAC	TGCACTTCGCAACTCGAGGGGCGGCTGCATTTTATTAATGGGTCAAATGA	1458
639	GCTAATTTAC	TGCACTTCGCAACTCGAGGGGCGGCTGCATTTTATTAATGGGTCAAATGA	580
1459	TTCACTTTT	TATGATGCTTCGCAAGGTCGCTTGCTCTCTTCCCACTGACAAATGCA	1518
579	TTCACTTTT	TATGATGCTTCGCAAGGTCGCTTGCTCTCTTCCCACTGACAAATGCA	520
1519	AAAGTTAG	AAAAATGATCATATATTTTATGATTAACAGAGCACTGGGCGACACCGATTTTA	1578
519	AAAGTTAG	AAAAATGATCATATATTTTATGATTAACAGAGCACTGGGCGACACCGATTTTA	460
1579	TAAATTAAC	TGAGACACTCTTTTAAACAAATGCGGCTTATTTTCTCAGATGATG	1638
459	TAAATTAAC	TGAGACACTCTTTTAAACAAATGCGGCTTATTTTCTCAGATGATG	400
1639	TTCAATCG	TGAATGCTTCAGGAAAGACCTTTTACCTTGACATATATGGCATTAATGATC	1698
399	TTCAATCG	TGAATGCTTCAGGAAAGACCTTTTACCTTGACATATATGGCATTAATGATC	340
1699	ACAAGCTC	TGAGGCTTCCTCTTCCATCCGCGGTGGACAGCTAAGACCTCAGTTTTCAT	1758
339	ACAAGCTC	TGAGGCTTCCTCTTCCATCCGCGGTGGACAGCTAAGACCTCAGTTTTCAT	280
1759	AGCATCTA	GAGCAGTGGGACTCAGCTGCGGATATTTTCGCCCCCATCTCCGCGGGAAATGT	1818
279	AGCATCTA	GAGCAGTGGGACTCAGCTGCGGATATTTTCGCCCCCATCTCCGCGGGAAATGT	220
1819	CTGAAGCA	ATTTTGGTTACTCAATGAGGAGGTGAGGAGGATACAGTGTCTACTACCA	1878
219	CTGAAGCA	ATTTTGGTTACTCAATGAGGAGGTGAGGAGGATACAGTGTCTACTACCA	160
1879	CTAGTGAT	TAAAGGCCAGGGATCTCTCTCAACTCTTACATGTACAGAGAGTCTCCCCA	1938
159	CTAGTGAT	TAAAGGCCAGGGATCTCTCTCAACTCTTACATGTACAGAGAGTCTCCCCA	100
1939	TTACAAC	TACCAATCCGAAGTGTCAACGTGTACAGGACATTAAGAAACCTCGTGTGGAG	1997
99	TTACAAC	TACCAATCCGAAGTGTCAACGTGTACAGGACATTAAGAAACCTCGTGTGGAG	40
1998	TAGA-AAA	GGGCTCGGAAG-AGGGGAGCCCAACAATCT	2034
39	TAGAA	AAAGGCGCTCGAAAGAGAGGGAGCCCAACAATCT	1

BX337228 1018 bp mRNA linear EST 08-APR-2004
 BX337228 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
 clone CS001039YG21 3-PRIME, mRNA sequence.
 BX337228
 BX337228 BX337228.2 GI:46283446
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1018)
 Li W.B., Gruber C., Jesssee J. and Polajsek D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30346952.
 contact: genoscope

Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 E-mail: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 742.r

FEATURES

source

Location/Qualifiers

1..1018

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1039G21"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 32.1%; Score 831.4; DB 5; Length 1018;
 Best Local Similarity 90.4%; Pred. No. 2,9e-227;
 Matches 922; Conservative 51; Mismatches 36; Indels 11; Gaps 9;

1550 AAACAGAGAGTGGGACACCGATTTTTAAATAAAGAGACCTCTTTTAAACAA 1609
 1018 AAACAGAGAGTGGGACACCGATTTTTAAATAAAGAGACCTCTTTTAAACAA 960
 1610 ACAAATGCGGGTTATTTCTCAGATATGTTTCCTGTAATGTCAGAGAGACCTT 1669
 959 ACAAATGCGGGTTATTTCTCAGATATGTTTCCTGTAATGTCAGAGAGACCTT 901
 1670 TCACTTCTATATGAGCATATGATGATCAAGACTCTAGAGCTTCTCTTTCACCTG 1729
 900 TACCCAGAGATATGAGCATATGATGATCAAGACTCTAGAGCTTCTCTTTCACCTG 841
 1730 CCGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1789
 840 CCGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 781
 1790 GATTTGGCCCCC-ATCTCGGGGGGAATGTCGAAGCAATTTTGGTTA--CCTCAATGA 1846
 780 GATTTGGCCCCC-ATCTCGGGGGGAATGTCGAAGCAATTTTGGTTA--CCTCAATGA 721
 1847 GGGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1906
 720 GGGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 661
 1907 CAACCTCTACCACTGACAGAGAGTCTCCCATTTACCACTGACAGAGAGTCTCAAC 1966
 660 CAACCTCTACCACTGACAGAGAGTCTCCCATTTACCACTGACAGAGAGTCTCAAC 601
 1967 TGTGTAGAGACTAAGAAACCTGTTTGTAGTGAAGAAAGGGCTGGAAGAGGGAGCCA 2026
 600 TGTGTAGAGACTAAGAAACCTGTTTGTAGTGAAGAAAGGGCTGGAAGAGGGAGCCA 541
 2027 ACAAACTGTGCTGCTT-CTCAGATATGCTTGGCAATTAAGCATTTCTGCTTTGGCT 2085
 540 ACAAACTGTGCTGCTT-CTCAGATATGCTTGGCAATTAAGCATTTCTGCTTTGGCT 481
 2086 GGTGCTCTGACAGAGAGAGCCAGAACTATTCGGGACCAAGATTAATCTCTCACTG 2144
 480 GGTGCTCTGACAGAGAGAGCCAGAACTATTCGGGACCAAGATTAATCTCTCACTG 421
 2145 ACGAGAGTTG--ACAAGAGCTTATGGGAAATG--CTGATGGGATTTATCTTCACTTGGAG 2201
 420 ACGAGAGTTGCAAGAGAGCTTATGGGAAATGAGCTGATGGGATTTATCTTCACTTGGAG 361

2202 C-TTCTAAGTTCTTTCCCTTCATTTACCTGACAGCCAAAGTCTGTAAAGAAATGCC 2260
 DB CGTTCTAAGTTCTTTCCCTTCATTTACCTGACAGCCAAAGTCTGTAAAGAAATGCC 301
 2261 TGAGTTTACGCTCAGGTTTCTTCTGATCTGAAATTTAGATCCAGACCTTCTGGCCACA 2320
 DB TGAGTTTACGCTCAGGTTTCTTCTGATCTGAAATTTAGATCCAGACCTTCTGGCCACA 241
 2321 ATTCAATTAAGGACCAACATATACCTTCATGACACACAGACCTTTTGAAGCA 2380
 DB ATTCAATTAAGGACCAACATATACCTTCATGACACACAGACCTTTTGAAGCA 181
 2381 AGGACATGACTGCTTGAATTTAGAGGCTTGAAGAAATGAAGCTTTGAAGAAATGACT 2440
 DB AGGACATGACTGCTTGAATTTAGAGGCTTGAAGAAATGAAGCTTTGAAGAAATGACT 121
 2441 TTGTTTCCAGCCCCCTTCCACACCTTCATGTTTAACTGCTTCTGGACCTGG 2500
 DB TTGTTTCCAGCCCCCTTCCACACCTTCATGTTTAACTGCTTCTGGACCTGG 61
 2501 AGCCAGGAGTACTGATTTACATGTTTGTATGAAGAACTGATTTTGAAGTTCTGATCTTC 2560
 DB AGCCAGGAGTACTGATTTACATGTTTGTATGAAGAACTGATTTTGAAGTTCTGATCTTC 1

RESULT 4

BX369964

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 925)

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

E-mail: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

742.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna7s=CS0BAG030ZA11_CS02865_1&c=742.r.

Location/Qualifiers

1..925

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1039G21"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

Location/Qualifiers

1..925

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1039G21"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna7s=CS0BAG030ZA11_CS02865_1&c=742.r.

Location/Qualifiers

1..925

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1039G21"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 31.0%; Score 801.4; DB 5; Length 925;
 Best Local Similarity 98.8%; Pred. No. 1.2e-218;
 Matches 827; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

411 TGAAGAGCTGACAGATGCTGGACCTACAAATGATATCATCATC-TTCTAA 469

```

Db      26 TGAAGAAAGTGCACACTCAGATGCTGGCACTTCAAAATGTTATATCAACACTTTCATAA 85
Qy      470 GGGAAAGGGGAAATGCTAATCTGAGTATTAATCTGAGCTTCACAGATCCCGAAGTGAAT 529
Db      86 GGGAAAGGGGAAATGCTAATCTGAGTATTAATCTGAGCTTCACAGATCCCGAAGTGAAT 145
Qy      530 GTGAGACTAATAATGCTCAGAGTCCAGAGCTTGGGCTGTGAGGCTCCCGATGTTCCCGAG 589
Db      146 GTGAGACTAATAATGCTCAGAGTCCAGAGCTTGGGCTGTGAGGCTCCCGATGTTCCCGAG 205
Qy      590 CCACAGTGTCTGTGGGCAATCCCAAGTGAACAGAGGAGCAACTTCTCGGAAGTCTCAAT 649
Db      206 CCACAGTGTCTGTGGGCAATCCCAAGTGAACAGAGGAGCAACTTCTCGGAAGTCTCAAT 265
Qy      650 ACCAGCTTTGAGCTGGAATCTGAGAAATGTCACATGAAAGTGTGTCTGTGCTTCAAT 709
Db      266 ACCAGCTTTGAGCTGGAATCTGAGAAATGTCACATGAAAGTGTGTCTGTGCTTCAAT 325
Qy      710 GTTACGATCAACAACACATCTCTGTATGATGAAATGACATTTGCCAAAGCAACAGG 769
Db      326 GTTACGATCAACAACACATCTCTGTATGATGAAATGACATTTGCCAAAGCAACAGG 385
Qy      770 GATATCAAAGTGACAGAAATCGAGATCAAAAGGCGAGTCACTACAGCTGTAACTCA 829
Db      386 GATATCAAAGTGACAGAAATCGAGATCAAAAGGCGAGTCACTACAGCTGTAACTCA 445
Qy      830 AAGCTTCTGTGTGTCTCTTCTTTCTTTGCTTCATGAGTGGGCACTTGTGCTCTCAAC 889
Db      446 AAGCTTCTGTGTGTCTCTTCTTTCTTTGCTTCATGAGTGGGCACTTGTGCTCTCAAC 505
Qy      890 CTTACCTGATGCTAAATATATGCTTGTGCTTGGCCCAAAAAGCATGCAAGTCAATGTTA 949
Db      506 CTTACCTGATGCTAAATATATGCTTGTGCTTGGCCCAAAAAGCATGCAAGTCAATGTTA 565
Qy      950 CAACAGGATCTACAGAACTATTTACACACAGATATGACCTAGTTTATATTTCTGGGA 1009
Db      566 CAACAGGATCTACAGAACTATTTACACACAGATATGACCTAGTTTATATTTCTGGGA 625
Qy      1010 GGAATGAAATTCATATCTAGAAAGTGTGAGTGGCAAAACAGAGCAAAACAAAGAA 1069
Db      626 GGAATGAAATTCATATCTAGAAAGTGTGAGTGGCAAAACAGAGCAAAACAAAGAA 685
Qy      1070 GCCAAAGAGAGAGGCTCCATATGAAACAGATATCTATCTTCAAGACATTTAGAA 1129
Db      686 GCCAAAGAGAGAGGCTCCATATGAAACAGATATCTATCTTCAAGACATTTAGAA 745
Qy      1130 GTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTG-TTAAAGTGAATGAATGCA 1188
Db      746 GTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTGTTAAAGTGAATGAATGCA 805
Qy      1189 GGTGAGAGCAAGTGCATCCCAAGATCTCAGGAGCTCCCTGCTGTCACTGGGG 1245
Db      806 GGTGAGAGCAAGTGCATCCCAAGATCTCAGGAGCTCCCTGCTGTCACTGGGG 862

```

```

RESULT 5
CA311913/c      779 bp      mRNA      linear      EST 04-NOV-2002
LOCUS      CA311913      779 bp      mRNA      linear      EST 04-NOV-2002
DEFINITION      UI-CF-FNO-afj-a-01-0-UI-afj UI-CF-FNO Homo sapiens cDNA clone
ACCESSION      CA311913
VERSION      CA311913.1 GI:24530011
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 779)
AUTHORS      Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
JOURNAL      Genome Res. 6 (9), 791-806 (1996)
MEDLINE      97044477

```

PUBMED COMMENT

8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul.mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source location/Qualifiers
1..779
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afj-a-01-0-UI"
/issue_type="Human lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (tl phage resistant)"
/clone_1lb="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 29.7%; Score 769; DB 6; Length 779;
Best Local Similarity 99.4%; Pred. No. 2,5e-209;
Matches 772; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 764 ACAGGGATATCAAGTGCAGAAATCGAGATCAAAAGGCGAGTCACTACAGCTGTA 823
Db 779 ACAGGGATATCAAGTGCAGAAATCGAGATCAAAAGGCGAGTCACTACAGCTGTA 720
Qy 824 AACTCAAAGCTTCTGTGTGTCTCTTCTTTTGGCCATGCTGGGCACTTGTGCTT 883
Db 719 AACTCAAAGCTTCTGTGTGTCTCTTCTTTTGGCCATGCTGGGCACTTGTGCTT 660
Qy 884 CTCAGCCCTTACCTGATGCTAAATATATGTCCTTGGCCCAAAAAGCATGCAAGTCA 943
Db 659 CTCAGCCCTTACCTGATGCTAAATATATGTCCTTGGCCCAAAAAGCATGCAAGTCA 600
Qy 944 TTGTTACAAAGGATCTACAGAACTATTTACACACAGATATGACCTAGTTTATATTT 1003
Db 599 TTGTTACAAAGGATCTACAGAACTATTTACACACAGATATGACCTAGTTTATATTT 540
Qy 1004 CTGGGAGGAAATTAATTCATATCTAGAAAGTCTGGATGAGCAAAACAGAGCAAAACA 1063
Db 539 CTGGGAGGAAATTAATTCATATCTAGAAAGTCTGGATGAGCAAAACAGAGCAAAACA 480
Qy 1064 AAAGAGCCAAAGAGAGGCTCCATATGAAACAGATTAATCTATCTTCAAGACATA 1123
Db 479 AAAGAGCCAAAGAGAGGCTCCATATGAAACAGATTAATCTATCTTCAAGACATA 420
Qy 1124 TTGAAGTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTGTTAAGAGTAAAGTAA 1183
Db 419 TTGAAGTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTGTTAAGAGTAAAGTAA 360
Qy 1184 ATGCAAGTGAAGCAAGTGCATCCCAAGATCTCAGGAGCTCCCTGCTGTCACTGG 1243

Db 359 ATGCAGCTGAGACAGATGCATCCAGATCTCAGGAGCCTCCCTGCCTGCACCTGG 300
QY 1244 GGAGTACAGAGACAGATAGTGTCTTCTTCTCTCAATTTTAACTTATGCTG 1303
Db 299 GGAGTACAGAGACAGATAGTGTCTTCTTCTCTCAATTTTAACTTATGCTG 240
QY 1304 TAATGTGCTCTGAGGAGAGCCCTGGAAGTCTATCCCAATATCCATCATCTTATATC 1363
Db 239 TAATGTGCTCTGAGGAGAGCCCTGGAAGTCTATCCCAATATCCATCATCTTATATC 180
QY 1364 CACAAATTAAGCTGTAGTATGTAACCTTAAGAGCGCTGTAATGACTGCGCACTTGGCACT 1423
Db 179 CACAAATTAAGCTGTAGTATGTAACCTTAAGAGCGCTGTAATGACTGCGCACTTGGCACT 120
QY 1424 CAGGGGCGCTGATTTTAACTTATGTAAGGTCATCACTTTTAACTTATGCTTCCAAAG 1483
Db 119 CAGGGGCGCTGATTTTAACTTATGTAAGGTCATCACTTTTAACTTATGCTTCCAAAG 60
QY 1484 GTGCTTGGCTTCTTCCCACTGACAAATGCGCAAGTTGAGAAAAATGATCATTA 1540
Db 59 GTGCTTGGCTTCTTCCCACTGACAAATGCGCAAGTTGAGAAAAATGATCATTA 3

RESULT 6
BM981657/c 751 bp mRNA linear EST 21-FEB-2003
LOCUS UI-CF-EN1-adi-m-02-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
DEFINITION UI-CF-EN1-adi-m-02-0-UI 3', mRNA sequence.
ACCESSION BM981657
VERSION BM981657.1 GI:19604370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 751)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYAT=Yes.

FEATURES

source
1. 751
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-adi-m-02-0-UI"
/issue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the

following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=human Lung Epithelial Cell lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 28.6%; Score 740.6; DB 5; Length 751;
Best Local Similarity 99.3%; Pred. No. 3.6e-201;
Matches 743; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 322 AGATGAGCTGTGCGAGAGATGAATGTTTCAAGAGCCGACAGAGTGTGCTGATCA 381
Db 751 AGATGAGCTGTGCGAGAGATGAATGTTTCAAGAGCCGACAGAGTGTGCTGATCA 692
QY 382 AGTGAATGTTGCAATGCTCTTTGCGGCTGAAAAACGTGAATCTCAGAGTCTGGCAC 441
Db 691 AGTGAATGTTGCAATGCTCTTTGCGGCTGAAAAACGTGAATCTCAGAGTCTGGCAC 632
QY 442 CTACAAATGTTATATCATCATCTTTAAAGGCAAGGGGAATGCTTAACTTGAATTAAC 501
Db 631 CTACAAATGTTATATCATCATCTTTAAAGGCAAGGGGAATGCTTAACTTGAATTAAC 572
QY 502 TGGAGCTTCAGATGCGGAGATGAATGTTGACTATATGCTGAGCTGAGACCTTGG 561
Db 571 TGGAGCTTCAGATGCGGAGATGAATGTTGACTATATGCTGAGCTGAGACCTTGG 512
QY 562 GTGTAGGCTCCCGATGGTTCCCGACCCACAGTGTCTGGGATCCCAAGTTGACCA 621
Db 511 GTGTAGGCTCCCGATGGTTCCCGACCCACAGTGTCTGGGATCCCAAGTTGACCA 452
QY 622 GGGAGCCAACTTCTGGAAGTCTCCATATCCAGCTTTGAGCTGAATGTTGAC 681
Db 451 GGGAGCCAACTTCTGGAAGTCTCCATATCCAGCTTTGAGCTGAATGTTGAC 392
QY 682 CATGAAGTGTGTGCTGCTTACATATGTTACATCAACACATCTCTGTATGAT 741
Db 391 CATGAAGTGTGTGCTGCTTACATATGTTACATCAACACATCTCTGTATGAT 332
QY 742 TGAATAATGACATTTGCAAGCAAGGGGATATCAAGTGAAGATCGAGATCAAAAG 801
Db 331 TGAATAATGACATTTGCAAGCAAGGGGATATCAAGTGAAGATCGAGATCAAAAG 272
QY 802 GGGAGTCCCTACAGCTCTTAACCTCAAGGCTCTGTGTGCTCTCTCTTTTGGC 861
Db 271 GGGAGTCCCTACAGCTCTTAACCTCAAGGCTCTGTGTGCTCTCTCTTTTGGC 212
QY 862 CATGAGCTGGGACCTTGTGCTCTGAGCCCTTACCTGATGCTAAATATATGTGCTGGC 921
Db 211 CATGAGCTGGGACCTTGTGCTCTGAGCCCTTACCTGATGCTAAATATATGTGCTGGC 152
QY 922 CACAAAAAGCATGCAAGATCATTTTACACAGGATCTACAGACTATTTTACACCA 981
Db 151 CACAAAAAGCATGCAAGATCATTTTACACAGGATCTACAGACTATTTTACACCA 92
QY 982 GATTAAGCTAGTTTATATTTCTGGAGAAATGAATTCATATCTAAGAGCTGAGAG 1041
Db 91 GATTAAGCTAGTTTATATTTCTGGAGAAATGAATTCATATCTAAGAGCTGAGAG 32
QY 1042 AGCAAAACAGACAGAAACAAAGAA 1069
Db 31 AGCAAAACAGACAGAAACAAAGAA 4

RESULT 7
CN259810 737 bp mRNA linear EST 16-MAY-2004
LOCUS 17000600184202 GRN_PRENUE Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN259810
VERSION CN259810.1 GI:47276224
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 737)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
CONTACT: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 737 Std Error: 0.00.
Location/Qualifiers
1. 737
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENUE"
/note="oligo dt primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic acid and mitogens."
ORIGIN
Query Match 28.0%; Score 725; DB 7; Length 737;
Best Local Similarity 99.9%; Pred. No. 1.1e-196;
Matches 736; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1374 GCTGTATGATGACCTTAAGACGCTGTAATGACTGCCACTTGGCAACTCAGGGGCGC 1433
DB 1 GCTGTATGATGACCTTAAGACGCTGTAATGACTGCCACTTGGCAACTCAGGGGCGC 60
QY 1434 TGCATTTTATGATGGTGCAATGATCCTTTTATGATGCTTCCAAAGTGCTTGGC 1493
DB 61 TGCATTTTATGATGGTGCAATGATCCTTTTATGATGCTTCCAAAGTGCTTGGC 120
QY 1494 TTCTCTTCCCACTGCAAAATGCGCAAGTTGAGAAAATGATCAATTTTATAGCATTAAC 1553
DB 121 TTCTCTTCCCACTGCAAAATGCGCAAGTTGAGAAAATGATCAATTTTATAGCATTAAC 180
QY 1554 AGAGCACTCGGCGACACCGATTTTATTAATTAATCTGAGCACTTCTTTTAAACAAACAA 1613
DB 181 AGAGCACTCGGCGACACCGATTTTATTAATTAATCTGAGCACTTCTTTTAAACAAACAA 240
QY 1614 ATGCGGGTTTATTTCTCAATGATGTTCAATCCGTAATGGTCCAGGAGAGACCTTTGAC 1673
DB 241 ATGCGGGTTTATTTCTCAATGATGTTCAATCCGTAATGGTCCAGGAGAGACCTTTGAC 300
QY 1674 CTGACATATATGGCATATGTCATCACAAGCTCGAGGCTTCTCTTCCATCCTGGGCTG 1733
DB 301 CTGACATATATGGCATATGTCATCACAAGCTCGAGGCTTCTCTTCCATCCTGGGCTG 360
QY 1734 GACAGCTAAGACCTCAGTTTTCATATAGCATCTAGAGAGCTGGGACTGAGCTGGGGTATT 1793
DB 361 GACAGCTAAGACCTCAGTTTTCATATAGCATCTAGAGAGCTGGGACTGAGCTGGGGTATT 420

QY 1794 TCGCCCCCATCTCCGGGGGAATGTCTGAAGACAATTTGGTTACTCTAATGAGGAGTG 1853
DB 421 TCGCCCCCATCTCCGGGGGAATGTCTGAAGACAATTTGGTTACTCTAATGAGGAGTG 480
QY 1854 GAGAGAGATACAGTGTCTACTACCACTAGTGATTAAGGCGAGGAGTGTCTCAACTTC 1913
DB 481 GAGAGAGATACAGTGTCTACTACCACTAGTGATTAAGGCGAGGAGTGTCTCAACTTC 540
QY 1914 CTACCATGTACAGAGAGCTTCCCCCATTTACCACTACCCCAATCCGAATGTCAATGTGTCA 1973
DB 541 CTACCATGTACAGAGAGCTTCCCCCATTTACCACTACCCCAATCCGAATGTCAATGTGTCA 600
QY 1974 GGAATAAGAAACCTGTTTGTAGTAAAGAGGCGCTGAAAGAGGAGGAGCCAAACAATC 2033
DB 601 GGAATAAGAAACCTGTTTGTAGTAAAGAGGCGCTGAAAGAGGAGGAGCCAAACAATC 660
QY 2034 TGCTGTGCTT-CTGACATTAATGATGCAATTAAGCAATTCGTCTTTGGCTGTGCT 2092
DB 661 TGCTGTGCTTCTCAATTAATGATGCAATTAAGCAATTCGTCTTTGGCTGTGCT 720
QY 2093 CAGCACAGAGAGCCACA 2109
DB 721 CAGCACAGAGAGCCACA 737
RESULT 8
BX358434 767 bp mRNA linear EST 08-APR-2004
LOCUS BX358434 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION BX358434 Clone CS0D1039YG21 5-PRIME, mRNA sequence.
ACCESSION BX358434
VERSION BX358434.2 GI:46285747
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 767)
Li, W. B., Gruber, C., Jessee, J., and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30366215.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1039AD10P1c=742.r.
FEATURES
Source
1. 767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 26.9%; Score 696.8; DB 5; Length 767;
Best Local Similarity 92.6%; Pred. No. 1.5e-188;
Matches 709; Conservative 36; Mismatches 19; Indels 2; Gaps 2;
QY 27 CCAGTACCAAGATACCTGGGAACCTTCCCGAGCCATGGCTTCCCTGGGGCAGATCTCT 86

```

Db      1 CCGGGATCCAGATACCCCTGGGAA-CTTCCCAGCCATGCTTCCCTGGGGAGATCCTCT 59
QY      87 TCTGGAGCAATTAATAGCATCATATATCTGGCTGAGCAATGTGACTCATCATTTGGCT 146
Db      60 TCTGGAGCAATTAATAGCATCATATATCTGGCTGAGCAATGTGACTCATCATTTGGCT 119
QY      147 TTGGTATTTCAAGGAGACATCTCCATCAGTCACTACTGTGCTGAGCTGGGAACATTTG 206
Db      120 TTGGTATTTCAAGGAGACATCTCCATCAGTCACTACTGTGCTGAGCTGGGAACATTTG 179
QY      207 GGGAGATGGAATCCTGAGCTGACCTTTTGAACCTGACATCAAACTTTTCTGATATGTGA 266
Db      180 GGGAGATGGAATCCTGAGCTGACCTTTTGAACCTGACATCAAACTTTTCTGATATGTGA 239
QY      267 TACAAATGCTGAAGGAAGGTGTTTGGCTGGTGTCCATAGATTCAAAGAAGCAAGATG 326
Db      240 TACAAATGCTGAAGGAAGGTGTTTGGCTGGTGTCCATAGATTCAAAGAAGCAAGATG 299
QY      327 AGCTGTCGAGAGCAGATGAAATGTTCAAGAGCCGAGCAGAGTGTGCTGATCAAGTGA 386
Db      300 AGCTGTCGAGAGCAGATGAAATGTTCAAGAGCCGAGCAGAGTGTGCTGATCAAGTGA 359
QY      387 TAGTTGGCAATGCTCTTTGGCGCTGAAAACCTGCACTCAGACATGCTGGCACTTACA 446
Db      360 TAGTTGGCAATGCTCTTTGGCGCTGAAAACCTGCACTCAGACATGCTGGCACTTACA 419
QY      447 AATGTATATATCATCTGTTAAAGGAGGGAATCTAACCCTGAGTAAATCACTGAG 506
Db      420 AATGTATATATCATCTGTTAAAGGAGGGAATCTAACCCTGAGTAAATCACTGAG 479
QY      507 CCTTCAGCATGCGGGAAGTGAATGTGACTATATATCCAGCTCAGAGACCTTGCGGTGTG 566
Db      480 CCTTCAGCATGCGGGAAGTGAATGTGACTATATATCCAGCTCAGAGACCTTGCGGTGTG 539
QY      567 AGGCTCCCGAGATGTTCCCGCAGCCCAAGTGTCTGGGCTATCCCACTTGACAGGAG 626
Db      540 AGGCTCCCGAGATGTTCCCGCAGCCCAAGTGTCTGGGCTATCCCACTTGACAGGAG 599
QY      627 CCAACTCTTCGGAAGTCTCCATATGAGCTTTGAGCTGGAACCTGGAATGTGACCATGA 686
Db      600 CCAACTCTTTTAAAGTCTCCATATGAGCTTTGAGCTGGAATGTGACCATGA 659
QY      687 AGGTTGTCTGTGCTCTCAATATGTACGATCAACAACATATCTCTGTATGATGA 746
Db      660 AGGTTGTCTGTGCTCTCAATATGTACGATCAACAACATATCTCTGTATGATGA 719
QY      747 ATGACATTTGCCAAGCAAGCAG-GGGATATCAAAATGACAGATCGG 791
Db      720 ATGATATTTGCCAAGCAAGCAGTGGATATTTAAGTACAGMATCGG 765

RESULT 9
CA313445/c 737 bp mRNA linear EST 04-NOV-2002
LOCUS      UI-CF-FNO-aeY-b-10-0-UI-s1 UI-CF-FNO Homo sapiens cDNA clone
DEFINITION UI-CF-FNO-aeY-b-10-0-UI 3', mRNA sequence.
ACCESSION  CA313445
VERSION     CA313445.1 GI:24531543
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 737)
AUTHORS     Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
PUBMED     8889548
COMMENT     Contact: McCray, PB
            McCray Lab

```

```

FEATURES
    source
        University of Iowa
        2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
        Tel: 319 356 4866
        Fax: 319 356 7171
        Email: paul-mccray@iowa.edu
        Tissue Procurement: Dr. M. J. Welsh, University of Iowa
        cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
        DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
        Clone Distribution: Researchers may obtain clones from Research
        Genetics (www.resgen.com) or from Open Biosystems
        (www.openbiosystems.com).
        The following repetitive elements were found in this cDNA
        sequence: 618-737, >MER20DNA/MER1_type (matched complement)
        Seq primer: M13 FORWARD
        POLYA=yes.
    Location/Qualifiers
        1..737
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="UI-CF-FNO-aeY-b-10-0-UI"
            /tissue="Human Lung Epithelial cells"
            /lab_host="RDH10B (Life Technologies) (Ti phage resistant)"
            /clone_lib="UI-CF-FNO"
            /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
            modified polylinker; Site 1: EcoR I; Site 2: Not I;
            UI-CF-FNO is a subtracted cDNA library derived from two
            normalized Human lung epithelial cell libraries (EN1
            and Dn1) The library was subtracted according to
            Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
            1996. For additional information, contact:
            bento-soares@uiowa.edu
            TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
            TAG_LIB=UI-CF-FNO
            TAG_SEQ=GCCTGTAGGC"

```

ORIGIN

```

Query Match      26.8%; Score 694; DB 6; Length 737;
Best Local Similarity 99.4%; Pred. No. 9,5e-186;
Matches 716; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```

```

QY      1869 CTACTACCAACTAGTGATTAAGGCGCAGGATGCTGCTCAACCTCTTACATGTACAGA 1928
Db      737 CTACTACCAACTAGT-GATTAAGGCGCAGGATGCTGCTCAACCTCTTACATGTACAGA 679
QY      1929 CGCTCCCATTAACAACATCCCAATCCGAAGTCAACTGTGTGAGACTAAGAAACCT 1988
Db      678 CGCTCCCATTAACAACATCCCAATCCGAAGTCAACTGTGTGAGACTAAGAAACCT 619
QY      1989 GGTTTTGAAGTAAAGAGGCGCTGAAAGAGGGAGCCCAAAATCTGTGTGCTT-CTGAC 2047
Db      618 GGTTTTGAAGTAAAGAGGCGCTGAAAGAGGGAGCCCAAAATCTGTGTGCTTCTGAC 559
QY      2048 ATTAGTCATTTGGCAATAATGAACATTTCTTTGGCTGCTGCTCCTGACAGAGAGCA 2107
Db      558 ATTAGTCATTTGGCAATAATGAACATTTCTTTGGCTGCTGCTCCTGACAGAGAGCA 499
QY      2108 GAACCTTATCGGGGACCCGAGATTAACATCTTCAGAGGAACAGATGTGACAGGCGCTATGGG 2167
Db      498 GAACCTTATCGGGGACCCGAGATTAACATCTTCAGAGGAACAGATGTGACAGGCGCTATGGG 439
QY      2168 AATAGCTGATGGGATTAATCTTCACTTGTGAGCTTCAAGTTCTTTCCCTCATTTCT 2227
Db      438 AATAGCTGATGGGATTAATCTTCACTTGTGAGCTTCAAGTTCTTTCCCTCATTTCT 379
QY      2228 ACCCTGCAAGCCAAAGTTCTGTAAGAAATGCTTGAAGTTCTAGCTCAGGTTTCTTACTC 2287
Db      378 ACCCTGCAAGCCAAAGTTCTGTAAGAAATGCTTGAAGTTCTAGCTCAGGTTTCTTACTC 319
QY      2288 TGAATTTAGATCTCCAGACCCCTTCTGGGCAAAATTTAAATTAAGGCAACAAATATAC 2347
Db      318 TGAATTTAGATCTCCAGACCCCTTCTGGGCAAAATTTAAATTAAGGCAACAAATATAC 259

```

QY 2348 CTTCCATGAGACACACAGACTTTTGAAGCAAGACATGACTGCTGAATTGAGGCC 2407
|
|
|
Db 258 CTTCCATGAGACACACAGACTTTTGAAGCAAGACATGACTGCTGAATTGAGGCC 199
|
|
|
QY 2408 TTGAGGAATGAAGCTTTGAAGAAAAGATACCTTTGTTCCAGCCCCCTTCCACACTCT 2467
|
|
|
Db 198 TTGAGGAATGAAGCTTTGAAGAAAAGATACCTTTGTTCCAGCCCCCTTCCACACTCT 139
|
|
|
QY 2468 TCAGTGTAAACCACTGCTTCTGAGACTTGGAGCCAGCTGACTGATTAATCATGTTGT 2527
|
|
|
Db 138 TCAGTGTAAACCACTGCTTCTGAGACTTGGAGCCAGCTGACTGATTAATCATGTTGT 79
|
|
|
QY 2528 TATAGAAACTGATTTTGAAGTTGATCGTTCAAGAGATGATTAATATACATTTCT 2587
|
|
|
Db 78 TATAGAAACTGATTTTGAAGTTGATCGTTCAAGAGATGATTAATATACATTTCT 19
|
|
|

RESULT 10
CN259813 714 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600041697 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259813
VERSION CN259813.1 GI:47276227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 714)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
TRANSCRIPTOME CHARACTERIZATION ELUCIDATES SIGNALING NETWORKS THAT
CONTROL HUMAN ES CELL GROWTH AND DIFFERENTIATION
Nat. Biotechnol. 22 (6), 707-716 (2004)
CONTACT: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 714 Std Error: 0.00.
Location/Qualifiers

FEATURES
source
1..714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Query Match 26.7%; Score 690; DB 7; Length 714;
Best Local Similarity 99.7%; Pred. No. 1.3e-186;
Matches 712; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 50 CTTTCCAGCAGCAGCTTCCCTGGGAGACATCTCTTGGAGCAATATTAGACATC 109
|
|
|
Db 1 CTTTCCAGCAGCAGCTTCCCTGGGAGACATCTCTTGGAGCAATATTAGACATC 60
|
|
|
QY 110 ATTATCTGCTGAGCAATTTGACATCATTTGGTATTTTCAGGAGACACTCC 169
|
|
|
Db 61 ATTATCTGCTGAGCAATTTGACATCATTTGGTATTTTCAGGAGACACTCC 120
|
|
|
QY 170 ATCAGACTACTACTGTGCTCCTAGCTGGAAACATTGGGAGAGATGGAAATCTGAGCTGC 229
|
|
|
Db 121 ATCAGACTACTACTGTGCTCCTAGCTGGAAACATTGGGAGAGATGGAAATCTGAGCTGC 180
|
|
|

QY 230 ACTTTGAACTGACATCAAACTTTCTGATATGATATACATGCTGAGAGAGTGT 289
|
|
|
Db 181 ACTTTGAACTGACATCAAACTTTCTGATATGATATACATGCTGAGAGAGTGT 240
|
|
|
QY 290 TTAGGCTTGGTCCATGATGTTCAAGAAGCAAGATGAGCTGCGAGCAGATGAATG 349
|
|
|
Db 241 TTAGGCTTGGTCCATGATGTTCAAGAAGCAAGATGAGCTGCGAGCAGATGAATG 300
|
|
|
QY 350 TTGAGAGCCCGGACAGAGTGTTCGATATCAAGTATGTTGGCAATGCTTTGGCG 409
|
|
|
Db 301 TTGAGAGCCCGGACAGAGTGTTCGATATCAAGTATGTTGGCAATGCTTTGGCG 360
|
|
|
QY 410 CTGAAAAACGTGCAACTCAAGATGCTGGCACTTAACAAATGTATATCATCTCTAA 469
|
|
|
Db 361 CTGAAAAACGTGCAACTCAAGATGCTGGCACTTAACAAATGTATATCATCTCTAA 420
|
|
|
QY 470 GGCAGGGGGAATCTAACCTTGATATATAAATGAGACCTTCAGATGCCGAAATGAT 529
|
|
|
Db 421 GGCAGGGGGAATCTAACCTTGATATATAAATGAGACCTTCAGATGCCGAAATGAT 480
|
|
|
QY 530 GTGACTATATATGCTGAGCTCAGAGACCTTCCGTGTGAGGCTCCCGATGTTCCCCAG 589
|
|
|
Db 481 GTGACTATATATGCTGAGCTCAGAGACCTTCCGTGTGAGGCTCCCGATGTTCCCCAG 540
|
|
|
QY 590 CCACAGTGGTCTGGGATCCCAAGTTGACACAGAGCCAACTTCTCGAAAGTCTCAAT 649
|
|
|
Db 541 CCACAGTGGTCTGGGATCCCAAGTTGACACAGAGCCAACTTCTCGAAAGTCTCAAT 600
|
|
|
QY 650 ACCAGCTTTGAGCTGAACTCTGAGATGAGACCATG-AAAGTTGTCTGTGCTTACAA 708
|
|
|
Db 601 ACCAGCTTTGAGCTGAACTCTGAGATGAGACCATGAAAGTTGTCTGTGCTTACAA 660
|
|
|
QY 709 TGTTAAGATCAACAAACATATC-TCTGTATGATTTGAAAATGATCATTTGCCAAG 761
|
|
|
Db 661 TGTTAAGATCAACAAACATATCCTGTATGATTTGAAAATGATCATTTGCCAAG 714
|
|
|

RESULT 11
CN259812 698 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600177307 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259812
VERSION CN259812.1 GI:47276226
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 698)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
TRANSCRIPTOME CHARACTERIZATION ELUCIDATES SIGNALING NETWORKS THAT
CONTROL HUMAN ES CELL GROWTH AND DIFFERENTIATION
Nat. Biotechnol. 22 (6), 707-716 (2004)
CONTACT: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 698 Std Error: 0.00.
Location/Qualifiers

FEATURES
source
1..698
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in

ORIGIN feeder-free conditions"

Query Match 26.2%; Score 676.6; DB 7; Length 698;
Best Local Similarity 99.3%; Pred. No. 9.5e-183;
Matches 690; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

710 GTTACGATCAACACACATATCTCTGTATGATTAAGAAATGACATTCGCAACACAGG 769
|||
4 GTCCGATCAACACACATATCTCTGTATGATTAAGAAATGACATTCGCAACACAGG 63
770 GATATCAAGTGAACAGATTCGAGATCAAAAGCGGAGTCACTTCAAGTCTAACTCA 829
64 GATATCAAGTGAACAGATTCGAGATCAAAAGCGGAGTCACTTCAAGTCTAACTCA 123
830 AAGGCTTCTGTGTCT 889
124 AAGGCTTCTGTGTCT 183
890 CCTTACCTGATGCTAAATATATATATATATATATATATATATATATATATATAT 949
184 CCTTACCTGATGCTAAATATATATATATATATATATATATATATATATATATAT 243
950 CAACAGGATCTACAGAACTATTTTCAACACAGATATGACTTATATATATATTTTGG 1009
244 CAACAGGATCTACAGAACTATTTTCAACACAGATATGACTTATATATATTTTGG 303
1010 GGAATGATTCATATCTAGAAATCTGAGTGAAGCAACAGAGCAAAACAAAGAA 1069
304 GGAATGATTCATATCTAGAAATCTGAGTGAAGCAACAGAGCAAAACAAAGAA 363
1070 GCCAAAGCAGAAAGCTCCAAATATGAACAGATATATCTATCTTCAAAACATATTA 1129
364 GCCAAAGCAGAAAGCTCCAAATATGAACAGATATATCTATCTTCAAAACATATTA 423
1130 GTTGGGAAAT 1189
424 GTTGGGAAAT 483
1190 GTGGAACAAGTGCATCCCAATCTCAGAGACCTCCCTGCTGCACCTGGGGAG 1249
484 GTGGAACAAGTGCATCCCAATCTCAGAGACCTCCCTGCTGCACCTGGGGAG 543
1250 AGAGCAGAGATAGTGCATCTTCTGTCTGATTTTATATATATATATATATATAT 1309
544 AGAGCAGAGATAGTGCATCTTCTGTCTGATTTTATATATATATATATATATAT 603
1310 TGCTTGAGAGAGCCCTGGAAGTCTATCCAAATATTCACATCTTATATTCACAA 1369
604 TGCTTGAGAGAGCCCTGGAAGTCTATCCCAATATTCACATCTTATATTCACAA 663
1370 TTTAGCTGTAT 1403
664 TTTAGCTGTAT 698

RESULT 12
BE741325 681 bp mRNA linear EST 15-SEP-2000
LOCUS BE741325
DEFINITION 601594166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947872 5',
mRNA sequence.
ACCESSION BE741325
VERSION BE741325.1 GI:10155317
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
REFERENCE 1 (bases 1 to 681)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-rc@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNU at: image.llnl.gov
Plate: L10M810 row: d column: 17
High quality sequence stop: 677.
Location/Qualifiers

FEATURES

source

1..681
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3947872"
/tissue_type="adenocarcinoma cell line"
/lab_host="VDH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 25.7%; Score 665.8; DB 2; Length 681;
Best Local Similarity 99.6%; Pred. No. 1.2e-179;
Matches 678; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

866 AGCTGGGACATCTCTCTCTCAGCCCTTACCTGATGCTAAATATATGCTTGGCCCA 925
1 AGCTGGGACATCTCTCTCTCAGCCCTTACCTGATGCTAAATATATGCTTGGCCCA 60
926 AAAAAGCATGCAAGTCAATGTTTACACAGGATCTACAGAACTATTTTACCAACAGATA 985
61 AAAAAGCATGCAAGTCAATGTTTACACAGGATCTACAGAACTATTTTACCAACAGATA 120
986 TGACCTAGTTTATATTTCTGGGAGAAATGAATCATATCTAGAAAGTCTGGAGTGA 1045
121 TGACCTAGTTTATATTTCTGGGAGAAATGAATCATATCTAGAAAGTCTGGAGTGA 180
1046 AACAGAGCAGAAACAAAGAGAGCAGAAAGCAGAAAGCTCCATATGAACAGATATA 1105
181 AACAGAGCAGAAACAAAGAGAGCAGAAAGCAGAAAGCTCCATATGAACAGATATA 240
1106 TCTATCTTCAAGACATATTTAGAAAGTGGGAAATATATCATGTGAACATGAGAGTG 1165
241 TCTATCTTCAAGACATATTTAGAAAGTGGGAAATATATCATGTGAACATGAGAGTG 300
1166 TTTAAGAGTAT 1225
301 TTTAAGAGTAT 360
1226 CCCCTGCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTGTAAT 1285
361 CCCCTGCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTGTAAT 420
1286 TTTTAT 1345
421 TTTTAT 480
1346 TATCCACATCTTAT 1405
481 TATCCACATCTTAT 540
1406 GACTGCACTTGCAGCACTCAGGGGCGGCTGCATTTTATATATATATATATATAT 1465
541 GACTGCACTTGCAGCACTCAGGGGCGGCTGCATTTTATATATATATATATATATAT 600
1466 TTTATATATCTTCCAAAGTGCCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGA 1525

Db 601 TTTATGATGCTCCAAAGTGCCTTGGCTTCTCTCCCACTGCAATGCGAAGTTGA 660
Qy 1526 GA-AAATGATCATTAATTTTA 1545
Db 661 GACCACTGATCATTAATTTTA 681

RESULT 13
BU632767/c 700 bp mRNA linear EST 23-SEP-2002
LOCUS BU632767
DEFINITION UI-H-FEI-bdy-k-03-0-UI.s1 NCI CGAP FEI Homo sapiens cDNA clone
UI-H-FEI-bdy-k-03-0-UI 3', mRNA sequence.
ACCESSION BU632767
VERSION BU632767.1 GI:23300022
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 700)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 623-700, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source Location/Qualifiers
1..700
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FEI-bdy-k-03-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI CGAP FEI"
/note="Organ: Chondrosarcoma; Vector: pRT73-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP FEI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA,
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCTACGAC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
TAG_LIB=UI-H-FEI
TAG_SEQ=CGCTACGAC"

ORIGIN
Query Match 25.7%; Score 665; DB 5; Length 700;
Best Local Similarity 99.9%; Pred. No. 2,1e-179;
Matches 676; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1912 TCCTACCATGTAGAGAGCTCTCCCATTAACAATCCAGATCGAAGTGTCACTGTGT 1971

Db 700 TCCTACCATGTAGAGAGCTCTCCCATTAACAATCCAGATCGAAGTGTCACTGTGT 641
Qy 1972 CAGACTTAAGAAACCTGTTTGTAGTAGAAAGGGCTGGAAAGAGGGAGCCAAACA 2031
Db 640 CAGACTTAAGAAACCTGTTTGTAGTAGAAAGGGCTGGAAAGAGGGAGCCAAACA 581
Qy 2032 TCTGTCTGCTT-CTCATTATGATTTGGAAATTAAGCATTTCTGTCTGTGCTGTC 2090
Db 580 TCTGTCTGCTTCTTCATTATGATTTGGAAATTAAGCATTTCTGTCTGTGCTGTC 521
Qy 2091 CTCAGACAGAGAGCCAGAACTCTATCGGGCACCAGATTAACATCTCTCAGTAAACGAG 2150
Db 520 CTCAGACAGAGAGCCAGAACTCTATCGGGCACCAGATTAACATCTCTCAGTAAACGAG 461
Qy 2151 TTGACAAAGGCTTATGGAAATGCGTGAATGGAATTAATCTTCACTTGTGAGCTTTAAGT 2210
Db 460 TTGACAAAGGCTTATGGAAATGCGTGAATGGAATTAATCTTCACTTGTGAGCTTTAAGT 401
Qy 2211 TTCTTTCCCTTCATTCTACCCCTGCAAGCCAGATTTGTAGAGAAATGCTGAGTTCTAG 2270
Db 400 TTCTTTCCCTTCATTCTACCCCTGCAAGCCAGATTTGTAGAGAAATGCTGAGTTCTAG 341
Qy 2271 CTCAGGTTTCTTACTCTGAAATTTAGATCTCCAGACCCCTCTGGCCACAATTCAATTA 2330
Db 340 CTCAGGTTTCTTACTCTGAAATTTAGATCTCCAGACCCCTCTGGCCACAATTCAATTA 281
Qy 2331 AGGCAACAAACATATACCTTCATGATGAGACACACAGACTTTTGAAGCAAGACAATGA 2390
Db 280 AGGCAACAAACATATACCTTCATGATGAGACACACAGACTTTTGAAGCAAGACAATGA 221
Qy 2391 CTCCTGAATGAGGCTTGAAGAAATGAGCTTTGAAGAAATTAATCTTGTTCAG 2450
Db 220 CTCCTGAATGAGGCTTGAAGAAATGAGCTTTGAAGAAATTAATCTTGTTCAG 161
Qy 2451 CCCCCTTCCCACTCTGATGTTTAAACCACTGCTTCTGACCTTGGACCTGGAGCCAGGTC 2510
Db 160 CCCCCTTCCCACTCTGATGTTTAAACCACTGCTTCTGACCTTGGAGCCAGGTC 101
Qy 2511 ACTGATTTACATGTTTATAGAAACGATTTTGAAGTTCTGATCGTTCAAGAGATGA 2570
Db 100 ACTGATTTACATGTTTATAGAAACGATTTTGAAGTTCTGATCGTTCAAGAGATGA 41
Qy 2571 TTTAATATACATTTCTCT 2587
Db 40 TTTAATATACATTTCTCT 24

RESULT 14
CB241729/c 691 bp mRNA linear EST 12-FEB-2003
LOCUS CB241729
DEFINITION UI-CF-FNO-efz-p-01-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
UI-CF-FNO-efz-p-01-0-UI 3', mRNA sequence.
ACCESSION CB241729
VERSION CB241729.1 GI:28363373
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 691)
Bonaldi, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171

Email: paul-mccray@iowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..691
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-af2-p-01-0-UI"
 /issue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subcloned cDNA library derived from two normalized Human Lung epithelial cell libraries (EN1 and DU1) The library was subcloned according to according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@iowa.edu
 TAG_LIB=UI-CF-FNO
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 25.6%; Score 661; DB 6; Length 691;
 Best Local Similarity 99.9%; Pired. No. 2.9e-178;
 Matches 672; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1916 ACCATGTACAGAGCGTCCGCCATCACTACCAATCCGAAGTGTCACTGTGACG 1975
 |||||
 691 ACCATGTACAGAGCGTCCGCCATCACTACCAATCCGAAGTGTCACTGTGACG 632
 |||||
 1976 ACTAAGAAACCCCTGTTTGTAGTAAAGAGGCTGAAAGAGGAGCCAAACAATCTG 2035
 |||||
 631 ACTAAGAAACCCCTGTTTGTAGTAAAGAGGCTGAAAGAGGAGCCAAACAATCTG 572
 |||||
 2036 TCTGCTT-CTCACTATAGTCATTTGGAATTAAGCATTTCTCTTGTGCTGCTGCTCA 2094
 |||||
 571 TCTGCTTCTCACTATAGTCATTTGGAATTAAGCATTTCTCTTGTGCTGCTGCTCA 512
 |||||
 2095 GCACAGAGAGCCAGAACTCTATCGGACACCGAGATTAACATCTCTCAGTAAAGAGTTGA 2154
 |||||
 511 GCACAGAGAGCCAGAACTCTATCGGACACCGAGATTAACATCTCTCAGTAAAGAGTTGA 452
 |||||
 2155 CAAGGCTATGGAATGCGCTGATGGAATTAATCTTCAAGTTGTTGAGCTTTCTAAGTTCT 2214
 |||||
 451 CAAGGCTATGGAATGCGCTGATGGAATTAATCTTCAAGTTGTTGAGCTTTCTAAGTTCT 392
 |||||
 2215 TTCCCTTCACTTCAACCTCGAAGCCAAAGTTCTGTAAAGAAAGCTGAGTTCTTACTCA 2274
 |||||
 391 TTCCCTTCACTTCAACCTCGAAGCCAAAGTTCTGTAAAGAAAGCTGAGTTCTTACTCA 332
 |||||
 2275 GGTTCCTTACTGTGAATTTAGATCTCAGAACCTCTCTGSCCAATTCATTAAGGC 2334
 |||||
 331 GGTTCCTTACTGTGAATTTAGATCTCAGAACCTCTCTGSCCAATTCATTAAGGC 272
 |||||
 2335 AACCAACATATACCTTTCATGAAGACACACAGACTTTTGAAGCAAGCAATGCTGC 2394
 |||||
 271 AACCAACATATACCTTTCATGAAGACACACAGACTTTTGAAGCAAGCAATGCTGC 212
 |||||
 2395 TTGAATTGAGGCTTGAAGAAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCC 2454
 |||||
 211 TTGAATTGAGGCTTGAAGAAATGAAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCC 152
 |||||

QY 2455 CTTCCACACTCTTCATGTTGTTAAACCACTGCTTCTGACCTTGGAGCCAGGTGACTG 2514
 |||||
 DB 151 CTTCCACACTCTTCATGTTGTTAAACCACTGCTTCTGACCTTGGAGCCAGGTGACTG 92
 |||||
 QY 2515 TATTACATGTTGTTTAAAGAAACGATATTTTGAAGTTTCGATTCGTTCAAGAGAAATATTA 2574
 |||||
 DB 91 TATTACATGTTGTTTAAAGAAACGATATTTTGAAGTTTCGATTCGTTCAAGAGAAATATTA 32
 |||||
 QY 2575 ATATACATTTCT 2587
 |||||
 DB 31 ATATACATTTCT 19
 |||||

RESULT 15
 CA314865/c 691 bp mRNA linear EST 04-NOV-2002
 LOCUS
 DEFINITION UI-CF-FNO-af1-e-12-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
 ACCESSION CA314865
 VERSION CA314865.1 GI:24532963
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 691)
 REFERENCE Ronaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and Subtraction: two approaches to facilitate gene
 TITLE discovery
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: McCray, PB
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@iowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..691
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-af1-e-12-0-UI"
 /issue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subcloned cDNA library derived from two normalized Human Lung epithelial cell libraries (EN1 and DU1) The library was subcloned according to according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@iowa.edu
 TAG_LIB=UI-CF-FNO
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

```
Query Match      25.5%; Score 660; DB 6; Length 691;
Best Local Similarity 99.7%; Pred. No. 5.7e-178;
Matches 671; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1916 ACCATGTACAGAGACGTCTCCCATTTACAACTACCAATCCGAGTGTCAACTGTGTGACAG 1975
    |||||
DB 691 ACCATGTACAGAGACGTCTCCCATTTACAACTACCAATCCGAGTGTCAACTGTGTGACAG 632
    |||||
QY 1976 ACTAGAAACCCCTGGTTTTGTAGTAAAGGCGCTGGAAAGGGAGCCCAACAAATCTG 2035
    |||||
DB 631 ACTAGAAACCCCTGGTTTTGTAGTAAAGGCGCTGGAAAGGGAGCCCAACAAATCTG 572
    |||||
QY 2036 TCTGCTT-CTGCATTTAGTCAATTTGCAAAATTAAGCATTTCTCTCTTTGGCTGTGCTCA 2094
    |||||
DB 571 TCTGCTTCTTCACTTAGTCAATTTGCAAAATTAAGCATTTCTCTCTTTGGCTGTGCTCA 512
    |||||
QY 2095 GCACAGAGAGCCAGAACTCTATCGGGCACAGATTAACATCTCTCAGTGAACAGAGTTGA 2154
    |||||
DB 511 GCACAGAGAGCCAGAACTCTATCGGGCACAGATTAACATCTCTCAGTGAACAGAGTTGA 452
    |||||
QY 2155 CAAGGCTTATGGGAAATGCGCTGATGAGTTATCTTCAGCTTGTGAGCTTTCTAAGTTTCT 2214
    |||||
DB 451 CAAGGCTTATGGGAAATGCGCTGATGAGTTATCTTCAGCTTGTGAGCTTTCTAAGTTTCT 392
    |||||
QY 2215 TTCCCTTCATTTCACTCCCTGCAAGCCAAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCA 2274
    |||||
DB 391 TTCCCTTCATTTCACTCCCTGCAAGCCAAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCA 332
    |||||
QY 2275 GGTTTTCTTACTCTGAATTTAGATCTCCAGACCCCTTCTGGCCAAATTCMAATTAAGGC 2334
    |||||
DB 331 GGTTTTCTTACTCTGAATTTAGATCTCCAGACCCCTTCTGGCCAAATTCMAATTAAGGC 272
    |||||
QY 2335 AACAAACATATTAACCTTCCATGAGACACACAGACTTTTGAAGCAAGACATGACTGC 2394
    |||||
DB 271 AACAAACATATTAACCTTCCATGAGACACACAGACTTTTGAAGCAAGACATGACTGC 212
    |||||
QY 2395 TTGAATTGAGGCTTGAAGAAATGAAGCTTGAAGAAATGAATCTTTGTTCCAGCCCC 2454
    |||||
DB 211 TTGAATTGAGGCTTGAAGAAATGAAGCTTGAAGAAATGAATCTTTGTTCCAGCCCC 152
    |||||
QY 2455 CTTCCCACTCTTCATGTGTTAAACACTGCTTCTGAGCCTTGAAGCCACGGTGACTG 2514
    |||||
DB 151 CTTCCCACTCTTCATGTGTTAAACACTGCTTCTGAGCCTTGAAGCCACGGTGACTG 92
    |||||
QY 2515 TATTACATGTGTATAGAAACATGATTTTGAAGTTCTGATCGTTCAAGAAATGATTTAA 2574
    |||||
DB 91 TATTACATGTGTATAGAAACATGATTTTGAAGTTCTGATCGTTCAAGAAATGATTTAA 32
    |||||
QY 2575 ATATACATTTCTT 2587
    |||||
DB 31 ATATACATTTCTT 19
    |||||
```

Search completed: May 31, 2005, 00:10:46
Job time : 10066.7 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 07:16:54 ; Search time 2657.37 Seconds

(without alignments)
10502.938 Million cell updates/sec

Title: US-09-763-978B-10

Sequence: 1 ttcaagactatagagc.....ttcacctgacatagc 576

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_hg: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_strs: 12: gb_sy: 13: gb_un: 14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	100.0	576	6	BD235839 A novel m
2	576	100.0	1567	6	BD264689 Compositi
3	576	100.0	1567	6	AR238092 Sequence
4	576	100.0	1567	6	AR257633 Sequence
5	576	100.0	1567	6	AR283679 Sequence
6	576	100.0	1567	6	AR443353 Sequence
7	576	100.0	1567	6	AR478431 Sequence
8	576	100.0	1567	6	AX366307 Sequence
9	576	100.0	1965	6	CQ41191 Sequence
10	576	100.0	2587	6	BD235830 A novel m
11	576	100.0	2603	6	AX403048 Sequence
12	576	100.0	2627	6	BD265002 Compositi
13	576	100.0	2627	6	AR238405 Sequence
14	576	100.0	2627	6	AR478744 Sequence
15	576	100.0	2627	6	AX156350 Sequence
16	576	100.0	2627	6	AX366624 Sequence
17	574.4	99.7	171595	9	AL391476 Human DNA
18	572.8	99.4	2671	9	BSM808167 Homo sapi
19	550.8	95.6	2626	6	AX375860 Sequence

20	549	95.3	595	6	CQ393186	CQ393186 Sequence
21	549	95.3	595	6	CQ39576	CQ39576 Sequence
22	549	95.3	643	6	CQ405961	CQ405961 Sequence
23	499.8	86.8	1658	6	CQ875680	CQ875680 Sequence
24	499.8	86.8	1658	6	AR252569	AR252569 Sequence
25	499.8	86.8	1658	6	AX092328	AX092328 Sequence
26	499.8	86.8	1658	6	AX376150	AX376150 Sequence
27	499.8	86.8	1658	6	AX395215	AX395215 Sequence
28	499.8	86.8	1658	6	AX403403	AX403403 Sequence
29	499.8	86.8	1658	6	AX468680	AX468680 Sequence
30	499.8	86.8	1658	6	AX58352	AX58352 Homo sapi
31	492	85.4	638	6	AX197664	AX197664 Sequence
32	491	85.4	625	6	AX208278	AX208278 Sequence
33	452	78.5	541	6	BD264643	BD264643 Compositi
34	452	78.5	541	6	AR238046	AR238046 Sequence
35	452	78.5	541	6	AR257587	AR257587 Sequence
36	452	78.5	541	6	AR283633	AR283633 Sequence
37	452	78.5	541	6	AR443307	AR443307 Sequence
38	452	78.5	541	6	AR478385	AR478385 Sequence
39	452	78.5	541	6	AX366261	AX366261 Sequence
40	449.2	78.0	9464	9	HSJ1025A1	AL080312 Human DNA
41	358.6	62.3	714	6	AX197570	AX197570 Sequence
42	358.6	62.3	714	6	AX208186	AX208186 Sequence
43	320	55.6	335	6	AX914817	AX914817 Sequence
44	320	55.6	335	6	BD050350	BD050350 Sequence
45	306.4	53.2	311	6	AX375857	AX375857 Sequence

ALIGNMENTS

BD235839 576 bp DNA linear PAT 17-JUL-2003
A novel method of diagnosing, monitoring, staging, imaging and
treating various cancers.

ACCESSION BD235839.1 GI:33045609
VERSION BD235839
KEYWORDS JP 2002523760-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 576)
AUTHORS Salceda,S., Sun,Y., Recipon,H. and Caffery,R.
TITLE A novel method of diagnosing, monitoring, staging, imaging and
treating various cancers
JOURNAL Patent: JP 2002523760-A 10 30-JUL-2002;
DIADEXUS INC

COMMENT OS Homo sapiens (human)
PN JP 2002523760-A/10
PD 30-JUL-2002
PF 01-SEP-1999 JP 2000567741
PR 02-SEP-1998 US 60/098880
PT SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFERY PC
G01N33/574, A61K39/395, A61K39/395, A61K39/395, A61K39/395 PC
PC A61K51/00, C07K16/32, C12N15/09, C12Q1/68, C12N15/00, A61K49/02 CC
A novel method of diagnosing, monitoring,
staging, imaging and
treating
CC various cancers
FH Key
FT source
Location/Qualifiers
1. 576
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source 1. 576
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 576;

C12N1/21, C12N5/06, C12N5/10, C12Q1/68, G01N33/53, G01N33/53, G01N33/566,

Compositions and methods for the therapy and diagnosis of

ovarian cancer	Location/Qualifiers
FH Key	
1	1557

FT	source	1..1567	/organism='Homo sapiens (human)'. location/analysis
FT			

Location/Qualifiers
1. .1567
/Organism="Homo sapiens"

```
/organism="Homo sapiens"  
/mol_type="genomic DNA"  
/db_xref="taxon:9606"
```

```
/db_xref="taxon:9606"
```

100.0%; Score 576; DB 6; Length 1567;
100.0%; Pred. No. 1.9e-151;

576; Conservativity 0; Mismatches 0; Indels 0; Gaps

1 TTCAAGACATATTAGAAGTTCGAAATAATTATGTCGAACTAGACAAGTGTGTTAAG

91 TTCAAAGACATATTAGAAGTTGGAAATAATTATGTGAACTAGACAAGTGTTAAG

61 GTGATAAGTAAATGCACGTGAGACAGTGCATCCCAATCTCAGGACCTCCCCCTT

51 GTGATTAAGTAAATGCACGCTGGAGACAAGTGTCATCCCAATCTCAGGACCTCCCT

21 CCTGTCACCTGGGAGTGAGAGGACAGGATAGTCATGTCCTTGTCTCTGAATTTTAA

CTGTCACTGGGAGTGAGAGGACAGGATAGTCATGTTCTTGTCTCGAATTTTAA

TTATATGCGCTGATGTGCTCTGAGGAAGCCCCCTGGAAGTCTATCCCAACATATCC

341 CATCTATATATTCACCAATTTAAGCTGTATGTATGCCCTAAGAGCGCTGCTAATTGACTG
371 TTAATATGCGCTGTATATGTTGCTCTGTAGGAGAGCCCTCTGAAAGTCTATATCCCMACATATCC

331 CATCTATATTCACCAATTAAAGCTGTAGTATGTACCCCTAAGAGCGTCCTAATTGACTGCTG
241 CATCTATATTCACCAATTAAAGCTGTAGTATGTACCCCTAAGAGCGTCCTAATTGACTGCTG

301 CACTTCGCACTCAGGGGCGGCTGCATTTTAGTAATGGGCAAAATGATTCACTTTTATT
331 CACTTAATATCCACAAATTAAGCGTAGAGTATGATCCCTTAAGAGCGCTCCTAAATGACCT

91 CACTTCGCAACTCAGGGGCGGCTGCATTTTAAAGTATGGTCAAATGATTCACCTTTTATT

ATGCTTCCAAAGGTGCTTGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA

451 ATGCTTCCAAAGGTGCCTTGCTCTCTTCCCACTGACAAATGCCAAGTGAGAAAA

421 TGATCATATTTAGCATAACAGAGCAGTCGGCACAACGATTTATAATAAAGTGA

511 TGATCATATTTTAGCATAACAGAGCAGTCGGGCAACCGATTTTATAAATAAACTGA

481 CACCCTCTTTTAAACAACAATGCGGTTTATTCTCAGATGATGTTTCATCCGTGAA

571 CACCTTCTTTAAACAACAATGCGGGTTATTCTCAGATGATGTTCAATCCGTGAA

541 GGTCAGGGAAGACCTTCACCTTGACTATATGCG 576

531 GGTCCAGGAGACCTTACCTTGACTATATGGC 666

AR238092 1567 bp DNA linear PAT 20-DE

Sequence 74 from patent US 6468546.
AR238092

AR238092.1 GI:27283056

Unknown.
Unknown.

Unclassified.
1 (bases 1 to 1567)

Mitcham, J.L., King, G.E. and Algate, P.A.
Compositions and methods for therapy and diagnosis of ovarian

JOURNAL Patent: US 6468546-A 74 22-OCT-2002;
FEATURES Location/Qualifiers
Source 1..1567
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No.1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTAGAGA 60
Db TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTAGAGA 150
Qy 61 GTGATTAAGTAAATGACAGTGGAGACAAGTGCATCCCAAGTCTCAGGGACCTCCCTG 120
Db GTGATTAAGTAAATGACAGTGGAGACAAGTGCATCCCAAGTCTCAGGGACCTCCCTG 210
Qy 121 CCTGTCACTGGGAGAGAGAGACAGATATGTCATGTTCTTTGTCTCTGAATTTTAA 180
Db CCTGTCACTGGGAGAGAGAGACAGATATGTCATGTTCTTTGTCTCTGAATTTTAA 270
Qy 211 CCTGTCACTGGGAGAGAGAGACAGATATGTCATGTTCTTTGTCTCTGAATTTTAA 270
Db TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCCA 240
Qy 181 TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCCA 240
Db TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCCA 330
Qy 241 CATCTTATATTCACAAATTAAGCTGTATATGTAACCTTAAGACGCTGAATTTGACTGC 300
Db CATCTTATATTCACAAATTAAGCTGTATATGTAACCTTAAGACGCTGAATTTGACTGC 390
Qy 331 CATCTTATATTCACAAATTAAGCTGTATATGTAACCTTAAGACGCTGAATTTGACTGC 390
Db 301 CACTTGGCACTCAGGGGGCGGCTGCATTTTAATATGATGATTAATCACTTTTATG 360
Qy 391 CACTTGGCACTCAGGGGGCGGCTGCATTTTAATATGATGATTAATCACTTTTATG 450
Db 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Qy 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 510
Db 421 TGAATCATATTTTAAAGATTAACAGAGAGATCGGCGACACCGATTTTAATAATACTGAG 480
Qy 511 TGAATCATATTTTAAAGATTAACAGAGAGATCGGCGACACCGATTTTAATAATACTGAG 570
Db 481 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 540
Qy 571 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 630
Db 541 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAGC 576
Qy 631 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAGC 666

RESULT 4
LOCUS AR257633 1567 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 74 from patent US 6468931.
ACCESSION AR257633
VERSION AR257633.1 GI:27307708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLE Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6468931-A 74 03-DEC-2002;
FEATURES Location/Qualifiers
Source 1..1567
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No.1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTAGAGA 60
Db TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTAGAGA 150
Qy 61 GTGATTAAGTAAATGACAGTGGAGACAAGTGCATCCCAAGTCTCAGGGACCTCCCTG 120
Db GTGATTAAGTAAATGACAGTGGAGACAAGTGCATCCCAAGTCTCAGGGACCTCCCTG 210
Qy 121 CCTGTCACTGGGAGAGAGAGACAGATATGTCATGTTCTTTGTCTCTGAATTTTAA 180
Db CCTGTCACTGGGAGAGAGAGACAGATATGTCATGTTCTTTGTCTCTGAATTTTAA 270
Qy 211 CCTGTCACTGGGAGAGAGAGACAGATATGTCATGTTCTTTGTCTCTGAATTTTAA 270
Db TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCCA 240
Qy 181 TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCCA 240
Db TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCCA 330
Qy 241 CATCTTATATTCACAAATTAAGCTGTATATGTAACCTTAAGACGCTGAATTTGACTGC 300
Db CATCTTATATTCACAAATTAAGCTGTATATGTAACCTTAAGACGCTGAATTTGACTGC 390
Qy 331 CATCTTATATTCACAAATTAAGCTGTATATGTAACCTTAAGACGCTGAATTTGACTGC 390
Db 301 CACTTGGCACTCAGGGGGCGGCTGCATTTTAATATGATGATTAATCACTTTTATG 360
Qy 391 CACTTGGCACTCAGGGGGCGGCTGCATTTTAATATGATGATTAATCACTTTTATG 450
Db 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Qy 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 510
Db 421 TGAATCATATTTTAAAGATTAACAGAGAGATCGGCGACACCGATTTTAATAATACTGAG 480
Qy 511 TGAATCATATTTTAAAGATTAACAGAGAGATCGGCGACACCGATTTTAATAATACTGAG 570
Db 481 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 540
Qy 571 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGATGATGTTCACTCCGTAAT 630
Db 541 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAGC 576
Qy 631 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAGC 666

RESULT 5
LOCUS AR283679 1567 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 74 from patent US 6528253.
ACCESSION AR283679
VERSION AR283679.1 GI:29720576
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLE Compositions and methods for diagnosis of ovarian cancer
JOURNAL Patent: US 6528253-A 74 04-MAR-2003;
FEATURES Location/Qualifiers
Source 1..1567
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No.1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTAGAGA 60
Db 91 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAACCTAGACAAGTGTAGAGA 150

QY 61 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCGAGATCTGAGGAGCCTCCCTG 120
|
|
|
Db 151 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCGAGATCTGAGGAGCCTCCCTG 210
|
|
|
QY 121 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTCTCTGTAATTTTNG 180
|
|
|
Db 211 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTCTCTGTAATTTTNG 270
|
|
|
QY 181 TTAATATGCTGTAAATGTTGCTCTGAGGAAAGCCCTGGAAGCTTAATCCCAATATCCA 240
|
|
|
Db 271 TTAATATGCTGTAAATGTTGCTCTGAGGAAAGCCCTGGAAGCTTAATCCCAATATCCA 330
|
|
|
QY 241 CATCTTAATATCCCAAAATTAAGCTGTATGTAATGTAATGTAATGTAATGTAATGTAATG 300
|
|
|
Db 331 CATCTTAATATCCCAAAATTAAGCTGTATGTAATGTAATGTAATGTAATGTAATGTAATG 390
|
|
|
QY 301 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGGTCAATGATTCACCTTTTATG 360
|
|
|
Db 391 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGGTCAATGATTCACCTTTTATG 450
|
|
|
QY 361 ATGCTTCCAAAGTGTGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 420
|
|
|
Db 451 ATGCTTCCAAAGTGTGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 510
|
|
|
QY 421 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAATCTGAG 480
|
|
|
Db 511 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAATCTGAG 570
|
|
|
QY 481 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 540
|
|
|
Db 571 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 630
|
|
|
QY 541 GGTCCAGGAGAGACCTTTACCTTACCTTAATATGCG 576
|
|
|
Db 631 GGTCCAGGAGAGACCTTTACCTTACCTTAATATGCG 666
|
|
|
RESULT 6
AR443353 1567 bp DNA linear PAT 20-FEB-2004
LOCUS AR443353
DEFINITION Sequence 74 from patent US 6670463.
ACCESSION AR443353
VERSION AR443353.1 GI:42671132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Prudakis,T.N. and King,G.E.
TITLE Compositions and methods for therapy of ovarian cancer
JOURNAL Patent: US 6670463-A 74 30-DEC-2003;
FEATURES
source Location/Qualifiers
1..1567
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTAAAGA 60
|
|
|
Db 91 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTAAAGA 150
|
|
|
QY 61 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCGAGATCTGAGGAGCCTCCCTG 120
|
|
|
Db 151 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCGAGATCTGAGGAGCCTCCCTG 210
|
|
|
QY 121 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTCTCTGTAATTTTNG 180
|
|
|
Db 211 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTCTCTGTAATTTTNG 270
|
|
|

QY 181 TTAATATGCTGTAAATGTTGCTCTGAGGAAAGCCCTGGAAGCTTAATCCCAATATCCA 240
|
|
|
Db 271 TTAATATGCTGTAAATGTTGCTCTGAGGAAAGCCCTGGAAGCTTAATCCCAATATCCA 330
|
|
|
QY 241 CATCTTAATATCCCAAAATTAAGCTGTATGTAATGTAATGTAATGTAATGTAATGTAATG 300
|
|
|
Db 331 CATCTTAATATCCCAAAATTAAGCTGTATGTAATGTAATGTAATGTAATGTAATGTAATG 390
|
|
|
QY 301 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGGTCAATGATTCACCTTTTATG 360
|
|
|
Db 391 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGGTCAATGATTCACCTTTTATG 450
|
|
|
QY 361 ATGCTTCCAAAGTGTGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 420
|
|
|
Db 451 ATGCTTCCAAAGTGTGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 510
|
|
|
QY 421 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAATCTGAG 480
|
|
|
Db 511 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAATCTGAG 570
|
|
|
QY 481 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 540
|
|
|
Db 571 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 630
|
|
|
QY 541 GGTCCAGGAGAGACCTTTACCTTACCTTAATATGCG 576
|
|
|
Db 631 GGTCCAGGAGAGACCTTTACCTTACCTTAATATGCG 666
|
|
|
RESULT 7
AR478431 1567 bp DNA linear PAT 14-MAY-2004
LOCUS AR478431
DEFINITION Sequence 74 from patent US 6699664.
ACCESSION AR478431
VERSION AR478431.1 GI:47237083
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W.,
Fanger,G.R., Reed,S.G., Vedvick,T.S. and Carter,D.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6699664-A 74 02-MAR-2004;
FEATURES
source Location/Qualifiers
1..1567
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTAAAGA 60
|
|
|
Db 91 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTAAGTGAACAGAGTGTAAAGA 150
|
|
|
QY 61 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCGAGATCTGAGGAGCCTCCCTG 120
|
|
|
Db 151 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCGAGATCTGAGGAGCCTCCCTG 210
|
|
|
QY 121 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTCTCTGTAATTTTNG 180
|
|
|
Db 211 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTCTCTGTAATTTTNG 270
|
|
|
QY 181 TTAATATGCTGTAAATGTTGCTCTGAGGAAAGCCCTGGAAGCTTAATCCCAATATCCA 240
|
|
|
Db 271 TTAATATGCTGTAAATGTTGCTCTGAGGAAAGCCCTGGAAGCTTAATCCCAATATCCA 330
|
|
|
QY 241 CATCTTAATATCCCAAAATTAAGCTGTATGTAATGTAATGTAATGTAATGTAATGTAATG 300
|
|
|

Db 331 CATCTTATATTCACAAATTAGCTGTATGATACCTTAAGAGCTGTAATTTGATGTC 390
Qy 301 CACTTGCAACTCAGGGGGCGGCTGCATTTTATGATAGGCTCAATGATTCACCTTTTATG 360
Db 391 CACTTGCAACTCAGGGGGCGGCTGCATTTTATGATAGGCTCAATGATTCACCTTTTATG 450
Qy 361 ATGCTTCCAAAGGAGCTTGGCTTCTCTCCCACTGACAAATGCCAAGTGTGAGAAAA 420
Db 451 ATGCTTCCAAAGGAGCTTGGCTTCTCTCCCACTGACAAATGCCAAGTGTGAGAAAA 510
Qy 421 TGATCATATTTTATGACATAAACAAGAGAGTGGGAGACCGATTTTATTAATAAATGAG 480
Db 511 TGATCATATTTTATGACATAAACAAGAGAGTGGGAGACCGATTTTATTAATAAATGAG 570
Qy 481 CACCTTCTTTTAAACAACAATGGGCTTTATTTCTCAGATGATGTCATCCGTAAT 540
Db 571 CACCTTCTTTTAAACAACAATGGGCTTTATTTCTCAGATGATGTCATCCGTAAT 630
Qy 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 576
Db 631 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 666

RESULT 8
AX366307 1567 bp DNA linear PAT 15-FEB-2002
LOCUS Sequence 74 from Patent WO0206317.
DEFINITION AX366307
ACCESSION AX366307
VERSION AX366307.1 GI:18697733
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Mitcham, J.L., King, G.E., Algate, P.A., Fling, S.P., Retter, M.W.,
Fanger, G.R., Reed, S.G., Vedvick, T.S., Carter, D., Hill, P. and
Albone, E.
Compositions and methods for the therapy and diagnosis of ovarian
cancer
Patent: WO 0206317-A 74 24-JAN-2002;
JOURNAL CORIXA CORPORATION (US)
FEATURES
source 1..1567
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAAAGACATATTAGAAAGTTGGGAAATATATTCATGTGAACGTGACAAAGTGTTAAGA 60
Db 91 TTCAAAAGACATATTAGAAAGTTGGGAAATATATTCATGTGAACGTGACAAAGTGTTAAGA 150
Qy 61 GTGATAAGTAAATATGACGCTGAGAGACAGTGCATCCCAAGATCTCAGGAGACCTCCCTG 120
Db 151 GTGATAAGTAAATATGACGCTGAGAGACAGTGCATCCCAAGATCTCAGGAGACCTCCCTG 210
Qy 121 CCTGTCACTGGGAGTGAAGAGACAGATATGTCATGTTCTTGTCTCTGAAATTTTATG 180
Db 211 CCTGTCACTGGGAGTGAAGAGACAGATATGTCATGTTCTTGTCTCTGAAATTTTATG 270
Qy 181 TTATATGTGCTGTATATGTTCTCTGAGAGAGCCCTGGAAGTCTATCCCAATATATCA 240
Db 271 TTATATGTGCTGTATATGTTCTCTGAGAGAGCCCTGGAAGTCTATCCCAATATATCA 330
Qy 241 CATCTTATATTCACAAATTAAGCTGTATGATACCTTAAGAGCTGCTAATTTGATGTC 300
Db 331 CATCTTATATTCACAAATTAAGCTGTATGATACCTTAAGAGCTGCTAATTTGATGTC 390

Qy 301 CACTTGCAACTCAGGGGGCGGCTGCATTTTATGATAGGCTCAATGATTCACCTTTTATG 360
Db 391 CACTTGCAACTCAGGGGGCGGCTGCATTTTATGATAGGCTCAATGATTCACCTTTTATG 450
Qy 361 ATGCTTCCAAAGGAGCTTGGCTTCTCTCCCACTGACAAATGCCAAGTGTGAGAAAA 420
Db 451 ATGCTTCCAAAGGAGCTTGGCTTCTCTCCCACTGACAAATGCCAAGTGTGAGAAAA 510
Qy 421 TGATCATATTTTATGACATAAACAAGAGAGTGGGAGACCGATTTTATTAATAAATGAG 480
Db 511 TGATCATATTTTATGACATAAACAAGAGAGTGGGAGACCGATTTTATTAATAAATGAG 570
Qy 481 CACCTTCTTTTAAACAACAATGGGCTTTATTTCTCAGATGATGTCATCCGTAAT 540
Db 571 CACCTTCTTTTAAACAACAATGGGCTTTATTTCTCAGATGATGTCATCCGTAAT 630
Qy 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 576
Db 631 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 666

RESULT 9
CO412191 1965 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 19262 from Patent WO0170979.
DEFINITION CO412191
ACCESSION CO412191
VERSION CO412191.1 GI:41319972
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 19262 27-SEP-2001;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
FEATURES
source 1..1965
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 576; DB 6; Length 1965;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAAAGACATATTAGAAAGTTGGGAAATATATTCATGTGAACGTGACAAAGTGTTAAGA 60
Db 1130 TTCAAAAGACATATTAGAAAGTTGGGAAATATATTCATGTGAACGTGACAAAGTGTTAAGA 1189
Qy 61 GTGATAAGTAAATATGACGCTGAGAGACAGTGCATCCCAAGATCTCAGGAGACCTCCCTG 120
Db 1190 GTGATAAGTAAATATGACGCTGAGAGACAGTGCATCCCAAGATCTCAGGAGACCTCCCTG 1249
Qy 121 CCTGTCACTGGGAGTGAAGAGACAGATATGTCATGTTCTTGTCTCTGAAATTTTATG 180
Db 1250 CCTGTCACTGGGAGTGAAGAGACAGATATGTCATGTTCTTGTCTCTGAAATTTTATG 1309
Qy 181 TTATATGTGCTGTATATGTTCTCTGAGAGAGCCCTGGAAGTCTATCCCAATATATCA 240
Db 1310 TTATATGTGCTGTATATGTTCTCTGAGAGAGCCCTGGAAGTCTATCCCAATATATCA 1369
Qy 241 CATCTTATATTCACAAATTAAGCTGTATGATACCTTAAGAGCTGCTAATTTGATGTC 300
Db 1370 CATCTTATATTCACAAATTAAGCTGTATGATACCTTAAGAGCTGCTAATTTGATGTC 1429
Qy 301 CACTTGCAACTCAGGGGGCGGCTGCATTTTATGATAGGCTCAATGATTCACCTTTTATG 360
Db 1430 CACTTGCAACTCAGGGGGCGGCTGCATTTTATGATAGGCTCAATGATTCACCTTTTATG 1489

QY 361 ATGCTTCCAAAGTGGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 420
DB 1490 ATGCTTCCAAAGTGGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 1549
QY 421 TGATCATTAATTTTACATTAACAGAGAGTGGCGACACCGATTATTAATAACTGAG 480
DB 1550 TGATCATTAATTTTACATTAACAGAGAGTGGCGACACCGATTATTAATAACTGAG 1609
QY 481 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTTCATCCGTAAT 540
DB 1610 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTTCATCCGTAAT 1669
QY 541 GGTCCAGGAGAGACCTTTACCTTGACTATATGCG 576
DB 1670 GGTCCAGGAGAGACCTTTACCTTGACTATATGCG 1705

RESULT 10
BD235830 2587 bp DNA linear PAT 17-JUL-2003
LOCUS A novel method of diagnosing, monitoring, staging, imaging and
DERIVATION creating various cancers.
ACCESSION BD235830
VERSION BD235830.1 GI:33045600
KEYWORDS JP 2002523760-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Salceda,S., Sun,Y., Recipon,H. and Cafferey,R.
AUTHORS A novel method of diagnosing, monitoring, staging, imaging and
TITLE treating various cancers
JOURNAL Patent: JP 2002523760-A 1 30-JUL-2002;
DIABEXUS INC
COMMENT OS Homo sapiens (human)
PN JP 2002523760-A/1
PD 30-JUL-2002
PF 01-SEP-1999 JP 2000567741
PR 02-SEP-1998 US 60/098880
PT SUSANA SALCEDA,YONGMING SUN,HERVE RECIPON,ROBERT CAFFEREY PC
G01N33/574,A61K39/395,A61K39/395,A61K39/395 PC
A61K49/00,A61K49/00,
PC A61K51/00,C07K16/32,C12N15/09,C12Q1/68,C12N15/00,A61K49/02 CC
A novel method of diagnosing, monitoring,
staging, imaging and
CC creating
various cancers
FH Key Location/Qualifiers
FT source 1..2587 /organism='Homo sapiens (human)'.
FT Location/Qualifiers
1..2587
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 2587;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATATTGAAGTTGGAAATTAATTCATGTGACATGACAGAGTGTGTTAAGA 60
DB 1112 TTCAAAGACATATTGAAGTTGGAAATTAATTCATGTGACATGACAGAGTGTGTTAAGA 1171
QY 61 GTGATAGTAAATGACGCTGAGACAGATGATCCCAAGATCTCAGGAGCTCCCTCG 120
DB 1172 GTGATAGTAAATGACGCTGAGACAGATGATCCCAAGATCTCAGGAGCTCCCTCG 1231
QY 121 CCTGTACCTGGGAGTGAAGACAGATGATGATGTTCTTGTCTGTGAATTTTAA 180

DB 1232 CCTGTACCTGGGAGTGAAGACAGATGATGATGTTCTTGTCTGTGAATTTTAA 1291
QY 181 TTATATGCTGTATATGTTGCTGTAGAGAGCCCTGGAAGTCTATCCCAATATCA 240
DB 1292 TTATATGCTGTATATGTTGCTGTAGAGAGCCCTGGAAGTCTATCCCAATATCA 1351
QY 241 CATCTTAATTTTCACAAAATTAAGCTGTATGATGATACCTTAATTTGACTGCG 300
DB 1352 CATCTTAATTTTCACAAAATTAAGCTGTATGATGATACCTTAATTTGACTGCG 1411
QY 301 CACTTGGACCTCAGAGGCGGCTGATTTTGTATAGGTCAAAATGATCACTTTTAA 360
DB 1412 CACTTGGACCTCAGAGGCGGCTGATTTTGTATAGGTCAAAATGATCACTTTTAA 1471
QY 361 ATGCTTCCAAAGTGGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 420
DB 1472 ATGCTTCCAAAGTGGCTTGGCTTCTTCCCACTGACAAATGCAAGTTGAGAAAA 1531
QY 421 TGATCATTAATTTTACATTAACAGAGAGTGGCGACACCGATTATTAATAACTGAG 480
DB 1532 TGATCATTAATTTTACATTAACAGAGAGTGGCGACACCGATTATTAATAACTGAG 1591
QY 481 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTTCATCCGTAAT 540
DB 1592 CACCTTCTTTTAAACAAATGCGGGTTTATTTCTGAGATGATGTTTCATCCGTAAT 1651
QY 541 GGTCCAGGAGAGACCTTTACCTTGACTATATGCG 576
DB 1652 GGTCCAGGAGAGACCTTTACCTTGACTATATGCG 1687

RESULT 11
AX403048 2603 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 1 from Patent WO0202624.
DERIVATION AX403048
ACCESSION AX403048
VERSION AX403048.1 GI:21388028
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Fox,G., Sullivan,J.K. and Fang,M.
AUTHORS B7-like molecules and uses thereof
TITLE Patent: WO 0202624-A 1 10-JAN-2002;
JOURNAL Amgen, Inc. (US)

FEATURES
source Location/Qualifiers
1..2603
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
53..901
/note='unamed protein product'
/codon_start=1
/protein_id='CAD33698.1'
/db_xref='GI:21388029'
/translation='MASHGQLFMSIISIIIIILAGAILIIGFISGRHSITVTVAS
AGNIGEDGILSCTPERDILKSDIVLQWKEGVLAGHFEKSGKDLSEODEFRGRTA
VPADQVYGNASLRKNQVLDADAGYKCIYITSGKGNANLEYKGAFSMPVVDYN
ASSETLRKAPRFPQPTVMAASVDQGANSEVSNTPELANSEVNTKQVSVLYNVT
INNTYSCEIENDIAKATGDIVTSEIRKSHLOLNSKASLCVSPFALISWALLPLS
PYLMK'

CDS
1..2603
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
53..901
/note='unamed protein product'

ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 2603;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATATTGAAGTTGGAAATTAATTCATGTGACATGACAGAGTGTGTTAAGA 60
DB 1103 TTCAAAGACATATTGAAGTTGGAAATTAATTCATGTGACATGACAGAGTGTGTTAAGA 1162

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
BD265002	Compositions and methods for the therapy and diagnosis of ovarian cancer.	BD265002	BD265002.1 GI:33074770	JP 2002532093-A/387.	Homo sapiens (human)	Mammalia; Eutheria; Primates; Carnivora; Hominiidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominiidae; Homo.	1 (bases 1 to 2627)	Michan J L., King G.E., Algate, P.A. and Frudakis, T.N. Compositions and methods for the therapy and diagnosis of ovarian Patent: JP 2002532093-A 387 02-OCT-2002;
CORIXA CORP									
OS	Homo sapiens (human)								
PN	JP 2002532093-A/387								
PD	02-OCT-2002								
PF	17-DEC-1999	JP 2000588356							
PR	17-DEC-1998	US 09/215681, 17-DEC-1998	US 09/216003	FR					
23-JUN-1999	US 09/338933, 24-SEP-1999	US 09/404879	PI						
JENNIFER L MITCHAM, GORDON E KING, PAUL A ALGATE, TONY N FRUDAKIS									
PC	CLN1S/09, A6IK31/7115, A6IK35/14, A6IK35/16, A6IK39/00, A6IK39/395, PC								
A6IK39/395,									
PC	A6IK48/00, A6IP35/00, A6IP37/04, C07K14/82, C07K19/00, CLN1/15, PC								
CLN1/19,									
PC	CLN1/21, CLN25/06, CLN25/10, CLN2Q1/68, GOIN33/53, GOIN33/53, GOIN33/								
566,									
PC	GOIN33/574, GOIN33/577, CLN1S/00, CLN25/00, CLN25/00 CC								
Compositions and methods for the therapy and diagnosis of CC									
Ovarian Cancer									
FH	Key	Location/Qualifiers							
FT	source	I..2627							

FEATURES	FT	/organism='Homo sapiens (human)'	
source	1..2627	Location/Qualifiers	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
ORIGIN			
Query Match	100.0%; Score 576; DB 6; Length 2627;		
Best Local Similarity	100.0%; Pred. No. 1,9e-151;		
Matches 576; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	TTCAAAGCATATTAGAAAGTTGGAAAAATAATTCATGTGAACATAGACAGTGTGTAAAGA	60
DB	1133	TTCAAAGCATATTAGAAAGTTGGAAAAATAATTCATGTGAACATAGACAGTGTGTAAAGA	11922
QY	61	GTCATTAAGTAAATAGCAGCTGGAGACAAGTGCATCCCAATCTCAGAGACCTCCCTG	120
DB	1193	GTCATTAAGTAAATAGCAGCTGGAGACAAGTGCATCCCAATCTCAGAGACCTCCCTG	12522
QY	121	CCGTGCACTGGGAGTGAAGAGACAGAGATAGTGCATGTTCTTGTCTGTGAATTTTAA	180
DB	1253	CCGTGCACTGGGAGTGAAGAGACAGAGATAGTGCATGTTCTTGTCTGTGAATTTTAA	1312
QY	181	TTATATGTCTGTATGTGCTCTGAGAGAACCCCTGGAAAGTCTATCCCAATATCCA	240
DB	1313	TTATATGTCTGTATGTGCTCTGAGAGAACCCCTGGAAAGTCTATCCCAATATCCA	1372
QY	241	CATCTTATATTCACAATTTAAGCTGTATGTATACCTTAAGAGCTGTATATGACTGC	300
DB	1373	CATCTTATATTCACAATTTAAGCTGTATGTATACCTTAAGAGCTGTATATGACTGC	14322
QY	301	CACCTTGCACATCGAGGGGCGGCTCATTTTATAGTAATGGGTCAAAATGATTAACCTTTATG	360
DB	1433	CACCTTGCACATCGAGGGGCGGCTCATTTTATAGTAATGGGTCAAAATGATTAACCTTTATG	1492
QY	361	ATGCTTCCAAAGTGCTGCTTGCCTTCTTCCCACTGACAAATGCAAAAGTTGAGAAAA	420
DB	1493	ATGCTTCCAAAGTGCTGCTTGCCTTCTTCCCACTGACAAATGCAAAAGTTGAGAAAA	1552
QY	421	TGATCATTAATTTTATAGCATTAACAGAGCATGTCGGGACACCGATTTTATAATTAACCTGAG	480
DB	1553	TGATCATTAATTTTATAGCATTAACAGAGCATGTCGGGACACCGATTTTATAATTAACCTGAG	1612
QY	481	CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTCATCCGTAAT	540
DB	1613	CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTCATCCGTAAT	1672
QY	541	GGTCCAGGAAAGACCTTTGACCTTGACTATATGGC	576
DB	1673	GGTCCAGGAAAGACCTTTGACCTTGACTATATGGC	1708
RESULT 13			
LOCUS	AR238405	2627 bp	DNA
DEFINITION	Sequence 391 from patent US 6468546.	linear	PAT 20-DEC-2002
ACCESSION	AR238405		
VERSION	AR238405.1	GI:27283369	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2627)		
AUTHORS	Mitcham,J.L., King,G.E. and Algate,P.A.		
TITLE	Compositions and methods for therapy and diagnosis of ovarian cancer		
JOURNAL	Patent: US 6468546-A 391 22-OCT-2002;		
FEATURES	Location/Qualifiers		
source	1..2627		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			

Query Match 100.0%; Score 576; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 1.9e-151; Indels 0; Gaps 0;
Matches 576; Conservative 0; Mismatches 0;

QY 1 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTGAAGTGAACAAGTGTGTTAAGA 60
DB 1133 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTGAAGTGAACAAGTGTGTTAAGA 1192
QY 61 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCCGAGATCTCAGGAGACCTCCCCCTG 120
DB 1193 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCCGAGATCTCAGGAGACCTCCCCCTG 1252
QY 121 CCGTACCTGGGGAGTGAAGACAGATAGCATGTCTTCTTGTCTCTGAATTTTATG 180
DB 1253 CCGTACCTGGGGAGTGAAGACAGATAGCATGTCTTCTTGTCTCTGAATTTTATG 1312
QY 181 TTATATGTCTGTATGTGCTCTGAGGAAGCCCTGAGAAAGTCTATCCCAACATATCCA 240
DB 1313 TTATATGTCTGTATGTGCTCTGAGGAAGCCCTGAGAAAGTCTATCCCAACATATCCA 1372
QY 241 CATCTTATATTCACAATTAAGCTGTAGTATGACCTTAAGACGCTGCTAATTTGACTGC 300
DB 1373 CATCTTATATTCACAATTAAGCTGTAGTATGACCTTAAGACGCTGCTAATTTGACTGC 1432
QY 301 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGTCAAAATGATTCACCTTTTATG 360
DB 1433 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGTCAAAATGATTCACCTTTTATG 1492
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGATTCACCTTTTATG 420
DB 1493 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGATTCACCTTTTATG 1552
QY 421 TGATCATATTTTATGACATTAACAGACAGTGGCGGACACCGATTTTATTAATAAATGAG 480
DB 1553 TGATCATATTTTATGACATTAACAGACAGTGGCGGACACCGATTTTATTAATAAATGAG 1612
QY 481 CACCTCTCTTTTAAACAACAATGCGGGTTATTTCTCAGATGATGTTCAATCCGTGAAT 540
DB 1613 CACCTCTCTTTTAAACAACAATGCGGGTTATTTCTCAGATGATGTTCAATCCGTGAAT 1672
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 576
DB 1673 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 1708

RESULT 14
AR478744 2627 bp DNA linear PAT 14-MAY-2004
LOCUS AR478744
DEFINITION Sequence 391 from patent US 6699664.
ACCESSION AR478744
VERSION AR478744.1 GI:47237396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham,J.L., King,G.B., Algate,P.A., Fling,S.P., Retter,M.W.,
Fanger,G.R., Reed,S.G., Vedrick,T.S. and Carter,D.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: US 6699664-A 391 02-MAR-2004;
FEATURES
source 1. 2627
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 1.9e-151; Indels 0; Gaps 0;
Matches 576; Conservative 0; Mismatches 0;

QY 1 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTGAAGTGAACAAGTGTGTTAAGA 60

DB 1133 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTGAAGTGAACAAGTGTGTTAAGA 1192
QY 61 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCCGAGATCTCAGGAGACCTCCCCCTG 120
DB 1193 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCCGAGATCTCAGGAGACCTCCCCCTG 1252
QY 121 CCGTACCTGGGGAGTGAAGACAGATAGCATGTCTTCTTGTCTCTGAATTTTATG 180
DB 1253 CCGTACCTGGGGAGTGAAGACAGATAGCATGTCTTCTTGTCTCTGAATTTTATG 1312
QY 181 TTATATGTCTGTATGTGCTCTGAGGAAGCCCTGAGAAAGTCTATCCCAACATATCCA 240
DB 1313 TTATATGTCTGTATGTGCTCTGAGGAAGCCCTGAGAAAGTCTATCCCAACATATCCA 1372
QY 241 CATCTTATATTCACAATTAAGCTGTAGTATGACCTTAAGACGCTGCTAATTTGACTGC 300
DB 1373 CATCTTATATTCACAATTAAGCTGTAGTATGACCTTAAGACGCTGCTAATTTGACTGC 1432
QY 301 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGTCAAAATGATTCACCTTTTATG 360
DB 1433 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATGGTCAAAATGATTCACCTTTTATG 1492
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGATTCACCTTTTATG 420
DB 1493 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGATTCACCTTTTATG 1552
QY 421 TGATCATATTTTATGACATTAACAGACAGTGGCGGACACCGATTTTATTAATAAATGAG 480
DB 1553 TGATCATATTTTATGACATTAACAGACAGTGGCGGACACCGATTTTATTAATAAATGAG 1612
QY 481 CACCTCTCTTTTAAACAACAATGCGGGTTATTTCTCAGATGATGTTCAATCCGTGAAT 540
DB 1613 CACCTCTCTTTTAAACAACAATGCGGGTTATTTCTCAGATGATGTTCAATCCGTGAAT 1672
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 576
DB 1673 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 1708

RESULT 15
AX156350 2627 bp DNA linear PAT 22-JUN-2001
LOCUS AX156350
DEFINITION Sequence 207 from Patent WO0140269.
ACCESSION AX156350
VERSION AX156350.1 GI:14537350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dillon,D.C., Day,C.H., Jiang,Y., Houghton,R.L., Mitcham,J.L. and
Wang,A.
TITLE Compositions and methods for therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0140269-A 207 07-JUN-2001;
CORIXA CORPORATION (US)
FEATURES
source 1. 2627
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 576; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 1.9e-151; Indels 0; Gaps 0;
Matches 576; Conservative 0; Mismatches 0;

QY 1 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTGAAGTGAACAAGTGTGTTAAGA 60
DB 1133 TTCAAAGACATATTAGAGTTGGGAAATTAATTCATGTGAAGTGAACAAGTGTGTTAAGA 1192
QY 61 GTGATTAAGTAAATGACGTGAGACAAAGTGCATCCCCGAGATCTCAGGAGACCTCCCCCTG 120

```
Db 1193 GTGATAGTAAATGACGTGAGACAAAGTCATCCCAAGTCTCAGGAGCCTCCCTG 1252
QY 121 CCTGTCACTGGGAGAGAGAGACAGATAGTGCATGTTCTTGTCTCTGAATTTTAG 180
Db 1253 CTTGTCACTGGGAGAGAGAGACAGATAGTGCATGTTCTTGTCTCTGAATTTTAG 1312
QY 181 TTATATGTGCTGTAATGTGCTCTGAGAAAGCCCTGAAAGTCTATCCACATATCA 240
Db 1313 TTATATGTGCTGTAATGTGCTCTGAGAAAGCCCTGAAAGTCTATCCACATATCA 1372
QY 241 CATCTTATATTCACAAATTAAGCTGTAGATGTACCTTAAGACGCTGTATTTGACTGC 300
Db 1373 CATCTTATATTCACAAATTAAGCTGTAGATGTACCTTAAGACGCTGTATTTGACTGC 1432
QY 301 CACTTGGCACTCAGGGGCGGCTGCATTTTAGTATAGGTCAAATGATTCATTTTATG 360
Db 1433 CACTTGGCACTCAGGGGCGGCTGCATTTTAGTATAGGTCAAATGATTCATTTTATG 1492
QY 361 ATGCTTCAAGGCTGCTGGCTTCTCTCCCACTGACAAATGSCAAAGTTGAGAAAA 420
Db 1493 ATGCTTCAAGGCTGCTGGCTTCTCTCCCACTGACAAATGSCAAAGTTGAGAAAA 1552
QY 421 TGATCATATTTTAGCATAAACAGAGCAGTCGGGACACCGATTTTAAATAAATGAG 480
Db 1553 TGATCATATTTTAGCATAAACAGAGCAGTCGGGACACCGATTTTAAATAAATGAG 1612
QY 481 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAAGATGATGTTCAATCCGTAAT 540
Db 1613 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAAGATGATGTTCAATCCGTAAT 1672
QY 541 GGTCCAGGGAAGGACCTTGACCTTGACTATATGGC 576
Db 1673 GGTCCAGGGAAGGACCTTGACCTTGACTATATGGC 1708
```

Search completed: May 30, 2005, 17:54:03
Job time : 2659.37 secs

THIS PAGE LEFT BLANK

en conjugated with a

CC Cytotoxic agent are useful for treating cancer. The present sequence
CC represents a CSG (clone ID: 16656542 and gene ID: 234617) fragment
XX
SQ Sequence 576 BP; 169 A; 118 C; 122 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 576; DB 3; Length 576;
 Best Local Similarity 100.0%; Pred. No. 3.1e-172;
 Matches 576; Conservative 0; Mismatches 0; Gaps 0;

Qy	1	TTCCAAAGACATATTAGAACTGGGAAAATAATTCATGGAACCTGACAAAGTGTTAG	60
Db	1	TTCAAAGACATTTAGAACTGGGAAAATAATTCATGGAACCTGACAAAGTGTTAG	60
Qy	61	GTGATTAAGTAAATGCACTGGAGCAAGTGCACTCCAGATCTCAGGAGCTCCCTG	120
Db	61	GTGATTAAGTAAATGCACTGGAGCAAGTGCACTCCAGATCTCAGGAGCTCCCTG	120
Qy	121	CCGTACACCTGGGAGTGGAGAGACAGATAGTGATCTCTGTAATTTTAG	180
Db	121	CCGTACACCTGGGAGTGGAGAGACAGATAGTGATCTCTGTAATTTTAG	180
Qy	181	TTATATGTGCTGAATGTGCTCTGAGGAAGCCCTGGAAAGTCAATCCACATCCA	240
Db	181	TTATATGTGCTGAATGTGCTCTGAGGAAGCCCTGGAAAGTCAATCCACATCCA	240
Qy	241	CATCTTAATATCCAAATTAAGCTGTAGTATGACCTTAAGACGCTGTAAATGACTGC	300
Db	241	CATCTTAATATCCAAATTAAGCTGTAGTATGACCTTAAGACGCTGTAAATGACTGC	300
Qy	301	CACCTTGGCACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAAATGATCACTTTTATG	360
Db	301	CACCTTGGCACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAAATGATCACTTTTATG	360
Qy	361	ATGCTTCCAAAGGTGGCTTGAGCTTCTCTTCCCACTGACAAATGSCAAAGTTGAGAAAA	420
Db	361	ATGCTTCCAAAGGTGGCTTGAGCTTCTCTTCCCACTGACAAATGSCAAAGTTGAGAAAA	420
Qy	421	TGATCATTAATTTTAGCATTAACAGAGCAGTCGGCAGACCGATTTTATAATAAACTGAG	480
Db	421	TGATCATTAATTTTAGCATTAACAGAGCAGTCGGCAGACCGATTTTATAATAAACTGAG	480
Qy	481	CACCTTCTTTTAAACAACAAATAAGGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT	540
Db	481	CACCTTCTTTTAAACAACAAATAAGGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT	540
Qy	541	GGTCCAGGGAAGACCTTTCACTTGAACATATAGCC	576
Db	541	GGTCCAGGGAAGACCTTTCACTTGAACATATAGCC	576

RESULT 2
AAA69764
ID AAA69764 standard; cDNA; 1567 BP.

AC	AAA69764;
XX	
DT	07-NOV-2000 (first entry)
XX	
DE	Human ovarian carcinoma antigen polynucleotide SEQ ID NO:74.
XX	
KW	Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW	tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200036107-A2.
XX	
PD	22-JUN-2000.
XX	
PF	17-DEC-1999; 99WO-US030270.
XX	
XX	17-DEC-1998; 98US-00215681.
PR	17-DEC-1998; 98US-00216003.

PR	23-JUN-1999;	99US-00338933.
PR	24-SEP-1999;	99US-00404879.
XX		
PA	(CORI-) CORIXA CORP.	

PI Mitcham JL, King GE, Algate PA, Frudakis TN,
XX
DR WPI; 2000-431589/37.

PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.

PS Claim 1; Fig 2; 299pp; English.

The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAH96961 to AAH70077 and AAH2552 to AAH1557, represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.

Query Match	100.0%	Score 576 ; DB 3 ;	Length 1567 ;
Best Local Similarity	100.0%	Pred. No. 5e-172 ;	
Matches 576 ;	Conservative 0 ;	Mismatches 0 ;	Gaps 0

OY	ITCAAAGACATATTGAAGTTGGGAAAATTAATCATGGAACCTGACAAAGTGTTAGA	60
Db	TTCAAAGACATATTGAAGTTGGGAAAATTAATCATGGAACCTGACAAAGTGTTAGA	150
OY	GTGATAAGTAATAATGCAACGTGAGACAAGTGATCCCAATCTCAGAGACCTCCCTG	120
Db	GTGATAAGTAATAATGCAACGTGAGACAAGTGATCCCAATCTCAGAGACCTCCCTG	210
OY	CTGTCAACCTGGGAGTGAAGACAGATAGTGCAATGTTCTTTGTCTCTGAATTTTAG	180
Db	CTGTCAACCTGGGAGTGAAGACAGATAGTGCAATGTTCTTTGTCTCTGAATTTTAG	270
OY	TTTATATGCTGTGAATATGTCCTGAGGAAGCCCTGGAAAGCTATCCCAACTATCCA	240
Db	TTTATATGCTGTGAATATGTCCTGAGGAAGCCCTGGAAAGCTATCCCAACTATCCA	330
OY	CATCTATATATCCACAATTTAAGCTGTAGTATGTACCTTAAGACGCTGTAATTGACTGC	300
Db	CATCTATATATCCACAATTTAAGCTGTAGTATGTACCTTAAGACGCTGTAATTGACTGC	390
OY	CACCTGCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAATGATTCATCTTTATG	360
Db	CACCTGCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAATGATTCATCTTTATG	450
OY	ATAGCTTCCAAAGGTGCTTGAGCTTCCTCTCCCACTGACAAATGCGCAAAGTGGGAAAA	420
Db	ATAGCTTCCAAAGGTGCTTGAGCTTCCTCTCCCACTGACAAATGCGCAAAGTGGGAAAA	510
OY	TGATCATTAATTTTAGCATTAACAGAGCAGTGGGACACCGATTTTATAATAAACTGAG	480
Db	TGATCATTAATTTTAGCATTAACAGAGCAGTGGGACACCGATTTTATAATAAACTGAG	570
OY	CACCTTCCTTTTAAACAAACAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT	540
Db	CACCTTCCTTTTAAACAAACAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT	630
OY	GGTCCAGGGAAGACCTTTCACCTGACATATGGC	576
Db	GGTCCAGGGAAGACCTTTCACCTGACATATGGC	666

RESULT 3

ABN72658
ID ABN72658 standard; DNA; 1567 BP.
XX
AC ABN72658;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma antigen polynucleotide #74.
XX
KW Human; immunostimulant; cytotoxic; cancer; ovarian carcinoma; ds.
XX
OS Homo sapiens.
XX
PN W0200206317-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-0067857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
XX (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2002-164781/21.
XX
DR
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
XX Example 1; Page 115; 408pp; English.
XX
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytotoxic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents DNA related
CC to the invention
XX
XX Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 576; DB 6; Length 1567;
Best Local Similarity 100.0%; Pred. No. 5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAAGTGAAGTGTGTTAGA 60
DB 91 TTCAAGACATATTAGAAAGTTGGGAAATATTCATGTGAAGTGAAGTGTGTTAGA 150
QY 61 GTGATAGTAAATAGCAGCTGGAGACAAGTGCATCCCAAGTCTCAGGACCTCCCTG 120
DB 151 GTGATAGTAAATAGCAGCTGGAGACAAGTGCATCCCAAGTCTCAGGACCTCCCTG 210
QY 121 CCTGTGACCTGGGAGTGAAGAGCAGAGTATGATGTCCTTTGTCCTGAATTTTAG 180
DB 211 CCTGTGACCTGGGAGTGAAGAGCAGAGTATGATGTCCTTTGTCCTGAATTTTAG 270
QY 181 TTATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCA 240
DB 271 TTATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCA 330
QY 241 CATCTTATATTCACCAATTAAGTGTAGTATGATACCTTAAGAGCGCTCTAATGATGC 300
DB 331 CATCTTATATTCACCAATTAAGTGTAGTATGATACCTTAAGAGCGCTCTAATGATGC 390
QY 301 CATCTTGAACCTGAGGCGGCTGCATTTTATGTAATGAGTCAATGATCACTTTTATG 360

DB 391 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGTAATGAGTCAATGATCACTTTTATG 450
QY 361 ATGCTTCAAAAGTGCTGCTTGTCTTCCCACTGACAAATGCCAAAGTTAGAAAA 420
DB 451 ATGCTTCAAAAGTGCTGCTTGTCTTCCCACTGACAAATGCCAAAGTTAGAAAA 510
QY 421 TGATCATTAATTTTATGATTAACAGAGAGTGGCGACACCGATTTTATTAATTAAGTAG 480
DB 511 TGATCATTAATTTTATGATTAACAGAGAGTGGCGACACCGATTTTATTAATTAAGTAG 570
QY 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAGATGATGTCCTGTAAT 540
DB 571 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAGATGATGTCCTGTAAT 630
QY 541 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAC 576
DB 631 GGTCCAGGAAAGACCTTTCACCTTGACTATATGAC 666
RESULT 4
ADA08823
ID ADA08823 standard; DNA; 1567 BP.
XX
XX ADA08823;
XX
AC ADA08823;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide #74.
XX
KW de; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REBD/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2003-532352/50.
XX
DR
XX
PT New isolated 0772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
XX Example 1; Fig 2; 371pp; English.
XX
CC The invention relates to an isolated 0772P polypeptide, which has the
CC structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma

CC antigen polynucleotide.

SQ Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;

Query Match 100.0%; Score 576; DB 9; Length 1567;

Best Local Similarity 100.0%; Pred. No. 5e-172;

Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAGACATATTAGAGTGGGAAATTAATCATGTGTAACATGACAGAGTGGTTAAGA 60
 |||
 DB 91 TTCAAGACATATTAGAGTGGGAAATTAATCATGTGTAACATGACAGAGTGGTTAAGA 150
 |||
 QY 61 GTGATAGTAAATGACGCTGAGACAGATGCCAGATCTCCAGAGACCTCCCTCG 120
 |||
 DB 151 GTGATAGTAAATGACGCTGAGACAGATGCCAGATCTCCAGAGACCTCCCTCG 210
 |||
 QY 121 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTCTTCTCTGTAATTTTATG 180
 |||
 DB 211 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTCTTCTCTGTAATTTTATG 270
 |||
 QY 181 TTATATGTGCTGTATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCA 240
 |||
 DB 271 TTATATGTGCTGTATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCA 330
 |||
 QY 241 CATCTTATATTCACAATTAAGCTGTATGTATGACCTTAAGAAGCTGTAAATGACTGC 300
 |||
 DB 331 CATCTTATATTCACAATTAAGCTGTATGTATGACCTTAAGAAGCTGTAAATGACTGC 390
 |||
 QY 301 CACTTGGCACTCAAGGGGGGGCTGCAATTTAGTAAGGTCATTAATATTCATCTTTTATG 360
 |||
 DB 391 CACTTGGCACTCAAGGGGGGGCTGCAATTTAGTAAGGTCATTAATATTCATCTTTTATG 450
 |||
 QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 420
 |||
 DB 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 510
 |||
 QY 421 TGATCATTAATTTAGCATTAACAGACAGTGGCGACACCGATTTTATAATTAACCTGAG 480
 |||
 DB 511 TGATCATTAATTTAGCATTAACAGACAGTGGCGACACCGATTTTATAATTAACCTGAG 570
 |||
 QY 481 CACCTTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGTTCAATCCGAT 540
 |||
 DB 571 CACCTTCTTTTAAACAAATGCGGTTTATTTCTAGATGATGTTCAATCCGAT 630
 |||
 QY 541 GGTCCAGGAAGACCTTTCACCTGACTATATGCG 576
 |||
 DB 631 GGTCCAGGAAGACCTTTCACCTGACTATATGCG 666
 |||

RESULT 5

ADP08570 standard; cDNA; 1567 BP.

XX ADP08570;

XX 12-FEB-2004 (first entry)

DE cDNA encoding secreted ovarian carcinoma antigen segid 74.

XX gene therapy; protein therapy; vaccine; antibody inhibition;
 KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
 KW secreted ovarian carcinoma antigen; gene; ss.

OS Homo sapiens.

XX US2003124140-A1.

XX 03-JUL-2003.

PF 17-JUL-2002; 2002US-00198053.

XX 17-DEC-1998; 98US-00215681.

PR 17-DEC-1998; 98US-00215603.

PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00657857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 PR 17-JUL-2001; 2001US-00907969.

XX (CORI-) CORIXA CORP.

XX Bangur CS, Retter MW, Fanger GR, Hill P;

XX WPI; 2003-897152/82.

PT Oncogenic nucleic acids useful for the prevention, diagnosis and

PT treatment of breast cancer.

XX Example 1; SEQ ID NO 74; 399pp; English.

CC The invention describes nucleic acids (I) and the polypeptides (II) they
 CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
 CC treating diseases related to their aberrant expression i.e. breast
 CC cancers. For example, (I) and (II) may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of (II) by expressing
 CC inactive proteins or to supplement the patients own production of (II).
 CC Additionally, (I) may be used to produce (II), by inserting (I) into a
 CC host cell and culturing the cell to express the protein (II). (I) And its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. The host cell may also be used as antigens in the production of
 CC antibodies against (II) and in assays to identify modulators of (II)'s
 CC expression and activity. The anti-(II) antibodies, agonists and
 CC antagonists may be used to regulate expression and activity and as
 CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
 CC immunoassay). This sequence represents a polynucleotide encoding a
 CC secreted ovarian carcinoma antigen.

SQ Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;

Query Match 100.0%; Score 576; DB 10; Length 1567;

Best Local Similarity 100.0%; Pred. No. 5e-172;

Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAGACATATTAGAGTGGGAAATTAATCATGTGTAACATGACAGAGTGGTTAAGA 60
 |||
 DB 91 TTCAAGACATATTAGAGTGGGAAATTAATCATGTGTAACATGACAGAGTGGTTAAGA 150
 |||
 QY 61 GTGATAGTAAATGACGCTGAGACAGATGCCAGATCTCCAGAGACCTCCCTCG 120
 |||
 DB 151 GTGATAGTAAATGACGCTGAGACAGATGCCAGATCTCCAGAGACCTCCCTCG 210
 |||
 QY 121 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTCTCTCTGTAATTTTATG 180
 |||
 DB 211 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTCTCTCTCTGTAATTTTATG 270
 |||
 QY 181 TTATATGTGCTGTATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCA 240
 |||
 DB 271 TTATATGTGCTGTATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCA 330
 |||
 QY 241 CATCTTATATTCACAATTAAGCTGTATGTATGACCTTAAGAAGCTGTAAATGACTGC 300
 |||
 DB 331 CATCTTATATTCACAATTAAGCTGTATGTATGACCTTAAGAAGCTGTAAATGACTGC 390
 |||
 QY 301 CACTTGGCACTCAAGGGGGGGCTGCAATTTAGTAAGGTCATTAATATTCATCTTTTATG 360
 |||
 DB 391 CACTTGGCACTCAAGGGGGGGCTGCAATTTAGTAAGGTCATTAATATTCATCTTTTATG 450
 |||
 QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 420
 |||
 DB 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAA 510
 |||

```

Qy 421 TGATCATATTTTGTAGTAAACAGAGAGTCGGGAGACCGATTTTAAATAAAGTGA 480
Db 511 TGATCATATTTTGTAGTAAACAGAGAGTCGGGAGACCGATTTTAAATAAAGTGA 570
Qy 481 CACCTTCTTTTAAACAAACAAATCGGGTTTATTTCTCAGATGATGTTCCGTAAT 540
Db 571 CACCTTCTTTTAAACAAACAAATCGGGTTTATTTCTCAGATGATGTTCCGTAAT 630
Qy 541 GGTCCAGGAAGACCTTTCACTTGAATATGAGC 576
Db 631 GGTCCAGGAAGACCTTTCACTTGAATATGAGC 666

RESULT 6
ADG46318
ID ADG46318 standard; cDNA; 1567 BP.
AC ADG46318;
XX
XX 26-FEB-2004 (first entry)
DE Human ovarian carcinoma polynucleotide #74.
XX
XX Human; ovarian carcinoma; gene; ss; OBE; ovarian cancer;
KM secreted tumour antigen; cytostatic; O772P.
XX
XX Homo sapiens.
OS
XX US2003165504-A1.
PN
XX 04-SEP-2003.
PD
XX 04-APR-2001; 2001US-00827271.
PF
XX 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
XX
XX (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
XX
XX Retter MW, Fanger GR;
PI
XX WPI; 2003-898035/82.
DR
XX
XX New isolated OBE or O772P polypeptides, useful for diagnosing,
PT preventing, treating and monitoring cancer, e.g. ovarian cancer,
PT stimulating the immune response in patient.
XX
XX Example 1; SEQ ID NO 74; 290pp; English.
PS
XX The invention relates to human ovarian carcinoma polypeptides, designated
CC OBE or O772P, and the polynucleotides encoding them. The invention also
CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC methods for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polynucleotide of the invention.
XX
XX Sequence 1567 BP; 460 A; 348 C; 333 G; 426 T; 0 U; 0 Other;
Query Match 100.0%; Score 576; DB 10; Length 1567;
Best Local Similarity 100.0%; Pred. No. 5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 TTCAAGACATATTAGAGTTGGGAAAATTAATTCATGTGAACTAGACAAGTGTGTTAGA 60
Db 91 TTCAAGACATATTAGAGTTGGGAAAATTAATTCATGTGAACTAGACAAGTGTGTTAGA 150
Qy 61 GTGATAAGTAAATTAAGACAGTGAAGACAGTGCATCCAGATCTCAGGAGCTCCCTG 120
Db 151 GTGATAAGTAAATTAAGACAGTGAAGACAGTGCATCCAGATCTCAGGAGCTCCCTG 210
Qy 121 CCGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGCTCTGAATTTTAA 180
Db 211 CCGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGCTCTGAATTTTAA 270
Qy 181 TTATATGTGCTGTAATGTTGCTCTGAAGAGAGCCCTGAAAGTCTATCCCAATATCCA 240
Db 271 TTATATGTGCTGTAATGTTGCTCTGAAGAGAGCCCTGAAAGTCTATCCCAATATCCA 330
Qy 241 CATCTTATATTCACAAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 300
Db 331 CATCTTATATTCACAAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 390
Qy 301 CACTTGCAACTGACAGGCGGCTGCACTTTAGTAAATGAGTCAATGATGATGATGATG 360
Db 391 CACTTGCAACTGACAGGCGGCTGCACTTTAGTAAATGAGTCAATGATGATGATGATG 450
Qy 361 ATGCTTCCAAAGGATGCTGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 451 ATGCTTCCAAAGGATGCTGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 510
Qy 421 TGATCATATTTTGTAGTAAACAGAGAGTCGGGAGACCGATTTTAAATAAAGTGA 480
Db 511 TGATCATATTTTGTAGTAAACAGAGAGTCGGGAGACCGATTTTAAATAAAGTGA 570
Qy 481 CACCTTCTTTTAAACAAACAAATCGGGTTTATTTCTCAGATGATGTTCCGTAAT 540
Db 571 CACCTTCTTTTAAACAAACAAATCGGGTTTATTTCTCAGATGATGTTCCGTAAT 630
Qy 541 GGTCCAGGAAGACCTTTCACTTGAATATGAGC 576
Db 631 GGTCCAGGAAGACCTTTCACTTGAATATGAGC 666

RESULT 7
ACN92433
ID ACN92433 standard; DNA; 1596 BP.
XX
XX ACN92433;
AC
XX 02-DEC-2004 (first entry)
DT
XX
XX Breast cancer related marker, seq id 13581.
DE
XX
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
KM
XX
XX Homo sapiens.
OS
XX
XX US2003099974-A1.
PN
XX 29-MAY-2003.
PD
XX 18-JUL-2002; 2002US-00198846.
PF
XX 18-JUL-2001; 2001US-0306220P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI
XX
XX WPI; 2003-787014/74.
DR
XX
XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX

```

PS Disclosure; SEQ ID NO 13583; 36bp; English.
XX
XX The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (SI). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?docID=20030099974
XX
SQ Sequence 1596 BP; 457 A; 354 C; 340 G; 424 T; 0 U; 21 Other;
Query Match 100.0%; Score 576; DB 11; Length 1596;
Best Local Similarity 100.0%; Pred. No. 5,1e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTTAAGA 60
DB 267 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTTAAGA 326
QY 61 GTGATAGTAAATGACGCTGGAGACAGATGTCATCCCAAGTCTCAGGACCTCCCTG 120
DB 327 GTGATAGTAAATGACGCTGGAGACAGATGTCATCCCAAGTCTCAGGACCTCCCTG 386
QY 121 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTGTCTCTGAATTTTAG 180
DB 387 CCTGTACCTGGGAGTGAAGAGACAGATGTCATGTTCTTGTCTCTGAATTTTAG 446
QY 181 TTATATGCTGTGAATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCA 240
DB 447 TTATATGCTGTGAATGTTGCTCTGAGAAAGCCCTGGAAGTCTATCCCAATATCA 506
QY 241 CATCTATATTCACAAATTAAGCTAGTATGATGTAACCTTAAGACGCTGTAATGACTG 300
DB 507 CATCTATATTCACAAATTAAGCTAGTATGATGTAACCTTAAGACGCTGTAATGACTG 566
QY 301 CACTTGGCAACTGAGGGGGCTGCAATTTTGAATGGTCAATGATTCACCTTTTATG 360
DB 567 CACTTGGCAACTGAGGGGGCTGCAATTTTGAATGGTCAATGATTCACCTTTTATG 626
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCCCAAGTGAACCAAGTTGAGAAAA 420
DB 627 ATGCTTCCAAAGGTGCTTGGCTTCTCCCAAGTGAACCAAGTTGAGAAAA 686
QY 421 TGATCATATTTTGAAGATAACAGACAGTCCGCGACACCGATTTTAAATTAACCTGAG 480
DB 687 TGATCATATTTTGAAGATAACAGACAGTCCGCGACACCGATTTTAAATTAACCTGAG 746
QY 481 CACCTTCTTTTAAACAAACAAATGGGGTTTATTTCTCAGATGATGTTGATCCGTAAT 540
DB 747 CACCTTCTTTTAAACAAACAAATGGGGTTTATTTCTCAGATGATGTTGATCCGTAAT 806
QY 541 GGTCCAGGAGGAGACCTTTCACCTGACTATATGGC 576
DB 807 GGTCCAGGAGGAGACCTTTCACCTGACTATATGGC 842

RESULT 8
ADL45372
ID ADL45372 standard; DNA; 1965 BP.
XX
XX ADL45372;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #19262.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
KW

XX
XX Homo sapiens.
OS
XX
XX MO200170979-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009126.
PF
XX
XX 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Lee J, Lillie J;
PI
XX
XX WPI; 2001-611502/70.
DR
XX
XX
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX
XX
XX Disclosure; SEQ ID NO 19262; 106bp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
XX
SQ Sequence 1965 BP; 557 A; 450 C; 452 G; 503 T; 0 U; 3 Other;
Query Match 100.0%; Score 576; DB 5; Length 1965;
Best Local Similarity 100.0%; Pred. No. 5,6e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTTAAGA 60
DB 1130 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTTAAGA 1189
QY 61 GTGATAGTAAATGACGCTGGAGACAGATGTCATCCCAAGTCTCAGGACCTCCCTG 120
DB 1190 GTGATAGTAAATGACGCTGGAGACAGATGTCATCCCAAGTCTCAGGACCTCCCTG 1249

QY 121 CCTGTGACCTGGGAGTGAAGAGCAGGATAGTCAATGTTCTTGTCTGAATTTTAG 180
DB 1250 CCTGTGACCTGGGAGTGAAGAGCAGGATAGTCAATGTTCTTGTCTGAATTTTAG 1309
QY 181 TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAAGTCTATCCCAACATATCCA 240
DB 1310 TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAAGTCTATCCCAACATATCCA 1369
QY 241 CATCTTATATTTCCCAAAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATATGACTGC 300
DB 1370 CATCTTATATTTCCCAAAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATATGACTGC 1429
QY 301 CACTTGGCACTGAGGGGCGGCTGCTATTTAGTAAATGGTCAATGTAATGACTTTTATG 360
DB 1430 CACTTGGCACTGAGGGGCGGCTGCTATTTAGTAAATGGTCAATGTAATGACTTTTATG 1489
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGSCAAAGTTGAGAAAA 420
DB 1490 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGSCAAAGTTGAGAAAA 1549
QY 421 TGAATCATATTTTGAATTAACAGAGAGTGGGAGACCGATTTTAAATAAATCTGAG 480
DB 1550 TGAATCATATTTTGAATTAACAGAGAGTGGGAGACCGATTTTAAATAAATCTGAG 1609
QY 481 CACCTTCTTTTAAACAAAGAAATGCGGGTTTATTTCTGAGATGATGATCCGTAAT 540
DB 1610 CACCTTCTTTTAAACAAAGAAATGCGGGTTTATTTCTGAGATGATGATCCGTAAT 1669
QY 541 GGTCCAGGAGGAGACCTTTCACTTGAATATGCG 576
DB 1670 GGTCCAGGAGGAGACCTTTCACTTGAATATGCG 1705

RESULT 9
AA290470
ID AA290470 standard; cDNA; 2587 BP.

XX AA290470;

DT 06-JUN-2000 (first entry)

DE Cancer specific gene (CSG) sequence (clone ID 16656542).

KM CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;

KW endometrial; uterine; lung; cytotoxic; ss.

OS Homo sapiens.

PN W0200012758-A1.

PD 09-MAR-2000.

PF 01-SEP-1999; 99WO-US019655.

PR 02-SEP-1998; 98US-0098880P.

PA (DIAD-) DIADEXUS LLC.

PI Salceda S, Sun Y, Recipon H, Cafferkey R;

XX WPI; 2000-256657/22.

PT Diagnosing, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer,
PT involves measuring cancer specific gene levels in cells and body fluids.

PS Claim 9; Page 44-45; 58pp; English.

CC The invention relates to detecting, diagnosing metastasis and staging
CC cancer by measuring levels of cancer specific genes (CSG) in cells,
CC tissues or body fluids. Their remission and progression, decreases and
CC increases in CSG levels, is also monitored, by periodic sample analysis.

CC The methods are useful for detecting cancers, especially gynecologic
CC cancers which include ovarian, breast, endometrial and uterine cancer and
CC lung cancer. Antibodies against the CSOs labeled with paramagnetic ions
CC or a radioisotope is useful for imaging cancer and when conjugated with a
CC cytotoxic agent are useful for treating cancer. The present sequence
CC represents a CSG sequence (clone ID: 16656542 and gene ID: 234617)
XX

SO Sequence 2587 BP; 737 A; 588 C; 580 G; 682 T; 0 U; 0 Other;

Query Match 100.0%; Score 576; DB 3; Length 2587;
Best Local Similarity 100.0%; Pred. No. 6, 4e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAAAGCATATTAAGTGGGAAATTAATTCATGTGAACATGACAGTGTGATAGA 60
DB 1112 TTGAAAGCATATTAAGTGGGAAATTAATTCATGTGAACATGACAGTGTGATAGA 1171
QY 61 GTGATAAGTAAATTAAGACGAGAGACAGTGCATCCCGAGATCTCAGGACCTCCCTG 120
DB 1172 GTGATAAGTAAATTAAGACGAGAGACAGTGCATCCCGAGATCTCAGGACCTCCCTG 1231
QY 121 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTGAAATTTTATG 180
DB 1232 CCTGTCACTGGGAGTGAAGAGACAGATAGTGCATGTTCTTGTCTGAAATTTTATG 1291
QY 181 TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAAGTCTATCCCAATATCCA 240
DB 1292 TTAATATGCTGTATATGTTGCTCTGAGAAAGCCCTGGAAAGTCTATCCCAATATCCA 1351
QY 241 CATCTTATATTTCCCAAAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATATGACTGC 300
DB 1352 CATCTTATATTTCCCAAAATTAAGCTGTATGTATGTAACCTTAAGACGCTGTATATGACTGC 1411
QY 301 CACTTGGCACTGAGGGGCGGCTGCAATTTTAAATGGTCAATGTAATGACTTTTATG 360
DB 1412 CACTTGGCACTGAGGGGCGGCTGCAATTTTAAATGGTCAATGTAATGACTTTTATG 1471
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGSCAAAGTTGAGAAAA 420
DB 1472 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGSCAAAGTTGAGAAAA 1531
QY 421 TGAATCATATTTTGAATTAACAGAGAGTGGGAGACCGATTTTAAATAAATCTGAG 480
DB 1532 TGAATCATATTTTGAATTAACAGAGAGTGGGAGACCGATTTTAAATAAATCTGAG 1591
QY 481 CACCTTCTTTTAAACAAAGAAATGCGGGTTTATTTCTGAGATGATGATCCGTAAT 540
DB 1592 CACCTTCTTTTAAACAAAGAAATGCGGGTTTATTTCTGAGATGATGATCCGTAAT 1651
QY 541 GGTCCAGGAGGAGACCTTTCACTTGAATATGCG 576
DB 1652 GGTCCAGGAGGAGACCTTTCACTTGAATATGCG 1687

RESULT 10
ABL57354
ID ABL57354 standard; cDNA; 2591 BP.

XX ABL57354;

DT 12-AUG-2002 (first entry)

DE Breast BS265 gene EST clone 3038129.

KM BS265; human; breast; cancer; tumour; metastasis; diagnosis;

KW gene therapy; expressed sequence tag; EST; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 61..909

FT /tag= a
/product= "BS265"

```

XX US2002034749-A1.
XX
XX 21-MAR-2002.
XX
XX 07-MAY-2001; 2001US-00850178.
XX
XX 18-NOV-1997; 97US-00972376.
XX 18-NOV-1998; 98US-00193944.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLE/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L A.
PA (RUSS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, KLAS MR, Kratochvil JD, Roberts-Rapp LA;
PI Russell JC, Stroupe SD;
XX
DR MPI: 2002-403712/43.
DR P-PSDB; ABB76274.
XX
PT New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
PT staging, monitoring, prognosticating, in vivo imaging, preventing,
PT treating, or determining the predisposition of an individual to breast
PT cancer.
XX
PS Claim 52; Page 41-42; 52pp; English.
XX
CC The present sequence is of human breast BS265 gene expressed sequence tag
CC (EST) clone 3038129. ESTs were derived from cDNA libraries made from
CC breast tumour tissues, breast non-tumour tissues and numerous other
CC tissues, and entered into a database as gene transcript images. They were
CC then evaluated to identify EST sequences that were representative
CC primarily of the breast tissue libraries, and were ranked according to
CC their abundance in the target libraries and absence from background
CC libraries. 4 Partial clones (see ABL57345-48) represented the minimum
CC number of clones that, together with the full-length sequence of clone
CC 3090752H1 (see ABL57349), were needed to form a contig and from which a
CC consensus sequence (see ABL57350) for BS265 was derived. Other clones
CC appeared at positions in the assembly upstream of the above sequences.
CC Clone 3038129 spanned the entire assembly, and encoded the protein given
CC in ABB76274. The set of contiguous and partially overlapping cDNA
CC sequences, designated as BS265 and transcribed from breast tissue, and
CC the polypeptides encoded by them, are useful for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing,
CC treating, or determining the predisposition of an individual to diseases
CC and conditions of the breast, especially tumours and metastases
XX
SO Sequence 2591 BP; 739 A; 591 C; 579 G; 682 T; 0 U; 0 Other:

```

```

Db 1231 CCTGTCACCTGGGGAGTGAGAGACAGATAGTGCATGTTCTTGTCTCTGAATTTTAG 1290
Qy 181 TTAATATGCTGATATGTTGCTCTGAGAGACCCCTGGAAAGTCAATCCAAATATCCA 240
Db 1291 TTAATATGCTGATATGTTGCTCTGAGAGACCCCTGGAAAGTCAATCCAAATATCCA 1350
Qy 241 CATCTTAATATTCACAAATTAAGCTGATATGTAACCTTAAGACGCTCTAATGACTGCG 300
Db 1351 CATCTTAATATTCACAAATTAAGCTGATATGTAACCTTAAGACGCTCTAATGACTGCG 1410
Qy 301 CACTTGGGAACCTCAGGGGCGGCTGCATTTTGTATATGGGTCAAAATGATTCATTTTAG 360
Db 1411 CACTTGGGAACCTCAGGGGCGGCTGCATTTTGTATATGGGTCAAAATGATTCATTTTAG 1470
Qy 361 ATGCTTCCAAAGAGTGCTTGGCTTCTCTTCCCAACTGACAAATGCAAGTTGAGAAAA 420
Db 1471 ATGCTTCCAAAGAGTGCTTGGCTTCTCTTCCCAACTGACAAATGCAAGTTGAGAAAA 1530
Qy 421 TGATCATATATTTTACATTAACAGACAGTGGGCAACCCGATTTTATTAATAAAGTGAAG 480
Db 1531 TGATCATATATTTTACATTAACAGACAGTGGGCAACCCGATTTTATTAATAAAGTGAAG 1590
Qy 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 540
Db 1591 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTCAGATGATGTTCAATCCGTGAAT 1650
Qy 541 GGTCCAGGGAAGACCTTTCACCTTGACTATATAGC 576
Db 1651 GGTCCAGGGAAGACCTTTCACCTTGACTATATAGC 1686

RESULT 11
AAD29253
ID AAD29253 standard; DNA; 2603 BP.
XX
AC AAD29253;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human B7-like protein (B7-L) DNA.
XX
KW Human; B7-like protein; B7-L; reproductive disorder; autoimmune disease;
KW proliferative disorder; infertility; hyperplasia; cancer; lung; breast;
KW brain; seminal vesicle; haematopoietic system; tumour; diabetes mellitus;
KW rheumatoid arthritis; systemic lupus erythematosus; toxic shock syndrome;
KW inflammatory bowel disease; psoriasis; allergy; Crohn's disease; vaccine;
KW Grave's disease; arteriosclerosis; multiple sclerosis; hypersensitivity;
KW nephropathy; skin disorder; endocrinopathy; vasculopathy; gynaecological;
KW myasthenia gravis; anaemia; lymphoproliferative disorder; neuroprotective;
KW cytosolic; multiple myeloma; tissue-degenerating disease; nephrotropic;
KW immunosuppressive; asthma; virucide; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 53..901
FT FT /*tag= a
FT FT /product= "Human B7-L protein"
FT sig_peptide 53..124
FT mat_peptide 125..898
FT FT /*tag= C
FT FT /product= "Human mature B7-L protein"
XX
PN WO200202624-A2.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021297.
XX
PR 30-JUN-2000; 2000US-0215645P.
XX
PA (AMGE-) AMGEN INC.

```

XX Fox M, Sullivan JK, Fang M;
PI WPI; 2002-171639/22.
DR P-PSDB; AAE18336.
XX
PT Novel B7-1-like polypeptides, polynucleotides and their modulators useful
PT for prevention and treatment of reproductive, immune and proliferative
PT disorders, e.g. cancer, arteriosclerosis.
XX
PS Claim 1; Fig 1A-1C; 133pp; English.
XX
CC The present invention relates to an isolated B7-1-like (B7-L) polypeptide
CC and its polynucleotide. B7-1 and its modulators are useful for treating
CC reproductive disorders (e.g. infertility, miscarriage, preterm labour and
CC delivery and endometriosis) and proliferative disorders. Antibodies,
CC soluble proteins comprising extracellular domains and other regulators of
CC B7-L are useful for enhancing the immune response to tumours. B7-1 plays
CC a role in growth and maintenance of cancer cells based on the observation
CC of seminal vesicle hyperplasia in transgenic mice overexpressing B7-1.
CC Modulators of B7-1 are useful for the treatment of cancer e.g. seminal
CC vesicle, lung, brain, breast, ovarian, testicular cancer and cancers of
CC haematopoietic system. B7-1 and their modulators are useful to treat
CC autoimmune diseases such as systemic lupus erythematosus, rheumatoid
CC arthritis, immune thrombocytopenic purpura and psoriasis, chronic
CC inflammatory disease such as inflammatory bowel disease (Crohn's disease
CC and ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and
CC diabetes mellitus. They are also useful as immunosuppressive agents for
CC bone marrow and organ transplantation or to prolong graft survival.
CC Modulators of B7-L are also useful for diagnosis and treatment of
CC diseases involving abnormal cell proliferation, arteriosclerosis and
CC vascular restenosis. Soluble B7-L serves as vaccine adjuvants.
CC Antagonists of B7-L are useful for alleviation of toxic shock syndrome or
CC allo sensitization due to blood transfusions, and for treatment of
CC multiple sclerosis, allergy, asthma and hypersensitivity reactions, and
CC nephropathies (e.g. glomerulonephritis), skin disorders (pemphigus and
CC pemphigoid), endocrinopathies, various neuropathies, vasculopathies,
CC coeliac disease, anaemia, thrombocytopenia, Guillain-Barre syndrome and
CC myasthenia gravis, and lymphoproliferative disorders such as multiple
CC myeloma. B7-L gene is useful in gene therapy and to map the locations of
CC B7-L gene and related genes on chromosomes, as hybridisation probes in
CC diagnostic assays, for isolating corresponding chromosomal B7-L genes,
CC and to identify heritable tissue-degenerating diseases. The present
CC sequence is human B7-L protein DNA
XX
SQ Sequence 2603 BP; 758 A; 589 C; 573 G; 682 T; 0 U; 1 Other;
Query Match 100.0%; Score 576; DB 6; Length 2603;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTCAAGACATATTAGAGAGTGGGAAATATTCATGTGAACTAGACAACTGTGTAAAGA 60
DB 1103 TTCAAGACATATTAGAGAGTGGGAAATATTCATGTGAACTAGACAACTGTGTAAAGA 1162
XX
QY 61 GTCATAGTAATATGACCTGAGACAAAGTCATCCCAATCTCAGGAGCTTCCCTCG 120
DB 1163 GTCATAGTAATATGACCTGAGACAAAGTCATCCCAATCTCAGGAGCTTCCCTCG 1222
XX
QY 121 CCTGTACCTGGGAGTGAAGAGACAGATAGTCATGTTCTTGTCTGCAATTTTAA 180
DB 1223 CCTGTACCTGGGAGTGAAGAGACAGATAGTCATGTTCTTGTCTGCAATTTTAA 1282
XX
QY 181 TTATATGTGCTGTATATGTTGCTGTAGGAAGCCCTTGAAAGTCTATCCCAATATCCA 240
DB 1283 TTATATGTGCTGTATATGTTGCTGTAGGAAGCCCTTGAAAGTCTATCCCAATATCCA 1342
XX
QY 241 CACTTATATTTCCAAATTAAGCTGTAGTATGACCTTAAGACGCTGCTAATTTGACTGC 300
DB 1343 CACTTATATTTCCAAATTAAGCTGTAGTATGACCTTAAGACGCTGCTAATTTGACTGC 1402
XX
QY 301 CACTTGCACATCAGGGGGCGGTGCAATTTAGTATGGGCAATGATTCACCTTTTAA 360

DB 1403 CACTTGCACATCAGGGGGCGGTGCAATTTAGTATGGGCAATGATTCACCTTTTAA 1462
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
DB 1463 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 1522
QY 421 TGAATCATATTTTATAGATTAAGACAGACATGCGGCGACCGATTTTATTAATTAACCTGAG 480
DB 1523 TGAATCATATTTTATAGATTAAGACAGACATGCGGCGACCGATTTTATTAATTAACCTGAG 1582
QY 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGATGTTTATCCGTAAT 540
DB 1583 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTGATGATGATGTTTATCCGTAAT 1642
QY 541 GGTCCAGGGAAGACCTTTTACCTTACCTATATATGCG 576
DB 1643 GGTCCAGGGAAGACCTTTTACCTTACCTATATATGCG 1678
XX
RESULT 12
AAA70077
ID AAA70077 standard; cDNA; 2627 BP.
XX
AC AAA70077;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:391.
XX
KM Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KM tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200036107-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US030270.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
PI WPI; 2000-431589/37.
XX
DR WPI; 2000-431589/37.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Claim 1; Page 204-205; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 100.0%; Score 576; DB 3; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  TTCAAAGCATATTGAAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTTAGA 60
XX      |||
DB      1133 TTCAAAGCATATTGAAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTTAGA 1192
QY      61  GTGATTAAGTAAATGACGCTGGAGACAGACAGATGCCAGATCTCAGGGACCTCCCTCG 120
XX      |||
DB      1193 GTGATTAAGTAAATGACGCTGGAGACAGACAGATGCCAGATCTCAGGGACCTCCCTCG 1252
QY      121 CCTGTACCTGGGGAGTGAAGAGACAGATAGTGAATGTTCTTGTCTGTGAATTTTNG 180
XX      |||
DB      1253 CCTGTACCTGGGGAGTGAAGAGACAGATAGTGAATGTTCTTGTCTGTGAATTTTNG 1312
QY      181 TTATATGTGCTGTAAATGTTGCTCTGAGGAAGCCCTCGAAAGTCTATCCCAATATCCA 240
XX      |||
DB      1313 TTATATGTGCTGTAAATGTTGCTCTGAGGAAGCCCTCGAAAGTCTATCCCAATATCCA 1372
QY      241 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGAAGCTGTGTAATGACTGC 300
XX      |||
DB      1373 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGAAGCTGTGTAATGACTGC 1432
QY      301 CACTTGGCAACTCAGGGGGGGGCGTGCATTTAGTAATGGGTCAAAATGATTCACTTTTATG 360
XX      |||
DB      1433 CACTTGGCAACTCAGGGGGGGGCGTGCATTTAGTAATGGGTCAAAATGATTCACTTTTATG 1492
QY      361 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
XX      |||
DB      1493 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
QY      421 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 480
XX      |||
DB      1553 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 1612
QY      481 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTGAGATGATGTTCACTCCGTAAT 540
XX      |||
DB      1613 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTGAGATGATGTTCACTCCGTAAT 1672
QY      541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 576
XX      |||
DB      1673 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 1708

RESULT 13
AAH55681
ID      AAH55681 standard; DNA; 2627 BP.
XX
AC      AAH55681;
XX
DT      04-SEP-2001 (first entry)
XX
DE      Human ovarian tumour-derived antigen O8E DNA sequence.
XX
KW      Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
XX      antigen; O8E; ds.
XX
OS      Homo sapiens.
XX
PN      WO200140269-A2.
PD      07-JUN-2001.
PF      29-NOV-2000; 2000WO-US032520.
PR      30-NOV-1999; 99US-00451651.
PR      22-FEB-2000; 2000US-00510662.
PR      10-MAR-2000; 2000US-00523586.
PR      07-APR-2000; 2000US-00545068.
PR      15-MAY-2000; 2000US-00571025.
XX
PA      (CORI-) CORIXA CORP.
PI      Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX      WPI; 2001-356154/37.
DR

```

```

DR      N-PSDB; AAB99204, AAB99205.
XX
XX      Breast tumor polypeptides and the nucleic acids that encode them, useful
PT      for the prevention, diagnosis and treatment of breast cancer.
XX
PS      Claim 24; Page 189; 221pp; English.
XX
CC      The present invention relates to human breast tumour protein coding
CC      sequences (see AAH5479-AAH5513, AAH5517-AAH55679 and AAH55682-
CC      AAH55762). The breast tumour protein DNA sequences may be used in the
CC      prevention, diagnosis and treatment of diseases associated with
CC      inappropriate expression of the breast tumour protein e.g. breast cancer.
CC      The present sequence is a human ovarian tumour-derived antigen coding
CC      sequence, which was used in an example from the present invention
SQ      Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match      100.0%; Score 576; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTCAAAGCATATTGAAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTTAGA 60
XX      |||
DB      1133 TTCAAAGCATATTGAAAGTTGGGAAAAATTAATTCATGTGACTAGACAAGTGTGTTAGA 1192
QY      61  GTGATTAAGTAAATGACGCTGGAGACAGATGCCAGATCTCAGGGACCTCCCTCG 120
XX      |||
DB      1193 GTGATTAAGTAAATGACGCTGGAGACAGATGCCAGATCTCAGGGACCTCCCTCG 1252
QY      121 CCTGTACCTGGGGAGTGAAGAGACAGATAGTGAATGTTCTTGTCTGTGAATTTTNG 180
XX      |||
DB      1253 CCTGTACCTGGGGAGTGAAGAGACAGATAGTGAATGTTCTTGTCTGTGAATTTTNG 1312
QY      181 TTATATGTGCTGTAAATGTTGCTCTGAGGAAGCCCTCGAAAGTCTATCCCAATATCCA 240
XX      |||
DB      1313 TTATATGTGCTGTAAATGTTGCTCTGAGGAAGCCCTCGAAAGTCTATCCCAATATCCA 1372
QY      241 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGAAGCTGTGTAATGACTGC 300
XX      |||
DB      1373 CATCTTATATTCACAAATTAAAGCTGTAGTATGATACCTTAAGAAGCTGTGTAATGACTGC 1432
QY      301 CACTTGGCAACTCAGGGGGGGGCGTGCATTTAGTAATGGGTCAAAATGATTCACTTTTATG 360
XX      |||
DB      1433 CACTTGGCAACTCAGGGGGGGGCGTGCATTTAGTAATGGGTCAAAATGATTCACTTTTATG 1492
QY      361 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
XX      |||
DB      1493 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
QY      421 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 480
XX      |||
DB      1553 TGATCATTAATTTTACATTAACAGACAGTGGCGACACCGATTTTATTAATTAACCTGAG 1612
QY      481 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTGAGATGATGTTCACTCCGTAAT 540
XX      |||
DB      1613 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTGAGATGATGTTCACTCCGTAAT 1672
QY      541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 576
XX      |||
DB      1673 GGTCCAGGAGAGACCTTTCACCTTGACTATATGCG 1708

RESULT 14
AAB72971
ID      AAB72971 standard; DNA; 2627 BP.
XX
AC      AAB72971;
XX
DT      02-JUL-2002 (first entry)
XX
DE      Ovarian carcinoma polynucleotide O8E.
XX
KW      Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
DR

```

```

XX OS Homo sapiens.
XX PN MO200206317-A2.
XX PD 24-JAN-2002.
XX PF 17-JUL-2001; 2001WO-US022635.
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.
XX PR 20-SEP-2000; 2000US-00667857.
XX PR 04-APR-2001; 2001US-00827271.
XX PR 18-JUN-2001; 2001US-00884441.
XX PA (CORI-) CORIXA CORP.
XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX DR WPI: 2002-164781/21.
XX DR P-PSDB; ABP30900, ABP30901.
XX PS Example 2; Page 319-320; 408bp; English.
XX CC This invention relates to polypeptides comprising an immunogenic portion
XX CC of an ovarian carcinoma protein which acts as an immunostimulant and is
XX CC cytoactive. The polypeptides, polynucleotides, antibodies, fusion
XX CC proteins, T cell populations and antigen presenting cells that express
XX CC the polypeptides are useful for stimulating an immune response in a
XX CC patient and treating ovarian cancer. This sequence represents DNA related
XX CC to the invention
XX SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 100.0%; Score 576; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAGAGTGGGAAATTAATCATGTGAACATGAGAGTGTGTTAGA 60
DB 1133 TTCAAGACATATTAGAGTGGGAAATTAATCATGTGAACATGAGAGTGTGTTAGA 1192
QY 61 GTGATTAAGTAAATGACGTCGAGACAAAGTCATCCCAATCTCAGAGACTCCCTG 120
DB 1193 GTGATTAAGTAAATGACGTCGAGACAAAGTCATCCCAATCTCAGAGACTCCCTG 1252
QY 121 CCTGTCACTGGGAGTGAAGAGACAGATAGTCATGTTCTTTGCTCTGGAATTTTAA 180
DB 1253 CCTGTCACTGGGAGTGAAGAGACAGATAGTCATGTTCTTTGCTCTGGAATTTTAA 1312
QY 181 TTATATGTGTGTAATGTTCTCTGAGAGAGCCCTGGAAAGTCTATCCCAATATCCA 240
DB 1313 TTATATGTGTGTAATGTTCTCTGAGAGAGCCCTGGAAAGTCTATCCCAATATCCA 1372
QY 241 CATCTTATATTCACAAATTAAGCTGATGATGTAACCTTAAGAGCGTCTAATTTGATGC 300
DB 1373 CATCTTATATTCACAAATTAAGCTGATGATGTAACCTTAAGAGCGTCTAATTTGATGC 1432
QY 301 CACTTGCAACTGACGAGGCGGCTGCACTTTTATGTAATGGGTCAATGATTCATTTTATG 360
DB 1433 CACTTGCAACTGACGAGGCGGCTGCACTTTTATGTAATGGGTCAATGATTCATTTTATG 1492
QY 361 ATGCTTCGAAAGGCTTGCTTCTTCCCAATGACAAATGCCAAATGTGAGAAAA 420
DB 1493 ATGCTTCGAAAGGCTTGCTTCTTCCCAATGACAAATGCCAAATGTGAGAAAA 1552
QY 421 TGATCATTAATTTAGCATTAAGACAGAGAGTGGGAGACCCGATTTTAAATAAAGTGA 480

```

```

DB 1553 TGATCATTAATTTAGCATTAAGACAGAGAGTGGGAGACCCGATTTTAAATAAAGTGA 1612
QY 481 CACCTTCTTTTAAACAAATGCGGCTTTATTTCTGAGATGATGTTATCGGTAAAT 540
DB 1613 CACCTTCTTTTAAACAAATGCGGCTTTATTTCTGAGATGATGTTATCGGTAAAT 1672
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 576
DB 1673 GGTCCAGGAGAGACCTTTCACCTTGACTATATGAGC 1708
RESULT 15
ADA08544
ID ADA08544 standard; cDNA; 2627 BP.
XX AC ADA08544;
XX DT 06-NOV-2003 (first entry)
XX DE Human ovarian carcinoma polynucleotide OBE.
XX KW ss; human; gene therapy; ovarian cancer; cancer.
XX OS Homo sapiens.
XX PN US2003091580-A1.
XX PD 15-MAY-2003.
XX PF 17-JUL-2001; 2001US-00907969.
XX PR 18-JUN-2001; 2001US-00884441.
XX PA (MITC/) MITCHAM J L.
XX PA (KING/) KING G E.
XX PA (ALGA/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PA (RETT/) RETTER M W.
XX PA (FANG/) FANGER G R.
XX PA (VEDV/) VEDVICK T S.
XX PA (CART/) CARTER D.
XX PA (HILL/) HILL P.
XX PA (ALBO/) ALBONE E.
XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX DR WPI: 2003-532352/50.
XX PT New isolated 0772P polypeptides and polynucleotides, useful in gene
XX PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
XX PT cancer.
XX PS Example 2; SEQ ID NO 391; 371pp; English.
XX CC The invention relates to an isolated 0772P polypeptide, which has the
XX CC structure fully defined in the specification. The composition containing
XX CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
XX CC or antigen presenting cells are useful for stimulating an immune response
XX CC and treating ovarian cancer. Detecting the presence of the
XX CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
XX CC carcinoma cDNAs and protein cDNAs were identified using microarray
XX CC technology. The present sequence represents a human ovarian carcinoma
XX CC antigen polynucleotide.
XX SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
Query Match 100.0%; Score 576; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 6.5e-172;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAAGACATATTAGAGTGGGAAATTAATCATGTGAACATGAGAGTGTGTTAGA 60

```

```
Db 1133 TTCAAGACATATTTAGAAAGTTGGGAAAATAATTCATGTGACTAGACAAGTGTTAAGA 1192
QY 61 GTGATTAAGTAAATATGACGTGAGACAAATGCAATCCCAATCTCAGGACCTCCCCCTG 120
Db 1193 GTGATTAAGTAAATATGACGTGAGACAAATGCAATCCCAATCTCAGGACCTCCCCCTG 1252
QY 121 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGCTCTGAAATTTTAG 180
Db 1253 CCTGTCACCTGGGGAGTGAAGAGACAGATAGTGCATGTTCTTTGCTCTGAAATTTTAG 1312
QY 181 TTATATGTCGTGAATGTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAATATCCA 240
Db 1313 TTATATGTCGTGAATGTGCTCTGAGAAAGCCCTGAAAGTCTATCCCAATATCCA 1372
QY 241 CATCTTAATTTCCAAATTAAGCTAGTATGTAACCTTAAGACGCTGCTAATGACTGC 300
Db 1373 CATCTTAATTTCCAAATTAAGCTAGTATGTAACCTTAAGACGCTGCTAATGACTGC 1432
QY 301 CACTTGCAACTCAGGGGGGCGCTGCATTTTAAGTGGTCAATGATTCACTTTTATG 360
Db 1433 CACTTGCAACTCAGGGGGGCGCTGCATTTTAAGTGGTCAATGATTCACTTTTATG 1492
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
Db 1493 ATGCTTCCAAAGGTGCTTGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 1552
QY 421 TGATCATATTTTAAGATTAACAGACAGTCCGGCGACACCGATTTTATTAATTAAGTGA 480
Db 1553 TGATCATATTTTAAGATTAACAGACAGTCCGGCGACACCGATTTTATTAATTAAGTGA 1612
QY 481 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTAAT 540
Db 1613 CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTAAT 1672
QY 541 GGTCCAGGGAAGACCTTTACCTTGACTAATATGC 576
Db 1673 GGTCCAGGGAAGACCTTTACCTTGACTAATATGC 1708
```

Search completed: May 30, 2005, 10:27:08
Job time : 354.272 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 17:54:16 ; Search time 395.201 Seconds
(without alignments)
8948.327 Million cell updates/sec

Title: US-09-763-978B-10

Perfect score: 576

Sequence: 1 ttcaagacattatagatgacg.....ttccactgacatatagc 576

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 5700845 seqs, 306979757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubpna/PCr_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubpna/PCrUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	1567	9	US-09-884-441-74
2	576	100.0	1567	10	US-09-907-969-74
3	576	100.0	1567	10	US-09-827-271-74
4	576	100.0	1567	15	US-10-198-053-74
5	576	100.0	1567	19	US-10-860-790-74
6	576	100.0	1567	14	US-10-198-846-13583
7	576	100.0	1965	10	US-09-814-353-19262
8	576	100.0	2591	9	US-09-850-178-23
9	576	100.0	2603	9	US-09-896-738-1
10	576	100.0	2627	9	US-09-778-320-207
11	576	100.0	2627	9	US-09-910-689-207

12	576	100.0	2627	9	US-09-884-441-391	Sequence 391, App
13	576	100.0	2627	10	US-09-907-969-391	Sequence 391, App
14	576	100.0	2627	10	US-09-827-271-391	Sequence 391, App
15	576	100.0	2627	13	US-10-010-742-207	Sequence 207, App
16	576	100.0	2627	15	US-10-198-053-391	Sequence 391, App
17	576	100.0	2627	18	US-10-714-389-207	Sequence 207, App
18	576	100.0	2627	18	US-10-717-296-207	Sequence 207, App
19	576	100.0	2627	19	US-10-860-790-391	Sequence 391, App
20	574.4	99.7	3357	17	US-10-023-339-2	Sequence 2, Appl1
21	550.8	95.6	2626	9	US-09-877-065-7	Sequence 7, Appl1
22	549	95.3	595	10	US-09-814-353-257	Sequence 257, App
23	549	95.3	595	10	US-09-814-353-6647	Sequence 6647, App
24	549	95.3	643	10	US-09-814-353-13032	Sequence 13032, A
25	529.4	91.9	2626	17	US-10-023-339-9	Sequence 9, Appl1
26	499.8	86.8	1658	9	US-09-989-722-290	Sequence 290, App
27	499.8	86.8	1658	9	US-09-989-723-290	Sequence 290, App
28	499.8	86.8	1658	9	US-09-989-729-290	Sequence 290, App
29	499.8	86.8	1658	9	US-09-989-727-290	Sequence 290, App
30	499.8	86.8	1658	9	US-09-989-731-290	Sequence 290, App
31	499.8	86.8	1658	9	US-09-989-732-290	Sequence 290, App
32	499.8	86.8	1658	9	US-09-991-073-290	Sequence 290, App
33	499.8	86.8	1658	9	US-09-990-442-290	Sequence 290, App
34	499.8	86.8	1658	9	US-09-991-163-290	Sequence 290, App
35	499.8	86.8	1658	9	US-09-993-604-290	Sequence 290, App
36	499.8	86.8	1658	9	US-09-990-456-290	Sequence 290, App
37	499.8	86.8	1658	9	US-09-989-721-290	Sequence 290, App
38	499.8	86.8	1658	9	US-09-992-598-290	Sequence 290, App
39	499.8	86.8	1658	9	US-09-989-933-290	Sequence 290, App
40	499.8	86.8	1658	9	US-09-989-735-290	Sequence 290, App
41	499.8	86.8	1658	9	US-09-990-444-290	Sequence 290, App
42	499.8	86.8	1658	9	US-09-991-181-290	Sequence 290, App
43	499.8	86.8	1658	9	US-09-989-730-290	Sequence 290, App
44	499.8	86.8	1658	9	US-09-990-436-290	Sequence 290, App
45	499.8	86.8	1658	9	US-09-993-687-290	Sequence 290, App

ALIGNMENTS

RESULT 1
US-09-884-441-74 Application US/09884441
Sequence 74, Appl1
Patent No. US2002019158A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C7
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapien
US-09-884-441-74

Query Match	100.0%; Score 576; DB 9; Length 1567;
Best Local Similarity	100.0%; Pred No. 1.5e-164; Indels 0; Gaps 0;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTCAAGACATATTAGAGTTGGGAATATTATTCATGTGAACCTAGCAACTGTGTAGAGA 60
DB	91 TTCAAGACATATTAGAGTTGGGAATATTATTCATGTGAACCTAGCAACTGTGTAGAGA 150
QY	61 GTGATAGTAAATGACGCGGAGACAAAGTGATCCCGAGTTCCGAGACCTCCCTG 120
DB	151 GTGATAGTAAATGACGCGGAGACAAAGTGATCCCGAGTTCCGAGACCTCCCTG 210
QY	121 CCTGACCTGGGAGTGAAGAGACGATAGTATGATCTTGTCTGTAATTTTAA 180


```
Db 211 CCTGTCACCTGGGAGTGAAGACAGATAGTGCATGTTCTTGTCTCTGAATTTTAG 270
QY 181 TTATATNGCTGTATATGTTGCTCTGAGAGAGCCCTGGAAAGCTATCCCAATATCCA 240
Db 271 TTATATNGCTGTATATGTTGCTCTGAGAGAGCCCTGGAAAGCTATATCCCAATATCCA 330
QY 241 CATCTTATATTCACAAATTTAAGCTGTAGTATGTACCTTAAGACGCTGTAAATTGACTGC 300
Db 331 CATCTTATATTCACAAATTTAAGCTGTAGTATGTACCTTAAGACGCTGTAAATTGACTGC 390
QY 301 CACTTGCACACTCAGGGGCGGCTGCATTTTATGATAGGGTCAATATGATCACTTTTAG 360
Db 391 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATAGGGTCAATATGATCACTTTTAG 450
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGAAAGTTGAGAAAA 420
Db 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGAAAGTTGAGAAAA 510
QY 421 TGATCATATTTTATGACATTAACAGAGCAGTGGCGACACCGATTTTATTAATAAATGAG 480
Db 511 TGATCATATTTTATGACATTAACAGAGCAGTGGCGACACCGATTTTATTAATAAATGAG 570
QY 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTAGATGATGTTCAATCCGTGAT 540
Db 571 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTAGATGATGTTCAATCCGTGAT 630
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATATGCG 576
Db 631 GGTCCAGGAGAGACCTTTCACCTTGACTATATATGCG 666
```

RESULT 2

```
US-09-907-969-74
; Sequence 74, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-969-74
```

```
Query Match 100.0%; Score 576; DB 10; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTCAAGAATATTTAAGTTGGGAAAAATATTCATGTGACATGACAAAGTGTGTTAAG 60
Db 91 TTCAAGAATATTTAAGTTGGGAAAAATATTCATGTGACATGACAAAGTGTGTTAAG 150
QY 61 GTGATAGTAAATGACAGTGAAGACAGATGATCCCAAGTCTGAGGAGCCCTCCCTG 120
Db 151 GTGATAGTAAATGACAGTGAAGACAGATGATCCCAAGTCTGAGGAGCCCTCCCTG 210
QY 121 CCTGTACCTGGGAGTGAAGACAGATGATGATGTTCTTGTCTGAAATTTTAG 180
```

```
Db 211 CCTGTCACCTGGGAGTGAAGACAGATAGTGCATGTTCTTGTCTCTGAATTTTAG 270
QY 181 TTATATNGCTGTATATGTTGCTCTGAGAGAGCCCTGGAAAGCTATCCCAATATCCA 240
Db 271 TTATATNGCTGTATATGTTGCTCTGAGAGAGCCCTGGAAAGCTATATCCCAATATCCA 330
QY 241 CATCTTATATTCACAAATTTAAGCTGTAGTATGTACCTTAAGACGCTGTAAATTGACTGC 300
Db 331 CATCTTATATTCACAAATTTAAGCTGTAGTATGTACCTTAAGACGCTGTAAATTGACTGC 390
QY 301 CACTTGCACACTCAGGGGCGGCTGCATTTTATGATAGGGTCAATATGATCACTTTTAG 360
Db 391 CACTTCGCAACTCAGGGGCGGCTGCATTTTATGATAGGGTCAATATGATCACTTTTAG 450
QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGAAAGTTGAGAAAA 420
Db 451 ATGCTTCCAAAGGTGCTTGGCTTCTCTCCCACTGACAAATGCGAAAGTTGAGAAAA 510
QY 421 TGATCATATTTTATGACATTAACAGAGCAGTGGCGACACCGATTTTATTAATAAATGAG 480
Db 511 TGATCATATTTTATGACATTAACAGAGCAGTGGCGACACCGATTTTATTAATAAATGAG 570
QY 481 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTAGATGATGTTCAATCCGTGAT 540
Db 571 CACCTTCTTTTAAACAAACAAATGCGGTTTATTTCTAGATGATGTTCAATCCGTGAT 630
QY 541 GGTCCAGGAGAGACCTTTCACCTTGACTATATATGCG 576
Db 631 GGTCCAGGAGAGACCTTTCACCTTGACTATATATGCG 666
```

RESULT 3

```
US-09-827-271-74
; Sequence 74, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-827-271-74
```

```
Query Match 100.0%; Score 576; DB 10; Length 1567;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTCAAGAATATTTAAGTTGGGAAAAATATTCATGTGACATGACAAAGTGTGTTAAG 60
Db 91 TTCAAGAATATTTAAGTTGGGAAAAATATTCATGTGACATGACAAAGTGTGTTAAG 150
QY 61 GTGATAGTAAATGACAGTGAAGACAGATGATCCCAAGTCTGAGGAGCCCTCCCTG 120
Db 151 GTGATAGTAAATGACAGTGAAGACAGATGATGATGTTCTTGTCTGAAATTTTAG 210
QY 121 CCTGTACCTGGGAGTGAAGACAGATGATGATGTTCTTGTCTGAAATTTTAG 180
Db 211 CCTGTACCTGGGAGTGAAGACAGATGATGATGTTCTTGTCTGAAATTTTAG 270
QY 181 TTATATNGCTGTATATGTTGCTCTGAGAGAGCCCTGGAAAGTCTATCCCAATATCCA 240
Db 271 TTATATNGCTGTATATGTTGCTCTGAGAGAGCCCTGGAAAGTCTATCCCAATATCCA 330
QY 241 CATCTTATATTCACAAATTTAAGCTGTAGTATGTACCTTAAGACGCTGTAAATTGACTGC 300
```

OY	1	TTCAAAGCATATTGAAGTTGGGAAAAATTAATCAATGGAATAGACAAGTGTGAAG	60
Dd	91	TTCAAAGCATATTGAAGTTGGGAAAAATTAATCAATGGAATAGACAAGTGTGAAG	150
OY	61	GTGATTAAGTAAATATGACAGTGGAGACAAGTGCATCCAGATCTCAGGAGCTCCCTG	120
Dd	151	GTGATTAAGTAAATATGACAGTGGAGACAAGTGCATCCAGATCTCAGGAGCTCCCTG	210
OY	121	CCTGTACCTGGGGAGTGAAGAGACAGGATAGTGCATGTTCTTTGTCTTGAATTTTATG	180
Dd	211	CCTGTACCTGGGGAGTGAAGAGACAGGATAGTGCATGTTCTTTGTCTTGAATTTTATG	270
OY	181	TTATATGCTGTATATGTTGCTCTGAGGAAGCCCTGGAGAAAGTATCCCAATATCA	240
Dd	271	TTATATGCTGTATATGTTGCTCTGAGGAAGCCCTGGAGAAAGTATCCCAATATCA	330
OY	241	CATCTTATATTCACCAATTAAGCTGTAGTATGTAACCTTAAGACGCTGTAAATTGACTG	300
Dd	331	CATCTTATATTCACCAATTAAGCTGTAGTATGTAACCTTAAGACGCTGTAAATTGACTG	390
OY	301	CACTTTCGAACTCAGGGGGCGCTGCATTTTAGTAAATGGGTCAAAATGATTCACTTTATG	360
Dd	391	CACTTTCGAACTCAGGGGGCGCTGCATTTTAGTAAATGGGTCAAAATGATTCACTTTATG	450
OY	361	ATGCTTCCAAAGGTGCTTTGGCTTCTCTCCCACTGACCAATGCGCAAGTTGAGAAAAA	420
Dd	451	ATGCTTCCAAAGGTGCTTTGGCTTCTCTCTCCCACTGACCAATGCGCAAGTTGAGAAAAA	510
OY	421	TGATCATATATTAGCATTAACAGAGACGTGGCAGACCGATTTTATTAATTAACCTGAG	480

|||||
Db 511 TGATCATATATTTAGCATAAACAGACAGCGCGACACCGATTTTATTAATAAATGAG 570
|||
Qy 481 CACCTCTTTTAAACAAATGGGTTTATTTCTGAGATNGTTCATCCCGGAT 540
|||
Db 571 CACCTCTTTTAAACAAATGGGTTTATTTCTGAGATNGTTCATCCCGGAT 630
|||
Qy 541 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 576
|||
Db 631 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 666
|||

RESULT 6

US-10-198-846-13583
; Sequence 13583, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 13583
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 1484, 1497,
; LOCATION: 1554, 1578, 1585, 1591, 1596
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13583

Query Match 100.0%; Score 576; DB 14; Length 1596;
Best Local Similarity 100.0%; Pred. No. 1.6e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 60
|||
Db 267 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 326
|||
Qy 61 GTGATAGTAAGTACGCGAGAGACAGATGATCCCGATCTCAGGACCTCCCTG 120
|||
Db 327 GTGATAGTAAGTACGCGAGAGACAGATGATCCCGATCTCAGGACCTCCCTG 386
|||
Qy 121 CCTGTACCTGGGAGTGAAGAGACAGATGATGTTCTTGTCTGTAATTTTAA 180
|||
Db 387 CCTGTACCTGGGAGTGAAGAGACAGATGATGTTCTTGTCTGTAATTTTAA 446
|||
Qy 181 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTCGAAAGCTATCCCAATATCCA 240
|||
Db 447 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTCGAAAGCTATCCCAATATCCA 506
|||
Qy 241 CATCTATATTCACAAATTAAGCTGATGATGATCCTTAAGCGCTGCTAATTTGACTG 300
|||
Db 507 CATCTATATTCACAAATTAAGCTGATGATGATCCTTAAGCGCTGCTAATTTGACTG 566
|||
Qy 301 CACTTGCAACTCAGGCGCGCTGATTTTAATGATGGTCAATGATTCATTTTATG 360
|||
Db 567 CACTTGCAACTCAGGCGCGCTGATTTTAATGATGGTCAATGATTCATTTTATG 626
|||
Qy 361 ATGCTTCGAAAGGTGCTTGTCTTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
|||
Db 627 ATGCTTCGAAAGGTGCTTGTCTTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 686
|||

Qy 421 TGATCATATATTTAGCATAAACAGACAGCGCGACACCGATTTTATTAATAAATGAG 480
|||
Db 687 TGATCATATATTTAGCATAAACAGACAGCGCGACACCGATTTTATTAATAAATGAG 746
|||
Qy 481 CACCTCTTTTAAACAAATGGGTTTATTTCTGAGATNGTTCATCCCGGAT 540
|||
Db 747 CACCTCTTTTAAACAAATGGGTTTATTTCTGAGATNGTTCATCCCGGAT 806
|||
Qy 541 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 576
|||
Db 807 GGTCCAGGAGAGACCTTTCACCTTACTATATGCG 842
|||

RESULT 7

US-09-814-353-19262
; Sequence 19262, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 19262
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 1965
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-19262

Query Match 100.0%; Score 576; DB 10; Length 1965;
Best Local Similarity 100.0%; Pred. No. 1.7e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 60
|||
Db 1130 TTCAAGACATATTAAGTTGGGAAATTAATTCATGTAACCTAGCAAGTGTGTAAGA 1189
|||
Qy 61 GTGATAGTAAGTACGCGAGAGACAGATGATCCCGATCTCAGGACCTCCCTG 120
|||
Db 1190 GTGATAGTAAGTACGCGAGAGACAGATGATCCCGATCTCAGGACCTCCCTG 1249
|||
Qy 121 CCTGTACCTGGGAGTGAAGAGACAGATGATGTTCTTGTCTGTAATTTTAA 180
|||
Db 1250 CCTGTACCTGGGAGTGAAGAGACAGATGATGTTCTTGTCTGTAATTTTAA 1309
|||
Qy 181 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTCGAAAGTCTATCCCAATATCCA 240
|||
Db 1310 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTCGAAAGTCTATCCCAATATCCA 1369
|||
Qy 241 CATCTATATTCACAAATTAAGCTGATGATGATCCTTAAGCGCTGCTAATTTGACTGC 300
|||

Db 1370 CATCTTATATTCACCAATTTAGCTAGATGATACCTTAAGCGCTGTAATTTGATGCG 1429
Qy 301 CACTTGGCAACTCAGGGGCGGCTGCACTTTTATGTAATGGGTCAATGATTCACCTTTTATG 360
Db 1430 CACTTCCCAACTCAGGGGCGGCTGCACTTTTATGTAATGGGTCAATGATTCACCTTTTATG 1489
Qy 361 ATGCTTCAGAAAGGCGCTTGGCTTCTGCTCCCACTGACAAATGSCCAAGTTGAGAAAA 420
Db 1490 ATGCTTCAGAAAGGCGCTTGGCTTCTGCTCCCACTGACAAATGSCCAAGTTGAGAAAA 1549
Qy 421 TGATCATATTTTATGATTAAGCAAGAGAGAGTGGCGACACCGATTTTATTAATAAATGAG 480
Db 1550 TGATCATATTTTATGATTAAGCAAGAGAGAGTGGCGACACCGATTTTATTAATAAATGAG 1609
Qy 481 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCGTGAAT 540
Db 1610 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCGTGAAT 1669
Qy 541 GGTCCAGGAGGACCTTTGACCTTGACTATATGCG 576
Db 1670 GGTCCAGGAGGACCTTTGACCTTGACTATATGCG 1705

RESULT 8
US-09-850-178-23

Sequence 23, Application US/09850178
Patent No. US20020034749A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Billings-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colipite, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Russell, John C.
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Scroupe, Stephen D.
APPLICANT: Gordon, Juliano
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
FILE REFERENCE: 6251 US.P1
CURRENT APPLICATION NUMBER: US/09/850,178
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 2591
TYPE: DNA
ORGANISM: Homo sapiens
US-09-850-178-23

Query Match 100.0%; Score 576; DB 9; Length 2591;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTTAGAGTTGGAAATTAATTCATGTGAACCTGAGCAAGTGTGTTAAGA 60
Db 1111 TTCAAGACATATTTAGAGTTGGAAATTAATTCATGTGAACCTGAGCAAGTGTGTTAAGA 1170
Qy 61 GTGATAAGTAAATGACGCTGAGAGCAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 120
Db 1171 GTGATAAGTAAATGACGCTGAGAGCAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 1230
Qy 121 CCGTCACTGGGAGGTGAGAGGACAGAGATGTCATGTTCTTTGCTCTGAATTTTAA 180
Db 1231 CCGTCACTGGGAGGTGAGAGGACAGAGATGTCATGTTCTTTGCTCTGAATTTTAA 1290

Qy 181 TTATATGCTGTATATGTTCTCTGAGAGAAAGCCCTGAAAGCTATATCCACATATCCA 240
Db 1291 TTATATGCTGTATATGTTCTCTGAGAGAAAGCCCTGAAAGCTATATCCACATATCCA 1350
Qy 241 CATCTTATATTTCCAAATTTAGCTGTATGATGATGATGATGATGATGATGATGATGATGATG 300
Db 1351 CATCTTATATTTCCAAATTTAGCTGTATGATGATGATGATGATGATGATGATGATGATGATG 1410
Qy 301 CACTTGGCAACTCAGGGGCGGCTGCACTTTTATGTAATGGGTCAATGATTCACCTTTTATG 360
Db 1411 CACTTGGCAACTCAGGGGCGGCTGCACTTTTATGTAATGGGTCAATGATTCACCTTTTATG 1470
Qy 361 ATGCTTCAGAAAGGCGCTTGGCTTCTGCTCCCACTGACAAATGSCCAAGTTGAGAAAA 420
Db 1471 ATGCTTCAGAAAGGCGCTTGGCTTCTGCTCCCACTGACAAATGSCCAAGTTGAGAAAA 1530
Qy 421 TGATCATATTTTATGATTAAGCAAGAGAGAGTGGCGACACCGATTTTATTAATAAATGAG 480
Db 1531 TGATCATATTTTATGATTAAGCAAGAGAGAGTGGCGACACCGATTTTATTAATAAATGAG 1590
Qy 481 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCGTGAAT 540
Db 1591 CACCTTCTTTTAAACAACAATGCGGGTTTATTTCTCAGATGATGTTCACTCGTGAAT 1650
Qy 541 GGTCCAGGAGGACCTTTGACCTTGACTATATGCG 576
Db 1651 GGTCCAGGAGGACCTTTGACCTTGACTATATGCG 1686

RESULT 9
US-09-896-738-1

Sequence 1, Application US/09896738
Patent No. US20020165347A1
GENERAL INFORMATION:
APPLICANT: Fox, Michael
APPLICANT: Sullivan, John K.
APPLICANT: Fang, Mei
TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
FILE REFERENCE: 00-513-A
CURRENT APPLICATION NUMBER: US/09/896,738
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,645
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 1
LENGTH: 2603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (53)..(901)
US-09-896-738-1

Query Match 100.0%; Score 576; DB 9; Length 2603;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTTAGAGTTGGAAATTAATTCATGTGAACCTGAGCAAGTGTGTTAAGA 60
Db 1103 TTCAAGACATATTTAGAGTTGGAAATTAATTCATGTGAACCTGAGCAAGTGTGTTAAGA 1162
Qy 61 GTGATAAGTAAATGACGCTGAGAGCAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 120
Db 1163 GTGATAAGTAAATGACGCTGAGAGCAAGTGCATCCCGAGATCTCAGGAGACTCCCGCTG 1222
Qy 121 CCGTCACTGGGAGGTGAGAGGACAGAGATGTCATGTTCTTTGCTCTGAATTTTAA 180
Db 1223 CCGTCACTGGGAGGTGAGAGGACAGAGATGTCATGTTCTTTGCTCTGAATTTTAA 1282
Qy 181 TTATATGCTGTATATGTTCTCTGAGAGAAAGCCCTGAAAGCTATATCCACATATCCA 240
Db 1283 TTATATGCTGTATATGTTCTCTGAGAGAAAGCCCTGAAAGCTATATCCACATATCCA 1342

QY	241	CATCTTAATTCACCAATTTAAGCTGTATGTATGACCTTAAGAGCGCTCTAATTCAC	300
Db	1343	CATCTTAATTCACCAATTTAAGCTGTATGTATGACCTTAAGAGCGCTCTAATTCAC	1402
QY	301	CACCTTGGCAACTCAGGGGCGGTGTCATTTTGTATGGTCAAAATGATTCACCTTTTATG	360
Db	1403	CACCTTGGCAACTCAGGGGCGGTGTCATTTTGTATGGTCAAAATGATTCACCTTTTATG	1462
QY	361	ATGCTTCCAAAGTGCTCTTGCTTCTCTCCCACTGACCAATGCGCAAGTTGAGAAAA	420
Db	1463	ATGCTTCCAAAGTGCTCTTGCTTCTCTCCCACTGACCAATGCGCAAGTTGAGAAAA	1522
QY	421	TGATCATATTTTATGACATPAAACAGAGCAGTGGCGACACCGATTTTATPAAATPAACTGAG	480
Db	1523	TGATCATATTTTATGACATPAAACAGAGCAGTGGCGACACCGATTTTATPAAATPAACTGAG	1582
QY	481	CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAATGATGTTTCATCCGTGAAT	540
Db	1583	CACCTTCTTTTAAACAAACAAATGCGGGTTTATTTCTCAATGATGTTTCATCCGTGAAT	1642
QY	541	GGTCCAGGAAAGACCTTCACCTTGACATATATGCG	576
Db	1643	GGTCCAGGAAAGACCTTCACCTTGACATATATGCG	1678

```

RESULT 10
US-09-778-320-207
; Sequence 207, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugui
; APPLICANT: Houston, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491CS
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-320-207

```

Query Match	100.0%	Score 576	DB 9	Length 2627
Best Local Similarity	100.0%	Pred. No. 2e-164		
Matches 576	Conservative	0	Mismatches 0	IndeIs 0
			Gaps 0	
Qy	1	TYCAAGCACTATTGAAGTTGGGAAATAATTCATGTGAACCTAGACAAGTGTGTTAAGA	60	
Db	1133	TTCAAGACATTTGAAAGTTGGGAAATTAATTCATGTGAACCTAGACAAGTGTGTTAAGA	1192	
Qy	61	GTGATAGTAAATATCAGCTGGAGACAAAGTCATCCCAAGTCTCAGGACCTCCCCCTG	120	
Db	1193	GTGATAAATTAATATCAGCTGGAGACAAAGTCATCCCAAGTCTCAGGACCTCCCCCTG	1252	
Qy	121	CCTGCACCTGGGGAGTGAAGGAAGATAGTGAATCTTCTTGCTGAATTTTGA	180	
Db	1253	CCTGCACCTGGGGAGTGAAGGAAGATAGTGAATCTTCTTGCTGAATTTTGA	1312	
Qy	181	TTATATGCTGTATGTGCTCTGAGGAAGCCCTGGAAAGTCATATCCCAATATCCA	240	
Db	1313	TTATATGCTGTATGTGCTCTGAGGAAGCCCTGGAAAGTCATATCCCAATATCCA	1372	
Qy	241	CATCTTATATTCACAAATTAAGCTGTAGATGTAACCTTAAGCGCTGTATTTGACTGC	300	

Db	1373	CATCTTATATTTCCCAAAATTAAGGTATAGATATGACCTTAAGCGCTGTAAATTAATGACG	1432
Oy	301	CACTTGGCACTCAGGGGCGGCTGCACTTTATATAGTATATGGTCAAAATGATTAACCTTTTATG	360
Db	1433	CACTTTCCCACTCAGGGGCGGCTGCACTTTATATAGTATATGGTCAAAATGATTAATCACTTTTATG	1492
Oy	361	ATGCTTCCAAAGTGCCTTGCGCTCTCTCCCACTGACAAATGCCCAAAGTTGAGAAAA	420
Db	1493	ATGCTTCCAAAGTGCCTTGCGCTCTCTCCCACTGACAAATGCCCAAAGTTGAGAAAA	1552
Oy	421	TGATCATATATTTTATGCAATAAACAAGACAGATGCGGACAACGATTTTATATTAATACTGAG	480
Db	1553	TGATCATATATTTTATGCAATAAACAAGACAGATGCGGACAACGATTTTATATTAATACTGAG	1612
Oy	481	CACCTTCTTTTAAACAACAATAATGCGGGTTATATTTCTCAGATGATGTTCAATCCGTGAT	540
Db	1613	CACCTTCTTTTAAACAACAATAATGCGGGTTATATTTCTCAGATGATGTTCAATCCGTGAT	1672
Oy	541	GGTCCAGGAAGACCTTTACCTTGACTATATGGC	576
Db	1673	GGTCCAGGAAGACCTTTACCTTGACTATATGGC	1708

```

RESULT 11
US-09-910-689-207
; Sequence 207, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yougu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-689-207

```

Query	March	Similarity	100.0%	Score	576	DB	9	length	2627	
Best	Local	Similarity	100.0%	Pred.	No.	28	164			
Matches	576	Conservative	0	Mismatches	0	Indels	0	Gaps	0	
Oy	1	TTCAAAGACATATTAGAAAGTTGGGAAAAATATTCATGTGAACTAAGACAGTGTCTTAAGA	60							
Db	1133	TTCAAAGACATATTAGAAAGTTGGGAAAAATATTCATGTGAACTAAGACAGTGTCTTAAGA	1192							
Oy	61	GTGATTAAGTAAATAGCAAGTGAACAAGTCATCCCGAGTCTCAGGAGCCTCCCTCG	120							
Db	1193	GTGATTAAGTAAATAGCAAGTGAACAAGTCATCCCGAGTCTCAGGAGCCTCCCTCG	1252							
Oy	121	CCTGTCACTCTGGGAGTGAGAGGACAGAGTATGTGCATGTTCTTTGTCTCTGAATTTTTCG	180							
Db	1253	CCTGTCACTCTGGGAGTGAGAGGACAGAGTATGTGCATGTTCTTTGTCTCTGAATTTTTCG	1312							
Oy	181	TTATATAGTCTGTATGTGCTCTGAGAGAACCCCTGGAAGGTATATCCCAACATATCCA	240							
Db	1313	TTATATAGTCTGTATGTGCTCTGAGAGAACCCCTGGAAGGTATATCCCAACATATCCA	1372							
Oy	241	CATCTTAATATCCAAATTAAGCTGTATGTATTAACCTTAAGACGCTGTCTAATTGACTGC	300							
Db	1373	CATCTTAATATCCAAATTAAGCTGTATGTATTAACCTTAAGACGCTGTCTAATTGACTGC	1432							

[illegible]

```

RESULT 12
US-09-884-441-391
; Sequence 391, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Patrick
; TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
; TITLE OF INVENTION: DIAGNOSIS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; .LENGTH: 2627
; .TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-441-391

Query Match: 100.0%; Score 576; DB 9; Length 2627;
Best Local Similarity 100.0%; Pred. No. 2e-164;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAGCATATTAGAGAGTTGGGAAATATATTCATGTGAACCTGACAGTGTTTAGA 60
DB 1133 TTCAAGCATATTAGAGAGTTGGGAAATATATTCATGTGAACCTGACAGTGTTTAGA 11922
QY 61 GTGATTAAGTAAATGACAGTGGAGACAAAGTCATCCCGAGTCTCAGGAGCCTCCCTG 120
DB 1193 GTGATTAAGTAAATGACAGTGGAGACAAAGTCATCCCGAGTCTCAGGAGCCTCCCTG 12522
QY 121 CCTGTACCTGGGAGTGAAGAGACAGATAGTGCAATCTTTGTCTCTGAATTTTAA 180
DB 1253 CCTGTACCTGGGAGTGAAGAGACAGATAGTGCAATCTTTGTCTCTGAATTTTAA 1312
QY 181 TTATATGCTGTATGTGCTCTGAGGAAACCCCTGGAAAGTCAATCCCAACATATCA 240
DB 1313 TTATATGCTGTATGTGCTCTGAGGAAACCCCTGGAAAGTCAATCCCAACATATCA 13722
QY 241 CATCTTATATTCACAAATTAAGCTGTATGTATGTACCTTAAGACGCTCTAATTGACTGC 300
DB 1373 CATCTTATATTCACAAATTAAGCTGTATGTATGTACCTTAAGACGCTCTAATTGACTGC 14322
QY 301 CACTTTCGCACTCAGGGGGCGGCTGCTATTTAGTATGGGTCAATGATTCACCTTTATG 360
DB 1433 CACTTTCGCACTCAGGGGGCGGCTGCTATTTAGTATGGGTCAATGATTCACCTTTATG 14922
QY 361 ATGCTTCCAAAGAGGCTTGCTCTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAAA 420
DB 1493 ATGCTTCCAAAGAGGCTTGCTCTCTCTCCCACTGACAAATGCAAAAGTTGAGAAAAA 15522

```

QY	422	TGATCAATAATTTT	AGCTAAACAGACAG	CGCGGACAACCGA	TTTTTATTAATAAAC	GTG	480
QY <td>1553</td> <td>TGATCAATAATTTT <td>AGCTAAACAGACAG <th>CGCGGACAACCGA</th> <th>TTTTTATTAATAAAC</th> <td>GTG</td> <td>1612</td> </td></td>	1553	TGATCAATAATTTT <td>AGCTAAACAGACAG <th>CGCGGACAACCGA</th> <th>TTTTTATTAATAAAC</th> <td>GTG</td> <td>1612</td> </td>	AGCTAAACAGACAG <th>CGCGGACAACCGA</th> <th>TTTTTATTAATAAAC</th> <td>GTG</td> <td>1612</td>	CGCGGACAACCGA	TTTTTATTAATAAAC	GTG	1612
Db <td>481</td> <td>CACCTCTTTT <td>TAACAAACAAATGCGG</td> <td>GTTPATTTCTCAGATG</td> <td>ATGTCGTCAAT</td> <td></td> <td>540</td> </td>	481	CACCTCTTTT <td>TAACAAACAAATGCGG</td> <td>GTTPATTTCTCAGATG</td> <td>ATGTCGTCAAT</td> <td></td> <td>540</td>	TAACAAACAAATGCGG	GTTPATTTCTCAGATG	ATGTCGTCAAT		540
QY <td>1613</td> <td>CACCTCTTTT <td>TAACAAACAAATGCGG</td> <td>GTTPATTTCTCAGATG</td> <td>ATGTCGTCAAT</td> <td></td> <td>1672</td> </td>	1613	CACCTCTTTT <td>TAACAAACAAATGCGG</td> <td>GTTPATTTCTCAGATG</td> <td>ATGTCGTCAAT</td> <td></td> <td>1672</td>	TAACAAACAAATGCGG	GTTPATTTCTCAGATG	ATGTCGTCAAT		1672
Db <td>541</td> <td>GGTCCAGGAAGAC</td> <td>CTTTCACCTTGCTAT</td> <td>TATGGC</td> <td></td> <td>576</td> <td></td>	541	GGTCCAGGAAGAC	CTTTCACCTTGCTAT	TATGGC		576	
QY <td>1673</td> <td>GGTCCAGGAAGAC</td> <td>CTTTCACCTTGCTAT</td> <td>TATGGC</td> <td></td> <td>1708</td> <td></td>	1673	GGTCCAGGAAGAC	CTTTCACCTTGCTAT	TATGGC		1708	

[illegible]

Db 1613 CACCTTCTTTTAAACAAGAAATCGGGTTTATTCTCAGATGATGTCATCCGTGAT 1672
Qy 541 GGTCCAGGGAAGACCTTTCACTTGACTATATGGC 576
Db 1673 GGTCCAGGGAAGACCTTTCACTTGACTATATGGC 1708

Search completed: May 31, 2005, 10:07:35
Job time : 396.201 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:48:09 ; Search time 2240.26 Seconds

(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978b-10

Perfect score: 576

Sequence: 1 ttcaagacatattagaagt.....ttcacctgacatattgac 576

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574.4	99.7	2431	3	CR603772 full-length
2	562	97.6	610	7	CN259817 17006000
3	526.4	91.4	939	5	BX371687 BX371687
4	523	90.8	622	7	CN259814 17006001
5	440.6	76.5	455	2	BE083024 RC2-BT064
6	433.4	75.2	624	7	CN259815 17006000
7	421	73.1	779	6	CA311913
8	419.8	72.9	661	2	BE741325
9	397	68.9	427	7	CN259816 17006000
10	314	54.5	737	7	CN259812 17006001
11	281	48.8	698	7	CN259812 17006001
12	260.8	45.3	481	5	BU679990 UT-CF-DU1
13	191	33.1	925	5	EX314963
14	121.4	21.2	925	5	EX314963
15	104.2	18.1	611	5	CR844392
16	94.6	16.0	812	8	BH280041
17	92	15.7	255	7	CK903676
18	90.4	15.7	351	1	AI698956
19	84.4	14.7	1018	5	EX317228
20	84.4	14.7	1018	5	EX317228
21	76	13.2	530	4	BI963964
22	58	10.1	728	9	CC473491
23	41.8	7.3	507	8	AZ332474
24	40.8	7.1	658	9	AG147829

25	40.4	7.0	501	8	BH697243	BH697243	BOWFOX06TR
26	40.2	7.0	1031	9	CNS00CF2	AL059199	Drosophila
27	40	6.9	1190	3	CR719416	CR719416	Terradon
28	39	6.8	1101	3	CNS01515	AL105502	Drosophila
29	38.8	6.7	302	5	BP068460	BP068460	BP068460
30	38.8	6.7	567	8	B2205357	B2205357	CH230-436
31	38.2	6.6	523	1	AL601909	DKFZP313P	AL601909
32	38	6.6	755	5	BU258011	BU258011	603747820
33	37.8	6.6	539	7	CV401235	CV401235	QV4-NN114
34	37.8	6.6	912	9	CG191398	CG191398	PUCAC65TD
35	37.8	6.6	926	9	CG191397	PUCAC65TB	CG191397
36	37.6	6.5	524	6	CA667778	w1Leu1.pk0	CA667778
37	37.6	6.5	843	9	CL426387	ZMMBB0044	CL426387
38	37.4	6.5	746	5	BU258987	BU258987	603743026
39	37.4	6.5	799	5	BX137735	Dario_rer	BX137735
40	37.4	6.5	839	5	BU111185	BU111185	603127240
41	37.4	6.5	894	5	BU355366	BU355366	603473992
42	37.2	6.5	576	6	CL372745	RPC144_30	CL372745
43	37.2	6.5	748	9	CR339430	Medicago	CR339430
44	37.2	6.5	1016	8	CC270576	CH261-119	CC270576
45	37.2	6.5	1201	9	CNS010CB	AL098789	Drosophila

ALIGNMENTS

RESULT 1	CR603772	2431 bp	mrna	linear	HTC 21-JUN-2004
LOCUS	CR603772	full-length cDNA clone	CS0D1039G21 of Placenta Cot 25-normalized		
DEFINITION	CR603772	full-length cDNA clone	CS0D1039G21 of Placenta Cot 25-normalized		
ACCESSION	CR603772	GI:50484579			
VERSION	CR603772.1	GI:50484579			
KEYWORDS	HTC; CNSUT_CDNA				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2431)				
AUTHORS	Li, W.B., Gruber, C., Jesse, J., and Polyes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact: Peng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 2431)				
REFERENCE	Genoscope.				
AUTHORS	Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage				
TITLE	Direct Submission				
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)				
COMMENT	Web: www.genoscope.cns.fr				
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime				
	end enriched, double-strand cDNA was digested with Not I and cloned				
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library				
	was normalized. Library was constructed by Life Technologies, a				
	division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1. 2431				
	/organism="Homo sapiens"				
	/mol_type="mrna"				
	/db_xref="taxon:9606"				
	/clone="CS0D1039G21"				
	/isue_type="Placenta Cot 25-normalized"				
	/plasmid="pCMVSPORT_6"				
ORIGIN					
Query Match	99.7%	Score 574.4	DB 3	Length 2431	
Best Local Similarity	99.8%	Pred. No. 2e-154	1	Indels 0	Gaps 0
Matches	575	Conservative	0	Mismatches	1
Qy	1	TTCAAGACATATTAGAGTTGGGAAATATTCATGTGACACTAGCAAGTGTGTAAAG	60		
Db	982	TTCAAGACATATTAGAGTTGGGAAATATTCATGTGACACTAGCAAGTGTGTAAAG	1041		

61 GTGATTAAGTAAATGACCTGGAGACAAGTGATCCCGATCTCAGGAGCTCCCTG 120
1042 GTGATTAAGTAAATGACCTGGAGACAAGTGATCCCGATCTCAGGAGCTCCCTG 1101
121 CCTGTACCTGGAGAGTGAAGACAGATGATGTTCTTTTGTCTGTAAATTTTNG 180
1102 CCTGTACCTGGAGAGTGAAGACAGATGATGTTCTTTTGTCTGTAAATTTTNG 1161
181 TTAATGCTGTAAGTGTCTGTGAAGCCCTGGAAGCTTATCCCAATATCA 240
1162 TTAATGCTGTAAGTGTCTGTGAAGCCCTGGAAGCTTATCCCAATATCA 1221
241 CATCTTAATTCACAAATTAAGTGTATGATGATCCCTAAGACGCTGTAATGATG 300
1222 CATCTTAATTCACAAATTAAGTGTATGATGATCCCTAAGACGCTGTAATGATG 1281
301 CACTTCGCACTGACGAGGCGGCTGCATTTTAAATGATGGTCAATGATTCATTTTATG 360
1282 CACTTCGCACTGACGAGGCGGCTGCATTTTAAATGATGGTCAATGATTCATTTTATG 1341
361 ATGCTTCCAAAGTGTCTGCTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
1342 ATGCTTCCAAAGTGTCTGCTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAA 1401
421 TGATCAATATTTAGATTAACAGACAGATCGCGACACCGATTTTAAATTAATGAG 480
1402 TGATCAATATTTAGATTAACAGACAGATCGCGACACCGATTTTAAATTAATGAG 1461
481 CACTTCTTTTAAACAACAATGCGGTTTATTTCTCAGATGATGTTCAATCGTGAAT 540
1462 CACTTCTTTTAAACAACAATGCGGTTTATTTCTCAGATGATGTTCAATCGTGAAT 1521
541 GGTCCAGGAGAGACCTTCACTTGACTATATGCG 576
1522 GGTCCAGGAGAGACCTTCACTTGACTATATGCG 1557

RESULT 2
CN259817 610 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600024783 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259817
VERSION CN259817.1 GI:47276231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 610)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Flak, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
CONTACT: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 610 Std Error: 0.00.
FEATURES
source
1..610
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_lib="GRN_PREHEP"
/note="oligo dT primed, full-length enriched cDNA library"

ORIGIN
Query Match 97.6%; Score 562; DB 7; Length 610;
Best Local Similarity 100.0%; Pred. No. 5,4e-121;
Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
From DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

15 AGAAGTGGGAAAATTAATTCATGTAAGTGAACAAGTGTGTAAGATGAATTAAT 74
6 AGAAGTGGGAAAATTAATTCATGTAAGTGAACAAGTGTGTAAGATGAATTAAT 65
75 GCACGTGAAGACAAATGATCCCATGATCTGAGGAGCTCCCTGCTGTACCTGGG 134
66 GCACGTGAAGACAAATGATCCCATGATCTGAGGAGCTCCCTGCTGTACCTGGG 125
135 AGTGAAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 194
126 AGTGAAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 185
195 ATGTTGCTCTGAGAGAGCCCTGGAAGTCTATCCCAATATCCCAATATCTTATATCA 254
186 ATGTTGCTCTGAGAGAGCCCTGGAAGTCTATCCCAATATCCCAATATCTTATATCA 245
255 CAATTAAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 314
246 CAATTAAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305
315 GGGGGGCTGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 374
306 GGGGGGCTGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 365
375 GCTTGGCTCTCTCTCCCACTGACAAATGATGATGATGATGATGATGATGATGAT 434
366 GCTTGGCTCTCTCTCCCACTGACAAATGATGATGATGATGATGATGATGATGAT 425
435 GCATTAACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 494
426 GCATTAACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
435 ACAACAAATGCGGTTTATTTCTCAGATGATGATGATGATGATGATGATGATGAT 554
446 ACAACAAATGCGGTTTATTTCTCAGATGATGATGATGATGATGATGATGATGAT 545
555 CTTTCACTTGACTATATGCG 576
546 CTTTCACTTGACTATATGCG 567

RESULT 3
BX371687/c 939 bp mRNA linear EST 28-APR-2004
LOCUS BX371687
DEFINITION BX371687 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
clone CS01031921 3-PRIME, mRNA sequence.
ACCESSION BX371687
VERSION BX371687.2 GI:46834026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 939)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459784.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BclI sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 742.r
 For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BA10212B08_CS01978_1ec=742.r.

FEATURES

source

```
1. .939
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039Y21"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

```
Query Match          91.4%; Score 526.4; DB 5; Length 939;
Best Local Similarity 98.4%; Pred. No. 1.2e-140;
Matches 571; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

QY 1 TTCAAAGACATA-TTGAAGTTGGGAAATTA-TTCATGTGAAGTACAG-TGTGTTA 57
DB 930 TTCAAAGACATATTGAAGTTGGGAAATTA-TTCATGTGAAGTACAG-TGTGTTA 871
QY 58 AGAGTGTAAATTAATGACAGTGGAGACAAGTCCCAAGATCTCAGGGA-CCTCC 116
DB 870 AGAGTGTAAATTAATGACAGTGGAGACAAGTCCCAAGATCTCAGGGA-CCTCC 811
QY 117 CCGACCTGTACCTGGGAGTGAAGAGACAGATAGTCAATGTTCTGTCTGATTT 176
DB 810 CCGACCTGTACCTGGGAGTGAAGAGACAGATAGTCAATGTTCTGTCTGATTT 751
QY 177 TTAGTTATATGTCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCACATA 236
DB 750 TTAGTTATATGTCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCACATA 691
QY 237 TCCACATCTTAATTTCCAAATTAAGCTGTATGATACCTTACAGCGTCTAATGA 296
DB 690 TCCACATCTTAATTTCCAAATTAAGCTGTATGATACCTTACAGCGTCTAATGA 631
QY 297 CTGCACTTGGCACTCAGGGGGGCTGCAATTTAGTAAGGTCGAATGATTCACCTTT 356
DB 630 CTGCACTTGGCACTCAGGGGGGCTGCAATTTAGTAAGGTCGAATGATTCACCTTT 571
QY 357 TATGATGCTTCCAAAGGTCCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGA 416
DB 570 TATGATGCTTCCAAAGGTCCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGA 511
QY 417 AAAATGATCAATATTTAGCATAAACAGACAGTGGCGACACCGATTTTAAATTAAC 476
DB 510 AAAATGATCAATATTTAGCATAAACAGACAGTGGCGACACCGATTTTAAATTAAC 451
QY 477 TGAGCACTCTTTTAAACAAATGGGGTTATTTCTGAGATGATGTTCAATCCCT 536
DB 450 TGAGCACTCTTTTAAACAAATGGGGTTATTTCTGAGATGATGTTCAATCCCT 391
QY 537 GAATGTCAGGAGACCTTTCACCTTACTATATGCG 576
DB 390 GAATGTCAGGAGACCTTTCACCTTACTATATGCG 351
```

```
RESULT 4
CN259814          622 bp      mRNA      linear      EST 16-MAY-2004
LOCUS             17006000107256 GRN_PREHER Homo sapiens cDNA 5', mRNA sequence.
DEFINITION        CN259814
ACCESSION         CN259814
VERSION           CN259814.1 GI:47276228
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 622)
 Brandenberger R., Wei H., Zhang S., Lei S., Muraige J., Pisk G. J., Li Y., Xu C., Fang R., Guegler K., Rao M. S., Mandalam R., Lebkowski J. and Stanton L. W.
 Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
 Insert length: 622 Std Error: 0.00.
 Location/Qualifiers

FEATURES

source

```
1. .622
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_lib="GRN PREHER"
/notes="oligo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"
```

ORIGIN

```
Query Match          90.8%; Score 523; DB 7; Length 622;
Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGAAGTACAGCAAGTGTGTTAGA 60
DB 100 TTCAAAGACATATTAGAAGTTGGGAAATTAATTCATGTGAAGTACAGCAAGTGTGTTAGA 159
QY 61 GTGATTAAGTAAATGACAGTGGAGACAAGTGCATCCCAAGTCTCAGGACCTCCCTG 120
DB 160 GTGATTAAGTAAATGACAGTGGAGACAAGTGCATCCCAAGTCTCAGGACCTCCCTG 219
QY 121 CCGTCACTGGGAGTGAAGAGACAGATAGTCAATGTTCTGTCTGATTTTATG 180
DB 220 CCGTCACTGGGAGTGAAGAGACAGATAGTCAATGTTCTGTCTGATTTTATG 279
QY 181 TTATATGTGCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCCAATATCCA 240
DB 280 TTATATGTGCTGTATGTTGCTCTGAGGAAGCCCTGAAAGTCTATCCCAATATCCA 339
QY 241 CATCTTAATTTCCAAATTAAGCTGTATGATGATACCTTACAGCGTCTAATGACTGC 300
DB 340 CATCTTAATTTCCAAATTAAGCTGTATGATGATACCTTACAGCGTCTAATGACTGC 399
QY 301 CACTTGGCACTCAGGGGGGCTGCAATTTAGTAAGGTCGAATGATTCACCTTTATG 360
DB 400 CACTTGGCACTCAGGGGGGCTGCAATTTAGTAAGGTCGAATGATTCACCTTTATG 459
QY 361 ATGCTTCCAAAGGTCCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 420
DB 460 ATGCTTCCAAAGGTCCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 519
QY 421 TGATCAATATTTAGCATAAACAGACAGTGGCGACACCGATTTTAAATTAATGAG 480
DB 520 TGATCAATATTTAGCATAAACAGACAGTGGCGACACCGATTTTAAATTAATGAG 579
QY 481 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGAT 523
DB 580 CACCTTCTTTTAAACAAATGCGGTTTATTTCTCAGAT 622
```

RESULT 5

BE083024

LOCUS BE083024 455 bp mRNA linear EST 12-JUN-2000
DEFINITION RC2-BT0642-240300-018-a02 BT0642 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE083024
VERSION BE083024.1 GI:8473332
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 455)
Dias Neco, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FADESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2-BT0642-240
300-018-a02&f=2000-03-24&t=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 455.
Location/Qualifiers
1..455
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="BT0642"
/note="Organ: breast; Vector: puc18; Site 1: Sma1; Site 2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 76.5%; Score 440.6; DB 2; Length 455;
Best Local Similarity 99.1%; Pred. No. 5.9e-116;
Matches 443; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 10 AATATTGAGAGTGGGAAATTAATTCATGTGAGCTAGACAGAGTGTGTAAGAGATTAAGT 69
DB 9 AATATTGAGAGTGGGAAATTAATTCATGTGAGCTAGACAGAGTGTGTAAGAGATTAAGT 68
QY 70 AAAATGCACTGTGAGAGCAAGATGATCCAGATCTCAGGAGACTCCCTGCTGCTGACC 129
DB 69 AAAATGCACTGTGAGAGCAAGATGATCCAGATCTCAGGAGACTCCCTGCTGCTGACC 128
QY 130 TGGGGAGTGAAGAGACAGATAGTGTCTTTTGTCTCTGTAATTTTAAATTATATG 189
DB 129 TGGGGAGTGAAGAGACAGATAGTGTCTTTTGTCTCTGTAATTTTAAATTATATG 188
QY 199 CTGTATATGTTGCTCTGAGAGAGCCCTGAGAAAGTCAATCCCAATATCAATCTTATA 249
DB 189 CTGTATATGTTGCTCTGAGAGAGCCCTGAGAAAGTCAATCCCAATATCAATCTTATA 248
QY 250 TTCACAAATTAAGCTGTATGTATGTAACCTAAGACGCTGCTAATGATGCCACTTGCA 309

|||||
DB 249 TTCACAAATTAAGCTGTATGTATGTAACCTAAGACGCTGCTAATGATGCCACTTGCG 308
QY 310 ACTCAGGGGCGGCTGCATTTTATGTAATGGGTCAATATGATCACTTTTATATGCTTCCA 369
DB 309 ACTCAGGGGCGGCTGCATTTTATGTAATGGGTCAATATGATCACTTTTATATGCTTCCA 368
QY 370 AAGTGCTGTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATPA 429
DB 369 AAGTGCTGTGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATPA 428
QY 430 TTTTATGATTAACAGACAGATGCGGCA 456
DB 429 TTTTATGATTAACAGACAGATGCGGCA 455

RESULT 6
CN259815
LOCUS CN259815 624 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700600019460 GRN_PRENEM Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN259815
VERSION CN259815.1 GI:47276229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 624)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandilam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 624 Std Error: 0.00.
Location/Qualifiers
1..624
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_1ib="GRN_PRENEM"
/note="oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

ORIGIN
Query Match 75.2%; Score 433.4; DB 7; Length 624;
Best Local Similarity 99.8%; Pred. No. 7.6e-114;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 GGACAGATAGTGCATGTTCTTGTCTGTAATTTTATGTAATGCTGTATGTTGC 201
DB 1 GGACAGATAGTGCATGTTCTTGTCTGTAATTTTATGTAATGCTGTATGTTGC 60
QY 202 TTTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCCAAATCTTATTCACAAATTA 261
DB 61 TTTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCCAAATCTTATTCACAAATTA 120
QY 262 AGCTATGATGTAACCTTAAGACGCTGCTAAATGCTGCCACTTGCACTGAGGGGCG 321
DB 121 AGCTATGATGTAACCTTAAGACGCTGCTAAATGCTGCCACTTGCACTGAGGGGCG 180
QY 322 CTGCAATTTTATGATAGGTCAAAATGATTCACCTTTTATGATGCTTCCAAAGTGCTTGG 381

Db 181 CTGATTTTGTAGTATGGGTCAATGATTCATTTTTATGATGCTTCCAAAGGTGCTGG 240
Qy 382 CTCTCTCTCCCACTGCAAAATGCCAAAGTTGAGAAAAATGATCATATTTTACATATA 441
Db 241 CTCTCTCTCTCCCACTGCAAAATGCCAAAGTTGAGAAAAATGATCATATTTTACATATA 300
Qy 442 CAGAGCAGTGGGAGACCCGATTTTATTAATACTGAGCACCCTTTTAAACAACA 501
Db 301 CAGAGCAGTGGGAGACCCGATTTTATTAATACTGAGCACCCTTTTAAACAACA 360
Qy 502 AATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGATGTCAGGAGGAGACCTTTCA 561
Db 361 AATGCGGGTTTATTTCTCAGATGATGTTCAATCCGTGATGTCAGGAGGAGACCTTTCA 420
Qy 562 CCTTGACTATATGGC 576
Db 421 CCTTGACTATATGGC 435

RESULT 7

CA311913/c 779 bp mRNA linear EST 04-NOV-2002
LOCUS UI-CF-FNO-afj-a-01-0-UI.e1 UI-CF-FNO Homo sapiens cDNA clone
DEFINITION UI-CF-FNO-afj-a-01-0-UI 3', mRNA sequence.
ACCESSION CA311913
VERSION CA311913.1 GI:24530011
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu

TISSUE Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.regen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source

1. .779 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afj-a-01-0-UI"
/issue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/clone_id="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Score 1; Site 2: Not 1;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS

ORIGIN

6hr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

Query Match 73.1%; Score 421; DB 6; Length 779;
Best Local Similarity 98.8%; Pred. No. 3.1e-110;
Matches 424; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTCAAGACATATTTAGAAAGTTGGAAAAATATATTCATGTGAACTAGACAAAGTGTGTAAGA 60
Db 431 TTCAAGACATATTTAGAAAGTTGGAAAAATATATTCATGTGAACTAGACAAAGTGTGTAAGA 372
Qy 61 GTCATAGTAAATTCACACCGTGAAGACAGATGTCATCCCAAGTCCAGGAGCCCTCCCTG 120
Db 371 GTATATAGTAAATTCACACCGTGAAGACAGATGTCATCCCAAGTCCAGGAGCCCTCCCTG 312
Qy 121 CTTGTACCTGGGAGTGAAGAGACAGATGTCATGTCATGTCCTGTCGTAATTTTAA 180
Db 311 CTTGTACCTGGGAGTGAAGAGACAGATGTCATGTCATGTCCTGTCGTAATTTTAA 252
Qy 181 TTATATGTGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCACATATCCA 240
Db 251 TTATATGTGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGTCTATCCACATATCCA 192
Qy 241 CATCTTATATTCACAAATTAAGCTGTATGATGATACCTTAAGACGCTGCTAATTTGACTGC 300
Db 191 CATCTTATATTCACAAATTAAGCTGTATGATGATACCTTAAGACGCTGCTAATTTGACTGC 132
Qy 301 CACTTGCAACTCAGAGGCGGCTGCTATTTAGTAAATGAGTCAATGATTCATCTTTTATG 360
Db 131 CACTTGCAACTCAGAGGCGGCTGCTATTTAGTAAATGAGTCAATGATTCATCTTTTATG 72
Qy 361 ATGCTTCCAAAGGTGCTTGGCTTCTTCTCCCACTGACAAATGCCAAAGTTGAGAAAAA 420
Db 71 ATGCTTCCAAAGGTGCTTGGCTTCTTCTCCCACTGACAAATGCCAAAGTTGAGAAAAA 12
Qy 421 TGATCATTA 429
Db 11 AAAAAAAAA 3

RESULT 8

BE741325 681 bp mRNA linear EST 15-SEP-2000
LOCUS 601594166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947872 5',
DEFINITION mRNA sequence.
ACCESSION BE741325
VERSION BE741325.1 GI:10155317
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
TISSUE Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNC810 row: d column: 17
High quality sequence strop: 677.

FEATURES
source

1. .681 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:3947872"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NH_MGC_9"
 /note="Organ: ovary; Vector: pOTB7, Site_1: XhoI, Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 72.9%; Score 419.8; DB 2; Length 681;
 Best Local Similarity 99.3%; Pred. No. 6,6e-110;
 Matches 432; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 TTCAAAGACATATTAGAGTTGGAAATATTATTCATGTAGCAAGAGTGTAAAGA 60
 DB 247 TTCAAAGACATATTAGAGTTGGAAATATTATTCATGTAGCAAGAGTGTAAAGA 306
 QY 61 GGTATAGTAAATGACGCTGAGAGCAATGCAATCCGAGTCTGAGGACCTCCCTCG 120
 DB 307 GGTATAGTAAATGACGCTGAGAGCAATGCAATCCGAGTCTGAGGACCTCCCTCG 366
 QY 121 CCTGTACCTGGGAGTGAAGAGACAGATAGTCATGTTCTTGTCTCTGAATTTTAG 180
 DB 367 CCTGTACCTGGGAGTGAAGAGACAGATAGTCATGTTCTTGTCTCTGAATTTTAG 426
 QY 181 TTATATGTCTGTATGTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCCA 240
 DB 427 TTATATGTCTGTATGTGCTCTGAGAGAGCCCTGAGAAAGTCTATCCCAATATCCA 486
 QY 241 CATCTTATTTCCAAATTAAGCTGTATAGTGTACCTTAAGCGTGTATATGATGCTG 300
 DB 487 CATCTTATTTCCAAATTAAGCTGTATAGTGTACCTTAAGCGTGTATATGATGCTG 546
 QY 301 CACTTGCAGCACTCAGGGGCGGCTGATTTAGTATGAGTCAATGATTCACCTTTTATG 360
 DB 547 CACTTGCAGCACTCAGGGGCGGCTGATTTAGTATGAGTCAATGATTCACCTTTTATG 606
 QY 361 ATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGA-AAA 419
 DB 607 ATGCTTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGACCAA 666
 QY 420 ATGATCATATTTTA 434
 DB 667 CTGATCATATTTTA 681

RESULT 9
 CN259816 427 bp mRNA linear EST 16-MAY-2004
 LOCUS CN259816
 DEFINITION 17000600060609 GRN_PRENNU Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN259816
 VERSION CN259816.1 GI:47276230
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J. and Stanton,L.W.
 JOURNAL Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
 COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)
 CONTACT: Brandenberger R
 JOURNAL
 COMMENT Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 427 Std Error: 0.00.
 Location/Qualifiers

FEATURES

source

1. 427
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
 /clone_lib="GRN_PRENNU"
 /note="Oligo dt primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic acid and mitogens."

ORIGIN

Query Match 68.9%; Score 397; DB 7; Length 427;
 Best Local Similarity 100.0%; Pred. No. 2,3e-103;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 GTTATATGCTGTATGTGCTGAGAGAGCCCTGGAAGTCTATCCCAATATCC 239
 DB 1 GTTATATGCTGTATGTGCTGAGAGAGCCCTGGAAGTCTATCCCAATATCC 60
 QY 240 ACATCTTATTTCCAAATTAAGCTGTATAGTATGATACCTTAAGAGCTGTATGACTG 299
 DB 61 ACATCTTATTTCCAAATTAAGCTGTATAGTATGATACCTTAAGAGCTGTATGACTG 120
 QY 300 CCACTTCCCACTCAGGGGCGGCTGATTTAGTATGAGTCAATGATTCACCTTTTAT 359
 DB 121 CCACTTCCCACTCAGGGGCGGCTGATTTAGTATGAGTCAATGATTCACCTTTTAT 180
 QY 360 GATGCTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 419
 DB 181 GATGCTCCAAAGGTGCTTGGCTTCTTCCCACTGACAAATGCCAAAGTTGAGAAAA 240
 QY 420 ATGATCATATTTTAAGCAATAACAGAGAGTGGGAGACCGATTTTAATAATAACTGA 479
 DB 241 ATGATCATATTTTAAGCAATAACAGAGAGTGGGAGACCGATTTTAATAATAACTGA 300
 QY 480 GCACCTTCTTTTAAACAAATGCGGTTATTTCTCAGATGATGTTCCCTGTAA 539
 DB 301 GCACCTTCTTTTAAACAAATGCGGTTATTTCTCAGATGATGTTCCCTGTAA 360
 QY 540 TGGTCAGGAGAGACCTTTGACCTTGACTATATGAGC 576
 DB 361 TGGTCAGGAGAGACCTTTGACCTTGACTATATGAGC 397

RESULT 10
 CN259810 737 bp mRNA linear EST 16-MAY-2004
 LOCUS CN259810
 DEFINITION 17000600184202 GRN_PRENNU Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN259810
 VERSION CN259810.1 GI:47276224
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J. and Stanton,L.W.
 JOURNAL Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
 COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)
 CONTACT: Brandenberger R
 JOURNAL
 COMMENT Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 737 Std Error: 0.00.
 Location/Qualifiers

FEATURES

Source
 1. 737
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_id="GRN_PRENEM"
 /note="Toligo dT primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic and mitogens."

ORIGIN

Query Match 54.5%; Score 314; DB 7; Length 737;
 Best Local Similarity 100.0%; Pred. No. 2.4e-79;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCTGTAGTATGACCTTAAAGCGCTGCTAAATGACCTCCACTTGCACCTCAGGGGCGGC 322
 DB 1 GCTGTAGTATGACCTTAAAGCGCTGCTAAATGACCTCCACTTGCACCTCAGGGGCGGC 60
 QY 323 TGCATTTTAAATGAGGTCAATGATTCACCTTTTAAATGATGCTTCCAAAGGCTTGGC 382
 DB 61 TGCATTTTAAATGAGGTCAATGATTCACCTTTTAAATGATGCTTCCAAAGGCTTGGC 120
 QY 383 TTCTCTCCCACTGACAAATGCGCAAGTTGAGAAAATGATCATATTTTAAAGCATTAAC 442
 DB 121 TTCTCTCCCACTGACAAATGCGCAAGTTGAGAAAATGATCATATTTTAAAGCATTAAC 180
 QY 443 AGAGCACTCGGCGCACCGCATTTTAAATTAATTAATGAGCACTTCTTTTAAACAAACA 502
 DB 181 AGAGCACTCGGCGCACCGCATTTTAAATTAATTAATGAGCACTTCTTTTAAACAAACA 240
 QY 503 ATCGGGTATTTTCTCAATGATGTTTCATCCGGAATGCTCCAGGAGACCTTTTAC 562
 DB 241 ATCGGGTATTTTCTCAATGATGTTTCATCCGGAATGCTCCAGGAGACCTTTTAC 300
 QY 563 CTGACTATATGCG 576
 DB 301 CTGACTATATGCG 314

RESULT 11

CN259812 698 bp mRNA linear EST 16-MAY-2004
 LOCUS CN259812
 DEFINITION 170006001.77307 GRN_PRENEM Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN259812
 VERSION CN259812.1 GI:47276226
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 698)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
 Li, Y., Xu, C., Fang, R., Gueglar, K., Rao, M. S., Mandalam, R.,
 Lebkowski, J. and Stanton, L. W.
 Transcriptional characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 698 Std Error: 0.00.

JOURNAL

COMMENT

FEATURES

Location/Qualifiers
 1. 698
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, DMSO-treated H9 cell
 line"
 /clone_id="GRN_PRENEM"
 /note="Toligo dT primed, full-length enriched cDNA library
 from DMSO-treated hES cell line H9 (p22) maintained in
 feeder-free conditions"

ORIGIN

Query Match 48.8%; Score 281; DB 7; Length 698;
 Best Local Similarity 99.7%; Pred. No. 8.2e-70;
 Matches 292; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCAAAGACATATTAGAAAGTTGGGAAATTAATCATGTGAACATGATGTTTAA 60
 DB 406 TTCAAAGACATATTAGAAAGTTGGGAAATTAATCATGTGAACATGATGTTTAA 465
 QY 61 GTGATTAATTAATTAATGACGTTGAGACATGATCCCAAGATCTCAGGACCTCCCTG 120
 DB 466 GTGATTAATTAATTAATGACGTTGAGACATGATCCCAAGATCTCAGGACCTCCCTG 525
 QY 121 CCTGTACCTGGGAGTGAAGACAGATAGTGTCTTCTTCTGAAATTTTAA 180
 DB 526 CCTGTACCTGGGAGTGAAGACAGATAGTGTCTTCTTCTGAAATTTTAA 565
 QY 181 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCACATATCA 240
 DB 586 TTATATGCTGTAAATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCACATATCA 645
 QY 241 CATCTTAATTTCCAAATTAATTAAGCTGTATATGA-CCCTAAGACGCTGTAA 292
 DB 646 CATCTTAATTTCCAAATTAATTAAGCTGTATATGATATCCCTAAGACGCTGTAA 698

RESULT 12

Bu679990 481 bp mRNA linear EST 07-OCT-2002
 LOCUS Bu679990
 DEFINITION UI-CF-DUI-aba-c-02-0-UI-.s1 UI-CF-DUI Homo sapiens cDNA clone
 UI-CF-DUI-aba-c-02-0-UI 3', mRNA sequence.
 ACCESSION Bu679990
 VERSION Bu679990.1 GI:23528471
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 481)
 Bonaldi, M. F., Lennon, G. and Soares, M. B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL MEDLINE
 PUBMED 8889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

Location/Qualifiers
1..481
/organism="Homo sapiens"
/mol_type="cDNA"
/db_xref="taxon:9606"
/clone="UI-CF-DUI-aba-c-02-0-U"
/issue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone.lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; UI-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGCTAGGC.
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-DUI
TAG_SEQ=GAGCTAGGC"

ORIGIN

Query Match 45.3%; Score 260.8; DB 5; Length 481;
Best Local Similarity 96.9%; Pred. No. 5.1e-64;
Matches 277; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

1 TTCAAGACATATTAGAGTGGGAAATTAATTCATGTAACAGCAAGTGTAAAGA 60
196 TTCAAGACATATTAGAGTGGGAAATTAATTCATGTAACAGCAAGTGTAAAGA 255
61 GTGATTAAGTAATGACGCTGAGACAGATGCCAGATCTCAGGAGCTCCCTCG 120
256 GTGATTAAGTAATGACGCTGAGACAGATGCCAGATCTCAGGAGCTCCCTCG 315
121 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTTAA 180
316 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTTAA 375
181 TTATATGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCA 240
376 TTATATGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGCTATCCCAATATCA 435
241 CATCTTA--TATTCACAATTAAGCTGATGATGATGATGATGATGATGATGAT 284
436 CATCTTAAGAGTTCACAAATTAATCCTGTATGATGATGATGATGATGATGAT 481

RESULT 13
AQ214963 510 bp DNA linear GSS 18-SEP-1998
LOCUS HS_3062_B2_E01_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3062 Col=2 Row=J, genomic survey
sequence.

ACCESSION AQ214963
VERSION AQ214963
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 510)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PubMed 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3062 Row: J column: 2
Class: BAC ends
High quality sequence stop: 510.

FEATURES

source

Location/Qualifiers
1..510
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3062 Col=2 Row=J"
/sex="male"
/clone.lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 33.2%; Score 191; DB 8; Length 510;
Best Local Similarity 78.6%; Pred. No. 7.6e-44;
Matches 257; Conservative 0; Mismatches 60; Indels 10; Gaps 2;

1 TTCAAGACATATTAGAGTGGGAAATTAATTCATGTAACAGCAAGTGTAAAGA 60
191 TTCCCCGAGCTATTCTTAATGCGGAGCTGTATTCTATCTGAACTACACTTGATTA-- 247
61 GTGATTAAGTAATGACGCTGAGACAGATGCCAGATCTCAGGAGCTCCCTCG 120
248 -----TCTTACTATCAAGAGACAGATGATGCCAGATCTCAGGAGCTCCCTCG 302
121 CCTGTACCTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTTAA 180
303 CCTATCACTGGGAGTGAAGACAGATGTCATGTTCTTGTCTCTGAATTTTAA 362
181 TTATATGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAG--TCTATCCCAATATC 238
363 TTATATGCTGTAATGTTGCTCTGAGAAAGCCCTGAAAGTCTCTATCCCAATATCA 422
239 CACATCTTATATTCACAATTAAGCTGATGATGATGATGATGATGATGATGAT 298
423 CACATCTTATATTCACAATTAAGCTGATGATGATGATGATGATGATGATGAT 482
299 GCCACTTGCACACTCAGAGGCGGCTGC 325
483 GCCCTACAGCACTCCGGAGCATTTGC 509

RESULT 14
BX369964 925 bp mRNA linear EST 26-APR-2004
LOCUS BX369964 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D103Y921 5-PRIME, mRNA sequence.

ACCESSION BX369964
VERSION BX369964
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 925)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0BA0302A11_CS02865_1sc=742.r.

FEATURES

source

Location/Qualifiers

1..925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 21.1%; Score 121.4; DB 5; Length 925;
Best Local Similarity 99.5%; Pred. No. 1.1e-23;
Matches 133; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 TTCAAGACATATTAGAGTTGGGAAATATTCATGTGACTGACAGAGTGTG-TTAA 59
Db 728 TTCAAGACATATTAGAGTTGGGAAATATTCATGTGACTGACAGAGTGTG 787
Qy 60 AGTATTAAGTAAATGACGCGGAGACAGTGCATCCCAATCTCAGGACCTCCCT 119
Db 788 AGTATTAAGTAAATGACGCGGAGACAGTGCATCCCAATCTCAGGACCTCCCT 847
Qy 120 GCCTGTCACTGGGG 134
Db 848 GCCTGTCACTGGGG 862

RESULT 15
CR844392/c 611 bp DNA linear GSS 27-SEP-2004
LOCUS GR0AAA79CH04FM1 INRA BAC Bos taurus genomic clone INRAD_713D08, DNA
DEFINITION sequence, genomic survey sequence.
ACCESSION CR844392
VERSION CR844392.1 GI:52780480
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Eggen, A., Schibler, L. and Roy, A.
TITLE Bovine BAC End sequences from the INRA bovine BAC library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 611)
AUTHORS
TITLE Genoscope.
JOURNAL Direct Submission
TITLE Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Contact: Andre Eggen
Department of Animal Genetics - LGBC
INRA
78350 Jouy-en-Josas, France
Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
Email: eggen@jouy.inra.fr
Clones are derived from the INRA bovine BAC library
(http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library

availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
(Evry) Plate: 713 row: D column: 08
Seq primer: M13 Forward
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..611
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Breed: Holstein"
/db_xref="taxon:9913"
/clone="INRAD_713D08"
/sex="Male"
/cell_type="fibroblast"
/clone_lib="INRA bovine BAC"
/note="Vector: pBelobAC11; Site 1: HindIII; Holstein bull;
INRA Bovine BAC library (Male) produced by Andre
Eggen-Genoscope sequence ID : GR0AAA79CH04FM1"

ORIGIN

Query Match 18.1%; Score 104.2; DB 9; Length 611;
Best Local Similarity 75.7%; Pred. No. 9.3e-19;
Matches 196; Conservative 0; Mismatches 53; Indels 10; Gaps 5;

Qy 325 CATTATAGTATGCGTCAATGATTCATCTTTATGATGCTTCGAAGGCTGGCTT 384
Db 280 CATTATAGTATGCGTCAATGATTCATCTTTATGATGCTTCGAAGGCTGGCTT 222
Qy 385 CTCTCCCACTGACAAATGCC-----AAAGTGAGAAAATGATCAATATTTAGCATA 439
Db 221 CTCTCCCACTGACAAATGCCAAAGAAAATGATCAATATTTAGCATA 162
Qy 440 AACAGACACTGCGGACACCC--GATTTTAAATAAATGACACCTCTTTT-AAAC 496
Db 161 AAAATAGTATGATGATGACACTGATTTTCTAAACTATGACACCTCTTTTAAAC 102
Qy 497 AAACAATGGGGTTTATTTCTGATGATGATTCATCCGATATGTCACGG-AAAGAC 555
Db 101 AAACAATGGGGTTTATTTCTGATGATGATTCATCCGATATGTCACGG-AAAGAC 42
Qy 556 CTTTCACTTGACTATATG 574
Db 41 CTTTCACTTGACTATATG 23

Search completed: May 31, 2005, 00:10:49
Job time : 2243.26 secs

THIS PAGE LEFT BLANK

Query Match	Score	DB	Length
100.0%	890	6	890

Db	2200	TCGAAATTAATCTTCAGCTGTTGAGCTTCAATGTTCTTCCCTTCAATCTACCCGCAAG	2259
Qy	541	CCAAAGTTCTGTAAAGAAATGCTTAGTCTTAGCTCAGGTTTCTTACTTGAATTTAGA	600
Db	2260	CCAAATTCCTGTAAAGAAATGCTTAGTCTCAGGTTTCTTACTTGAATTTAGA	2319
Qy	601	TCCTCAGACCCCTTCTGCGCAATTTCAATTAAGGCAACAAACATACCTTCATGAA	660
Db	2320	TCCTCAGACCCCTTCTGCGCAATTTCAATTAAGGCAACAAACATACCTTCATGAA	2379
Qy	661	GCACACACAGACTTTTGAAGCAAGACATGACTGTTGAATTAGGCTTGAAGATG	720
Db	2380	GCACACACAGACTTTTGAAGCAAGACATGACTGTTGAATTAGGCTTGAAGATG	2439
Qy	721	AAGCTTTGAAGAAAAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA	780
Db	2440	AAGCTTTGAAGAAAAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA	2499
Qy	781	ACCACTGCTTCTCTGGAAGCTTGGAGCCACGCGTGAATGATTAACATGTTGTTATGAAAC	840
Db	2500	ACCACTGCTTCTCTGGAAGCTTGGAGCCACGCGTGAATGATTAACATGTTGTTATGAAAC	2559
Qy	841	TGAATTTAGAGTTCTGATGCTTCAAGAGAAATGATTAATATACATTTCT	890
Db	2560	TGAATTTAGAGTTCTGATGCTTCAAGAGAAATGATTAATATACATTTCT	2609
RESULT 3			
AR238405		2627 bp	DNA
LOCUS	AR238405		linear
DEFINITION	Sequence 391 from patent US 6468546.		PAT 20-DEC-2002
ACCESSION	AR238405		
VERSION	AR238405.1		GI:27283369
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2627)		
TITLE	Mitcham, J. L., King, G. E. and Algate, P. A.		
JOURNAL	Compositions and methods for therapy and diagnosis of ovarian		
FEATURES	Patent: US 6468546-A 391-22-OCT-2002;		
SOURCE	Location/Qualifiers		
	1..2627		
	/organism="Unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match	98.7%;	Score 878;	DB 6;
Best Local Similarity	99.9%;	Pred. No. 2e-258;	
Matches	889;	Conservative 0;	Mismatches 0;
		Indels 1;	Gaps 1;
Qy	1	C A A G C T T G A G G C T T C T C T T T C C A T C C T G G T G A C A G C T T A A G A C C T C A G T T T T C A T A	60
Db	1721	C A A G C T T G A G G C T T C T C T T T C C A T C C T G C G T G A C A G C T T A A G A C C T C A G T T T T C A T A	1780
Qy	61	G C A T T T A G A G C A G T G G A C T A G C T G G G A T G A T T T G C C C C C A A T C T C G G G A A T G T C	120
Db	1781	G C A T T T A G A G C A G T G G A C T A G C T G G G A T G A T T T G C C C C C A A T C T C G G G A A T G T C	1840
Qy	121	T G A A G A C A A T T T G G T T A C C T C A A T G A G G A G T G A G A G A G A T A C A G T C T A C C A A C	180
Db	1841	T G A A G A C A A T T T G G T T A C C T C A A T G A G G A G T G A G A G A G A T A C A G T C T A C C A A C	1900
Qy	181	T A G T G A A T A A A G G C C A G G A A G C T G C T C A A C T C T T A C A T G T A C A G G A A G T C T C C C C A	240
Db	1901	T A G T G A A T A A A G G C C A G G A A G C T G C T C A A C T C T T A C A T G T A C A - G A A G T C T C C C A	1959
Qy	241	T T A C A A C T A C C A A T C C G A A G T G T C A A C T G T C A G A C T A A G A A A C C C T G T T T T G A G T	300
Db	1960	T T A C A A C T A C C A A T C C G A A G T G T C A A C T G T C A G A C T A A G A A A C C C T G T T T T G A G T	2019
Qy	301	A G A A A A G G C C T G G A A A G G G G A C C A A C A A T C T G T C T G C T T C T T C A C A T T A G C A T T	360

Db	2020	AGAAAGGGGCGTGGAAAGGGGAGCCAAACAATCTGTCTCTCTTCTTCACTTATGTCAATT	2079
Qy	361	GGCAAAATAGCAATTCGTCTCTTTGGCTGCTGCTCCAGACAGAGAGCCAGAACTATC	420
Db	2080	GGCAAAATAGCAATTCGTCTCTTTGGCTGCTGCTCCAGACAGAGAGCCAGAACTATC	2139
Qy	421	GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCTATGGGAAATGCTCGA	480
Db	2140	GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCTATGGGAAATGCTCGA	2139
Qy	481	TGGGATTAATCTTCAGCTTGTGAGCTTCAAGTTCTTCCCTCAATTCATCCCTGCAAG	540
Db	2200	TGGGATTAATCTTCAGCTTGTGAGCTTCAAGTTCTTCCCTCAATTCATCCCTGCAAG	2258
Qy	541	CCAAATTCTGAAGAAGAAATGCCGAGTTCTAGCTCAGATTTTCTTACTCGAATTTTGA	600
Db	2260	CCAAATTCTGAAGAAGAAATGCCGAGTTCTAGCTCAGATTTTCTTACTCGAATTTTGA	2319
Qy	601	TCTCCAGACCCCTTCCTGGCCCAATTCGAAATTAAGGCAACAACATATACCTTCATGAA	660
Db	2320	TCTCCAGACCCCTTCCTGGCCCAATTCGAAATTAAGGCAACAACATATATACCTTCATGAA	2379
Qy	661	GCACACACAGCTTTTGAAGACAGCAATGACTGCTGAATTGAGGCCCTTGAGGAAATG	720
Db	2380	GCACACACAGCTTTTGAAGACAGCAATGACTGCTGAATTGAGGCCCTTGAGGAAATG	2439
Qy	721	AAGCTTTGAAGAAAGAAATGACTTTGTTTCAGAGCCCTCCACACTCTCATGTGTGA	780
Db	2440	AAGCTTTGAAGAAAGAAATGACTTTGTTTCAGAGCCCTCCACACTCTCATGTGTGA	2499
Qy	781	ACCACTGCTTCTCTGAGCCTTGAGCCACAGGTGACTGTATTACATGTTGTATAGAAAC	840
Db	2500	ACCACTGCTTCTCTGAGCCTTGAGCCACAGGTGACTGTATTACATGTTGTATAGAAAC	2559
Qy	841	TGATTTTGAAGTTCGTGATCTTCAAGAGATGATTAATATACATTTTCTT	890
Db	2560	TGATTTTGAAGTTCGTGATCTTCAAGAGATGATTAATATACATTTTCTT	2609
RESULT 4			
LOCUS	AR478744	2627 bp	DNA linear PAT 14-MAY-2004
DEFINITION	Sequence 391 from patent US 6699664.		
ACCESSION	AR478744		
VERSION	AR478744.1	GI:47237396	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2627)		
TITLE	Mitchem,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W.,		
JOURNAL	Fanger,G.R., Reed,S.G., Vedvick,T.S. and Carter,D.		
FEATURES	Compositions, and methods for the therapy and diagnosis of ovarian		
source	Patent: US 6699664-A 391 02-MAR-2004;		
ORIGIN	Location/Qualifiers		
	1..2627		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	98.7%;	Score 878;	DB 6; Length 2627;
Best Local Similarity	99.9%;	Pred. No. 2e-258;	
Matches	889;	Conservative 0;	Mismatches 0; Indels 1; Gaps 1;
Qy	1	CAAGCTCTGAAGCTTCTCTTCCATCTGCGTGAACAGCTAAGACCTCAGTTTCAATA	60
Db	1721	CAAGCTCTGAAGCTTCTCTTCCATCTGCGTGAACAGCTAAGACCTCAGTTTCAATA	1780
Qy	61	GCATCTGAGACAGTGGAGCTCAGTGGGGGTGATTTGGCCCCCATCTTCGGGGGAATGTC	120
Db	1781	GCATCTGAGACAGTGGAGCTCAGTGGGGGTGATTTGGCCCCCATCTTCGGGGGAATGTC	1840

QY 121 TGAAGCAATTTTGGTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
1841 TGAAGCAATTTTGGTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
QY 181 TAGTGATTAAGGCGCAGGAGTGTCTCACTCTTACCATGTACAGGAGCTCTCCCA 240
1901 TAGTGATTAAGGCGCAGGAGTGTCTCACTCTTACCATGTACAGGAGCTCTCCCA 1959
QY 241 TTACAACTACCAATCCGAAGTGTCAAGTGTCAAGACTTAAGAAACCTGGTTTGAAT 300
1960 TTACAACTACCAATCCGAAGTGTCAAGTGTCAAGACTTAAGAAACCTGGTTTGAAT 2019
QY 301 AGAAAAAGGCGCTGGAAGAGGAGGCAACAAATCTGTCTGTCTTCCCTCAATTAAGTCAAT 360
2020 AGAAAAAGGCGCTGGAAGAGGAGGCAACAAATCTGTCTGTCTTCCCTCAATTAAGTCAAT 2079
QY 361 GGCAAATTAAGCAATCTGTCTCTTTGGCTGTCTGTCTGACACAGAGAGCCAACTCTATC 420
2080 GGCAAATTAAGCAATCTGTCTCTTTGGCTGTCTGTCTGACACAGAGAGCCAACTCTATC 2139
QY 421 GGGCACACAGATTAACATCTCTCAGTGAAGAGTTGACAAAGGCTTAAGGAAATGCTCTA 480
2140 GGGCACACAGATTAACATCTCTCAGTGAAGAGTTGACAAAGGCTTAAGGAAATGCTCTA 2199
QY 481 TGGGATTAATCTTCAAGCTGTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTACCTGCAAG 540
2200 TGGGATTAATCTTCAAGCTGTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTACCTGCAAG 2259
QY 541 CCAGATTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTGAATTGA 600
2260 CCAGATTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTGAATTGA 2319
QY 601 TCTCCAGACCCCTTCGCGCAATTCOAATTAAGGCAACAAATATCTTCCATGAA 660
2320 TCTCCAGACCCCTTCGCGCAATTCOAATTAAGGCAACAAATATCTTCCATGAA 2379
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTCTTGAATTGAGGCTTGAGGAATG 720
2380 GCACACACAGACTTTTGAAGCAAGCAATGACTCTTGAATTGAGGCTTGAGGAATG 2439
QY 721 AAGCTTTGAAGAAAGAAATACCTTTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 780
2440 AAGCTTTGAAGAAAGAAATACCTTTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 2499
QY 781 ACCACTGCTTCTTGAAGCAAGTGAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
2500 ACCACTGCTTCTTGAAGCAAGTGAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2559
QY 841 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATTAATTAATTAATTAATTAATTAAT 890
2560 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATTAATTAATTAATTAATTAATTAAT 2609
Db

RESULT 5
AX156350 2627 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 207 from Patent WO0140269.
AX156350
VERSION AX156350.1 GI:14537350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Dillon,D.C., Day,C.H., Jiang,Y., Houghton,R.L., Mitcham,J.L. and
TITLE Compositions and methods for therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0140269-A 207 07-JUN-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..2627

ORIGIN
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 98.7%; Score 878; DB 6; Length 2627;
Best Local Similarity 99.9%; Pred. No. 2e-258;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTCCATCTGCTGAGGAGCACTTAAGACTCAGTTTTCATA 60
1721 CAAGCTGAGGCTTCTCTTCCATCTGCTGAGGAGCACTTAAGACTCAGTTTTCATA 1780
Db

QY 61 GCATTAAGAGAGTGGAGCTCAGCTGAGGTAATTTGCCCCCATCTCCGAGGAAATGTC 120
1781 GCATTAAGAGAGTGGAGCTCAGCTGAGGTAATTTGCCCCCATCTCCGAGGAAATGTC 1840
Db

QY 121 TGAAGCAATTTTGGTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
1841 TGAAGCAATTTTGGTTACCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
Db

QY 181 TAGTGATTAAGGCGCAGGAGTGTCTCACTCTTACCATGTACAGGAGCTCTCCCA 240
1901 TAGTGATTAAGGCGCAGGAGTGTCTCACTCTTACCATGTACAGGAGCTCTCCCA 1959
Db

QY 241 TTACAACTACCAATCCGAAGTGTCAAGTGTCAAGACTTAAGAAACCTGGTTTGAAT 300
1960 TTACAACTACCAATCCGAAGTGTCAAGTGTCAAGACTTAAGAAACCTGGTTTGAAT 2019
Db

QY 301 AGAAAAAGGCGCTGGAAGAGGAGGCAACAAATCTGTCTGTCTTCCCTCAATTAAGTCAAT 360
2020 AGAAAAAGGCGCTGGAAGAGGAGGCAACAAATCTGTCTGTCTTCCCTCAATTAAGTCAAT 2079
Db

QY 361 GGCAAATTAAGCAATCTGTCTCTTTGGCTGTCTGTCTGACACAGAGAGCCAACTCTATC 420
2080 GGCAAATTAAGCAATCTGTCTCTTTGGCTGTCTGTCTGACACAGAGAGCCAACTCTATC 2139
Db

QY 421 GGGCACACAGATTAACATCTCTCAGTGAAGAGTTGACAAAGGCTTAAGGAAATGCTCTGA 480
2140 GGGCACACAGATTAACATCTCTCAGTGAAGAGTTGACAAAGGCTTAAGGAAATGCTCTGA 2199
Db

QY 481 TGGGATTAATCTTCAAGCTGTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTACCTGCAAG 540
2200 TGGGATTAATCTTCAAGCTGTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTACCTGCAAG 2259
Db

QY 541 CCAGATTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTGAATTGA 600
2260 CCAGATTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTGAATTGA 2319
Db

QY 601 TCTCCAGACCCCTTCGCGCAATTCOAATTAAGGCAACAAATATCTTCCATGAA 660
2320 TCTCCAGACCCCTTCGCGCAATTCOAATTAAGGCAACAAATATCTTCCATGAA 2379
Db

QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTCTTGAATTGAGGCTTGAGGAATG 720
2380 GCACACACAGACTTTTGAAGCAAGCAATGACTCTTGAATTGAGGCTTGAGGAATG 2439
Db

QY 721 AAGCTTTGAAGAAAGAAATACCTTTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 780
2440 AAGCTTTGAAGAAAGAAATACCTTTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 2499
Db

QY 781 ACCACTGCTTCTTGAAGCAAGTGAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
2500 ACCACTGCTTCTTGAAGCAAGTGAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2559
Db

QY 841 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATTAATTAATTAATTAATTAATTAAT 890
2560 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATTAATTAATTAATTAATTAATTAAT 2609
Db

RESULT 6
AX366624 2627 bp DNA linear PAT 15-FEB-2002
LOCUS AX366624

DEFINITION Sequence 391 from Patent WO0206317.
ACCESSION AX366624
VERSION AX366624.1 GI:18698046
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W.,
Fanger,G.R., Reed,S.G., Vedvick,T.S., Carter,D., Hill,P. and
Albone,E.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: WO 0206317-A 391 24-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..2627
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 98.7%; Score 878; DB 6; Length 2627;
Best Local Similarity 99.9%; Pred. No. 2e-258;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTCTGCGTGAGACGTAAGACCTCACTTTCAATA 60
DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTCTGCGTGAGACGTAAGACCTCACTTTCAATA 1780
QY 61 GCATCTAGACGAGGAGCTCAGCTGGGGGATTTGCGCCCATCTCGGGGGAAATGTC 120
DB 1781 GCATCTAGACGAGGAGCTCAGCTGGGGGATTTGCGCCCATCTCGGGGGAAATGTC 1840
QY 121 TGAAGACAATTTTGTTTACCTCAATGAGGAGTGAGAGAGATACAGTGTACTACCAAC 180
DB 1841 TGAAGACAATTTTGTTTACCTCAATGAGGAGTGAGAGAGATACAGTGTACTACCAAC 1900
QY 181 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCTCACTGACGAGGAGCTGTCCCA 240
DB 1901 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCTCACTGACGAGGAGCTGTCCCA 1959
QY 241 TTAACAATAACCAATCCGAAGTGTCACTGTGTCAGGACCTAAGAAACCGGTTTGGAT 300
DB 1960 TTAACAATAACCAATCCGAAGTGTCACTGTGTCAGGACCTAAGAAACCGGTTTGGAT 2019
QY 301 AGAAAAGGCGCTGGAAGAGGAGGAGCCCAAAATCTGTCTGTCTCTCACTTAATGTCATT 360
DB 2020 AGAAAAGGCGCTGGAAGAGGAGGAGCCCAAAATCTGTCTGTCTCTCACTTAATGTCATT 2079
QY 361 GGGCAATAAGCAATTTCTCTTCTTGTGCTGTCTGCTCCAGCAAGAGAGCCGAATCTATC 420
DB 2080 GGGCAATAAGCAATTTCTCTTCTTGTGCTGTCTGCTCCAGCAAGAGAGCCGAATCTATC 2139
QY 421 GGGCACAGGATTAACATCTCTCAGTGAAGAGTGCAAGGCTTAAGGGAATGCTGCA 480
DB 2140 GGGCACAGGATTAACATCTCTCAGTGAAGAGTGCAAGGCTTAAGGGAATGCTGCA 2199
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTCACTCGAG 540
DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTCACTCGAG 2259
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTCTAAGTCAAGTTTCTTACTGTGAATTTAGA 600
DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTCTAAGTCTAAGTTTCTTACTGTGAATTTAGA 2319
QY 601 TCTCCAGACCTCTCGGCAATTCGAATTAAGCAAAATTAAGCAATTAATTAATTAAGCA 660
DB 2320 TCTCCAGACCTCTCGGCAATTCGAATTAAGCAAAATTAAGCAATTAATTAATTAAGCA 2379
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTTGAGGCGCTTGAAGATG 720

DB 2380 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTTGAGGCGCTTGAAGATG 2439
QY 721 AACCTTGAGAGAAAGAAATTAATTTTCCAGCCCTTCCACACTCTCAATGTGTTA 780
DB 2440 AACCTTGAGAGAAAGAAATTAATTTTCCAGCCCTTCCACACTCTCAATGTGTTA 2499
QY 781 ACCACTGCTTCTTGACCTTGAGGACGAGGAGTGTATTAATGTTTATAGAAAC 840
DB 2500 ACCACTGCTTCTTGACCTTGAGGACGAGGAGTGTATTAATGTTTATAGAAAC 2559
QY 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGAATTAATTAATTAATTTCTT 890
DB 2560 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGAATTAATTAATTAATTTCTT 2609
RESULT 7
AX403048 2603 bp DNA linear PAT 07-JUN-2002
LOCUS
DEFINITION Sequence 1 from Patent WO020624.
ACCESSION AX403048
VERSION AX403048.1 GI:21388028
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fox,G., Sullivan,J.K. and Fang,M.
TITLE B7-like molecules and uses thereof
JOURNAL Patent: WO 020624-A 1 10-JAN-2002;
Amgen, Inc. (US)
FEATURES
source Location/Qualifiers
1..2603
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
53..901
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD33698.1"
/db_xref="GI:21388029"
/translation="MASLQOILFWSIISIIILAGALALIGFGISGRHSITVTTVAS
ASGIDGILSCFEPDILSDIVIOMLEGVGLVHFEKEGDELSDDEMRGRTA
VRADQYIVGNASILRLKNVOLTGATGKYKIIISKSGNANLEKTAFAFPEPVNVN
ASSETIRCAAPRPFQPTVYMASQVDQGANFSEVSTSELSENVMTMYVSVLYVVT
INNTYSCMIENDIAKATGDIKVTSEIKRSHDQLNLSFASLCVSSFPAISWALPLS
PYLMNK"
ORIGIN
Query Match 98.6%; Score 877.6; DB 6; Length 2603;
Best Local Similarity 99.8%; Pred. No. 2.e-258;
Matches 888; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 CAAGCTGAGGCTTCTCTTCCATCTCTGCGTGACACTAAGACCTCACTTTCAATA 60
DB 1691 CAAGCTGAGGCTTCTCTTCCATCTCTGCGTGACACTAAGACCTCACTTTCAATA 1750
QY 61 GCATCTAGAGCAAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 120
DB 1751 GCATCTAGAGCAAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 1810
QY 121 TGAAGCAATTTTGGTTTACTCAATGAAGGAGTGAGAGAGATACAGTGTACTACCAAC 180
DB 1811 TGAAGCAATTTTGGTTTACTCAATGAAGGAGTGAGAGAGATACAGTGTACTACCAAC 1870
QY 181 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCTAAGATGAAGAGAGCTGTCCCA 240
DB 1871 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCTAAGATGAAGAGAGCTGTCCCA 1929
QY 241 TTAACAATAACCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTGTGTTGAGT 300
DB 1930 TTAACAATAACCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTGTGTTGAGT 1989

QY 301 AGAAAAAGGCGCTGAGAAAGAGGAGCCAAATCTGTCTGCTCTCAATTAATGATC 360
|
|
Db 1990 AGAAAAAGGCGCTGAGAAAGAGGAGCCAAATCTGTCTGCTCTCAATTAATGATC 2049
QY 361 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTGACACAGAGAGCCAGAACTCTATC 420
|
|
Db 2050 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTGACACAGAGAGCCAGAACTCTATC 2109
QY 421 GGGCACCGAGATTAACATCTCTGAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGA 480
|
|
Db 2110 GGGCACCGAGATTAACATCTCTGAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGA 2169
QY 481 TGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTTCCCTCAATTCACCTGCAAG 540
|
|
Db 2170 TGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTTCCCTCAATTCACCTGCAAG 2229
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTTACCTCAAGTTTCTTACTCTGAATTTAGA 600
|
|
Db 2230 CCAAGTTCTGTAAAGAAATGCTGAGTTCTTACCTCAAGTTTCTTACTCTGAATTTAGA 2289
QY 601 TCTCCGAGACCTTCCCTGGGCGCAATTCAAATTAAGGCAACAAATATACCTTCCATGAA 660
|
|
Db 2290 TCTCCGAGACCTTCCCTGGGCGCAATTCAAATTAAGGCAACAAATATACCTTCCATGAA 2349
QY 661 GCACACACAGACTTTTGAAGAGCAAGACATGACTGCTTGAATTGAGGCTTGAAGAAATG 720
|
|
Db 2350 GCACACACAGACTTTTGAAGAGCAAGACATGACTGCTTGAATTGAGGCTTGAAGAAATG 2409
QY 721 AAGCTTTGAAGAAAGAAATACTTTGTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 780
|
|
Db 2410 AAGCTTTGAAGAAAGAAATACTTTGTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 2469
QY 781 ACCACTGCTCTCTGAGACCTTGGAGCAGGAGTGAATTAATGATTTAGTATTAAGAAAC 840
|
|
Db 2470 ACCACTGCTCTCTGAGACCTTGGAGCAGGAGTGAATTAATGATTTAGTATTAAGAAAC 2529
QY 841 TGAATTTAGAGTTCTGATCGTTTCAGAGATGAATTAATATACATTTCT 890
|
|
Db 2530 TGAATTTAGAGTTCTGATCGTTTCAGAGATGAATTAATATACATTTCT 2579

RESULT 8
AX375860 2626 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 7 from Patent W00194641.
DEFINITION AX375860
ACCESSION AX375860
VERSION AX375860.1 GI:19170332
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Ople, E., McLachlan, K. and Heard, C.
Gene targets and ligands that bind thereto for treatment and
diagnosis of ovarian carcinomas
Patent: WO 0194641-A 7 13-DEC-2001;
Idac Pharmaceuticals Corporation (US)
Location/Qualifiers
1. .2626
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.5%; Score 876.4; DB 6; Length 2626;
Best Local Similarity 99.8%; Pred. No. 6, 1e-258;
Matches 888; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 CAAAGCTCTGAGGCTTCTCTTTCATCTCGCTGAGACAGCTAGACTCTGTTTCAATA 60
|
|
|
Db 1699 CAAAGCTCTGAGGCTTCTCTTTCATCTCGCTGAGACAGCTAGACTCTGTTTCAATA 1758

QY 61 GCATCTAGACAGATGAGGAGCTCAGCTGGGTGATTTTCGCCCCCATCTCGGGGGAAATGTC 120
|
|
Db 1759 GCATCTAGACAGATGAGGAGCTCAGCTGGGTGATTTTCGCCCCCATCTCGGGGGAAATGTC 1818
QY 121 TGAAGACAAATTTGGTTACCTCAATAGAGGAGTGGAGAGGATTCAGTCTACTACCAAC 180
|
|
Db 1819 TGAAGACAAATTTGGTTACCTCAATAGAGGAGTGGAGAGGATTCAGTCTACTACCAAC 1878
QY 181 TAGTGATTAAGAGCCAGAGGATGCTGCTCAACCTCTCAACATGTACAGGAGGCTGCCCA 240
|
|
Db 1879 TAGTGATTAAGAGCCAGAGGATGCTGCTCAACCTCTCAACATGTACAGGAGGCTGCCCA 1937
QY 241 TTACACTACCCCAATCCGAAGTGTCACTGTGTGACAGCTAAGAAACCTGTTTGAAT 300
|
|
Db 1938 TTACACTACCCCAATCCGAAGTGTCACTGTGTGACAGCTAAGAAACCTGTTTGAAT 1997
QY 301 AGAAAAAGGCGCTGAGAAAGAGGAGCCAAATCTGTCTGCTCTCAATTAATGATC 360
|
|
Db 1998 AGAAAAAGGCGCTGAGAAAGAGGAGCCAAATCTGTCTGCTCTCAATTAATGATC 2057
QY 361 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTGACACAGAGAGCCAGAACTCTATC 420
|
|
Db 2058 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTGACACAGAGAGCCAGAACTCTATC 2117
QY 421 GGGCACCGAGATTAACATCTCTGAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGA 480
|
|
Db 2118 GGGCACCGAGATTAACATCTCTGAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGA 2177
QY 481 TGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTTCCCTCAATTCACCTGCAAG 540
|
|
Db 2178 TGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTTCCCTCAATTCACCTGCAAG 2237
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTTACCTCAAGTTTCTTACTCTGAATTTAGA 600
|
|
Db 2238 CCAAGTTCTGTAAAGAAATGCTGAGTTCTTACCTCAAGTTTCTTACTCTGAATTTAGA 2297
QY 601 TCTCCGAGACCTTCCCTGGGCGCAATTCAAATTAAGGCAACAAATATACCTTCCATGAA 660
|
|
Db 2298 TCTCCGAGACCTTCCCTGGGCGCAATTCAAATTAAGGCAACAAATATACCTTCCATGAA 2357
QY 661 GCACACACAGACTTTTGAAGAGCAAGACATGACTGCTGAATTGAGGCTTGAAGAAATG 720
|
|
Db 2358 GCACACACAGACTTTTGAAGAGCAAGACATGACTGCTGAATTGAGGCTTGAAGAAATG 2417
QY 721 AAGCTTTGAAGAAAGAAATACTTTGTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 780
|
|
Db 2418 AAGCTTTGAAGAAAGAAATACTTTGTTTCAGCCCCCTTCCACACTCTTCAATGTGTTA 2477
QY 781 ACCACTGCTCTCTGAGACCTTGGAGCAGGAGTGAATTAATGATTTAGTATTAAGAAAC 840
|
|
Db 2478 ACCACTGCTCTCTGAGACCTTGGAGCAGGAGTGAATTAATGATTTAGTATTAAGAAAC 2537
QY 841 TGAATTTAGAGTTCTGATCGTTTCAGAGATGAATTAATATACATTTCT 890
|
|
Db 2538 TGAATTTAGAGTTCTGATCGTTTCAGAGATGAATTAATATACATTTCT 2587

RESULT 9
AL391476/c 171595 bp DNA linear PRI 03-AUG-2001
LOCUS Human DNA sequence from clone RP11-229A19 on chromosome 1, complete
DEFINITION AL391476
ACCESSION AL391476
VERSION AL391476.20 GI:15131484
KEYWORDS
HTG. Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Wallis, J.
Direct Submission
Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT

CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:14970375.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; SW; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
RP11-229A19 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see
<http://www.choi.org/bacpac/home.htm>
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-229A19 The true left end of clone RP11-287H9 is at 67254 in this sequence. The true right end of clone RP4-570D9 is at 57439 in this sequence.

FEATURES

Source

Location/Qualifiers
1. .171595
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-229A19"
/clone_1b="RPCT-11.1"
324. .685
/note="L1M3 repeat: matches 5769. .6141 of consensus"
repeat_region
745. .1182
/note="L1M2 repeat: matches 5890. .6341 of consensus"
repeat_region
1261. .1466
/note="AluX repeat: matches 1. .183 of consensus"
repeat_region
1471. .1567
/note="L1 repeat: matches 5042. .5132 of consensus"
repeat_region
1568. .1880
/note="AluX repeat: matches 1. .312 of consensus"
repeat_region
1881. .2391
/note="L1 repeat: matches 4471. .5042 of consensus"
repeat_region
2392. .2668
/note="AluY repeat: matches 1. .291 of consensus"
repeat_region
2669. .2813
/note="L1 repeat: matches 4336. .4471 of consensus"
repeat_region
3066. .3198
/note="FLAM_C repeat: matches 1. .133 of consensus"
repeat_region
3264. .3367
/note="MIR repeat: matches 32. .134 of consensus"
repeat_region
3758. .4064
/note="AluX repeat: matches 1. .305 of consensus"
repeat_region
4312. .4610
/note="AluX repeat: matches 1. .306 of consensus"
repeat_region
5330. .5607
/note="LIP45 repeat: matches 5866. .6143 of consensus"
repeat_region
6639. .6803
/note="MIR repeat: matches 27. .189 of consensus"
repeat_region
7176. .7218
/note="L2 repeat: matches 2654. .2698 of consensus"
repeat_region
7287. .7593
/note="MER7A repeat: matches 1. .346 of consensus"
repeat_region
8914. .8963

/note="MADE1 repeat: matches 31. .80 of consensus"
9335. .9484
/note="L1MCS repeat: matches 7699. .7849 of consensus"
repeat_region
9485. .9784
/note="AluSc repeat: matches 1. .300 of consensus"
repeat_region
9785. .9811
/note="L1MCS repeat: matches 7673. .7699 of consensus"
repeat_region
9812. .9975
/note="FAM repeat: matches 1. .170 of consensus"
repeat_region
9976. .10469
/note="L1MCS repeat: matches 7185. .7673 of consensus"
repeat_region
11613. .11858
/note="L1PA16 repeat: matches 5857. .6157 of consensus"
repeat_region
13950. .14280
/note="MER44A repeat: matches 1. .333 of consensus"
repeat_region
14390. .14493
/note="L2 repeat: matches 2601. .2705 of consensus"
repeat_region
16020. .16325
/note="AluX repeat: matches 1. .308 of consensus"
repeat_region
16726. .16892
/note="MIR repeat: matches 79. .261 of consensus"
repeat_region
17071. .17373
/note="AluSq repeat: matches 1. .301 of consensus"
repeat_region
17708. .18140
/note="MER68A repeat: matches 1. .435 of consensus"
repeat_region
19282. .19574
/note="Aluub repeat: matches 1. .294 of consensus"
repeat_region
19774. .19904
/note="FLAM_A repeat: matches 1. .133 of consensus"
repeat_region
20023. .20325
/note="AluY repeat: matches 1. .303 of consensus"
repeat_region
20904. .21029
/note="Aluub repeat: matches 10. .136 of consensus"
repeat_region
22334. .22596
/note="AluX repeat: matches 1. .264 of consensus"
repeat_region
23089. .23144
/note="2 copies 28 mer 98% conserved"
repeat_region
23310. .23345
/note="9 copies 4 mer tglg 94% conserved"
repeat_region
24358. .24654
/note="AluX repeat: matches 1. .297 of consensus"
repeat_region
25318. .25615
/note="AluY repeat: matches 1. .297 of consensus"
repeat_region
26469. .26775
/note="AluU repeat: matches 1. .304 of consensus"
repeat_region
31909. .32321
/note="L2 repeat: matches 2035. .2515 of consensus"
repeat_region
33438. .33739
/note="AluG repeat: matches 1. .302 of consensus"
repeat_region
35428. .35499
/note="MIR repeat: matches 78. .145 of consensus"
repeat_region
35687. .35843
/note="MER58C repeat: matches 9. .45 of consensus"
repeat_region
36245. .36311
/note="L1M3 repeat: matches 7674. .7739 of consensus"
repeat_region
36338. .36699
/note="L1M4 repeat: matches 7358. .7643 of consensus"
repeat_region
36702. .36938
/note="L2 repeat: matches 1141. .1372 of consensus"
repeat_region
37430. .37621
/note="L2 repeat: matches 2088. .2281 of consensus"
repeat_region
37655. .38005
/note="L2 repeat: matches 2335. .2710 of consensus"
repeat_region
38922. .39220
/note="AluU repeat: matches 1. .299 of consensus"
repeat_region
39802. .39885
/note="3 copies 28 mer 96% conserved"
repeat_region
39931. .40073
/note="MULTI1 repeat: matches 11. .157 of consensus"
repeat_region
40191. .40247
/note="Char1e4 repeat: matches 1906. .1961 of consensus"
repeat_region
40286. .40363
/note="MULTI1 repeat: matches 288. .372 of consensus"

```
repeat_region 40657. .40734
                /note="MIR repeat: matches 28. .99 of consensus"
repeat_region 40735. .41048
                /note="AluSc repeat: matches 1. .309 of consensus"
repeat_region 41049. .41092
                /note="MIR repeat: matches 99. .144 of consensus"
repeat_region 41248. .41351
                /note="MIR repeat: matches 57. .167 of consensus"
repeat_region 42498. .42761
                /note="AluSg repeat: matches 1. .265 of consensus"
repeat_region 43527. .43770
                /note="L2 repeat: matches 2465. .2742 of consensus"
repeat_region 44795. .44944
                /note="L2 repeat: matches 2620. .2749 of consensus"
repeat_region 44945. .45231
                /note="AluYb repeat: matches 21. .307 of consensus"
repeat_region 45232. .45629
                /note="L2 repeat: matches 2129. .2620 of consensus"
repeat_region 45628. .45864
                /note="L2 repeat: matches 1162. .1409 of consensus"
repeat_region 45880. .46206
                /note="MUTB repeat: matches 43. .390 of consensus"
misc_feature 45990. .46265
                /note="Sequence from overlapping clone RP4-570D9
                (AL139248). Assembly confirmed by restriction digest."
repeat_region 46271. .47156
                /note="L2 repeat: matches 3. .1061 of consensus"
repeat_region 47227. .47442
                /note="MER20 repeat: matches 2. .218 of consensus"
repeat_region 47449. .47755
                /note="AluSg repeat: matches 1. .304 of consensus"
repeat_region 48722. .49035
                /note="AluSg repeat: matches 1. .307 of consensus"
repeat_region 51378. .51522
                /note="FRAM repeat: matches 4. .162 of consensus"
repeat_region 53299. .53600
                /note="AluJo repeat: matches 1. .296 of consensus"
repeat_region 55969. .56042
                /note="MIR repeat: matches 106. .187 of consensus"
repeat_region 56386. .56695

Query Match 98.1%; Score 873.2; DB 9; Length 171595;
Best Local Similarity 99.6%; Pred. No. 8.1e-257;
Matches 886; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CAAAGCTCTAGAGGCTTCCTTCCTTCATCCGCGTGAAGCTAGACTCAAGTTTCAATA 60
    |||||
DB 81543 CAAAGCTCTAGAGGCTTCCTTCCTTCATCCGCGTGAAGCTAGACTCAAGTTTCAATA 81484

QY 61 GCATCTAGAGCAGTGGAGACTCAGCTGGGAGTATTTGCCGCCCATCTCCGGGGAAATGTC 120
    |||||
DB 81483 GCATCTAGAGCAGTGGAGACTCAGCTGGGAGTATTTGCCGCCCATCTCCGGGGAAATGTC 81424

QY 121 TGAAGCAATTTTGTTTACTCTCAATGAGGAGTGAAGAGATACAGTGTACTTACCAAC 180
    |||||
DB 81423 TGAAGCAATTTTGTTTACTCTCAATGAGGAGTGAAGAGATACAGTGTACTTACCAAC 81364

QY 181 TAGTGATTAAGGCCGAGGATGCTGCTCAACCTCCATACATGATGAGGACGCTCCCA 240
    |||||
DB 81363 TAGTGATTAAGGCCGAGGATGCTGCTCAACCTCCATACATGATGAGGACGCTCCCA 81305

QY 241 TTTCACACTCCCAATCCGAAGTGTCAATGTCAGAGCTTAAGAAACCCTGTTTGAGT 300
    |||||
DB 81304 TTTCACACTCCCAATCCGAAGTGTCAATGTCAGAGCTTAAGAAACCCTGTTTGAGT 81245

QY 301 AGAAAAAGGCGCTTGAAAAAGAGGGAGCCAAATCTGTCTGCTTCTCAATTAGTCATT 360
    |||||
DB 81244 AGAAAAAGGCGCTTGAAAAAGAGGGAGCCAAATCTGTCTGCTTCTCAATTAGTCATT 81185

QY 361 GGGAAATTAAGCAATTCGTCTCTTTGGCTGTGCTTCAAGCAACAAGAGCCGAATCTATC 420
    |||||
DB 81184 GGGAAATTAAGCAATTCGTCTCTTTGGCTGTGCTTCAAGCAACAAGAGCCGAATCTATC 81125
```

```
QY 421 GGGACACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGGGAATGCCCTGA 480
    |||||
DB 81124 GGGACACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGGGAATGCCCTGA 81065

QY 481 TGGGATTTATCTTCAGCTTGTTGAGGCTTAAAGTTCTTCCCTTCATTCTACCCCTGCAAG 540
    |||||
DB 81064 TGGGATTTATCTTCAGCTTGTTGAGGCTTAAAGTTCTTCCCTTCATTCTACCCCTGCAAG 81005

QY 541 CCAGTTCTGTAAGAAATGCTGAGTCTTACGTCAGGTTTCTTACTGTAATTTAG 600
    |||||
DB 81004 CCAGTTCTGTAAGAAATGCTGAGTCTTACGTCAGGTTTCTTACTGTAATTTAG 80945

QY 601 TCTCCAGACCTTCTCTGCGCACATTCAAATTAAGGCAACAACTATACCTTCATGAA 660
    |||||
DB 80944 TCTCCAGACCTTCTCTGCGCACATTCAAATTAAGGCAACAACTATACCTTCATGAA 80885

QY 661 GCACACAGACTTTTGAAGCAAGATGACTGCTTGAATTGAGGCTTGAGGAATG 720
    |||||
DB 80884 GCACACAGACTTTTGAAGCAAGATGACTGCTTGAATTGAGGCTTGAGGAATG 80825

QY 721 AAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTTA 780
    |||||
DB 80824 AAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTTA 80765

QY 781 ACCACTGCTCTCTGAGACCTTGAGCCACGCGTACTGTATTCATGTTTATAGAAAC 840
    |||||
DB 80764 ACCACTGCTCTCTGAGACCTTGAGCCACGCGTACTGTATTCATGTTTATAGAAAC 80705

QY 841 TGATTTTGAAGTTCGATCGTTCAAGAGATGATTAATATACATTTCT 890
    |||||
DB 80704 TGATTTTGAAGTTCGATCGTTCAAGAGATGATTAATATACATTTCT 80655

RESULT 10
HSR808167 2671 bp mRNA linear PRI 30-AUG-2003
LOCUS HSR808167
DEFINITION Homo sapiens mRNA; cDNA DKFZp779B1717 (from clone DKFZp779B1717).
ACCESSION BX648021
VERSION BX648021.1 GI:34367180
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2671)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German Human cDNA Consortium
CONSTRM Direct Submision
TITLE Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
JOURNAL Neuberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp779B1717) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
FEATURES
Location/Qualifiers
source 1..2671
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp779B1717"
/tissue_type="liver"
/clone_lib="779 (anonymous; hmccl). Vector pSport1_Sfi; host
DH10B; sites SfiI + SfiIB"
/dev_stage="fetal"
2599..2604
polyA_signal
```

polYA_site 2616
ORIGIN

Query Match	97.8%	Score 870;	DB 9;	length 2671;
Best Local Similarity	99.3%	Pred. No. 5, 7e-256;		
Matches 884;	Conservative	0;	Mismatches 5;	Indels 1;
			Gaps	1;

Qy	1	CAACCTCGAAGGCTCTCTCTTCCATCTCGGTGAGCAAGCTAAAGCCCTCAGTTTCAATA	60
Db	1728	CAAGCTCGAAGGCTCTCTCTTCCATCTCGGTGAGCAAGCTAAAGCTCAGTTTCAATA	1787
Qy	61	GCATCTAGAGCAGTGGGATCTAGCTGGGGTAAATTTCCGCCCCATCTTCGGGGGAATGTC	120
Db	1788	GCATCTAGAGCAGTGGGATCTAGCTGGGGTAAATTTCCGCCCCATCTTCGGGGGAATGTC	1847
Qy	121	TGAAGACAAATTTGGTTACTCAATGAAAGGAGTGAAGGAGATACAGTGCTAACATCAAC	180
Db	1848	TGAAGACAAATTTGGTTACTCAATGAAAGGAGTGAAGGAGATACAGTGCTAACATCAAC	1907
Qy	181	TATGTGATTAAGGCCAGGATGCTGCTCAACCTCTTACATGTACAGGGAAGTCTCCCA	240
Db	1908	TATGTGATTAAGGCCAGGATGCTGCTCAACCTCTTACATGTGACA -GGAGCTCTCCCA	1966
Qy	241	TTACAACATCCCAATCCGAATGTCAATGTGTCAAGATCAAGAAACCTTGTTAGT	300
Db	1967	TTACAACATCCCAATCCGAATGTCAATGTGTCAAGGATCAAGAAACCTTGTTAGT	2026
Qy	301	AGAAAAGGGCTGTGAAGAGGGGAGCCAACAATCTGCTCTTCTCACTTAATGACTT	360
Db	2027	AGAAAAGGGCTGTGAAGAGGGGAGCCAACAATCTGCTCTTCTCACTTAATGACTT	2086
Qy	361	GGCAATTAAGACTTCTGTCTTTTGGCTGCTCAGACACAGAGGACAGAACTTATC	420
Db	2087	GGCAATTAAGACTTCTGTCTTTTGGCTGCTCAGACACAGAGGACAGAACTTATC	2146
Qy	421	GGGACACAGATTAATCATCTCTCAGTGAAACAAGTTGAACAAGGCTATGGGAAATGCCGA	480
Db	2147	GGGACACAGATTAATCATCTCTCAGTGAAACAAGTTGAACAAGGCTATGGGAAATGCCGA	2206
Qy	481	TGGGATTAATCTTCAAGCTGTGTAGCTCTTAAGTTCTTCCCTCAATTCTACCTGCAAG	540
Db	2207	TGGGATTAATCTTCAAGCTGTGTAGCTCTTAAGTTCTTCCCTCAATTCTACCTGCAAG	2266
Qy	541	CCAAATTCTGTAAGAAATGCTGAGTTCTAAGCTCAGGTTTTCTTACTCTGAATTTAGA	600
Db	2267	CCAAATTCTGTAAGAAATGCTGAGTTCTAAGCTCAGGTTTTCTTACTCTGAATTTAGA	2326
Qy	601	TCTCCAGACCTTCTCTGGCCACAATTCAAATTAAGGCAACAACATTAATCTTCATGAA	660
Db	2327	TCTCCAGACCTTCTCTGGCCACAATTCAAATTAAGGCAACAACATTAATCTTCATGAA	2386
Qy	661	GCACACACAGACTTTTGAAGCAAGACCAATGACGCTTGAATTAAGGCTTGAAGATG	720
Db	2387	GCACACACAGACTTTTGAAGCAAGACCAATGACGCTTGAATTAAGGCTTGAAGATG	2446
Qy	721	AAGCTTTGAAGAAAGAAATACCTTGTTCAGGCCCTTCCCACTCTTCAGTGTGA	780
Db	2447	AAGCTTTGAAGAAAGAAATACCTTGTTCAGGCCCTTCCCACTCTTCAGTGTGA	2506
Qy	781	ACCACTGCTTCTCTGACCTTGAAGCCACGGGTGACTGATTAACATGTTGTATGAANAAC	840
Db	2507	ACCACTGCTTCTCTGACCTTGAAGCCACGGGTGACTGATTAACATGTTGTATGAANAAC	2566
Qy	841	TGATTTTAAGATTCTGATCTTTCAAAGAAATGATTTAAATTAACATTTCT	890
Db	2567	TGATTTTAAGATTCTGATCTTTCAAAGAAATGATTTAAATTAACATTTCT	2616

RESULT 11	
BD264689	
LOCUS	BD264689
DEFINITION	1567 bp DNA linear PAT 17-JUL-2003
	Compositions and methods for the therapy and diagnosis of ovarian cancer.

ACCESSION	BD264689	GI:33074457
VERSION	BD264689.1	
KEYWORDS	JP 2002532093-A/74.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE
1 (pages 1 to 1567)
AUTHORS
Mitchem,J.L., King,G.E., Algate,P.A. and Frudakis,T.N.
TITLE
Compositions and methods for the therapy and diagnosis of ovarian
JOURNAL
Patent: JP 2002532093-A 74 02-OCT-2002;
codex.com

COMMENT	OS	Homo sapiens (human)
PN	TP	2002532093-A/74

PF 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681, 17-DEC-1998 US 09/216003 PR
23-JUN-1999 US 09/338933, 24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM, GORDON E KING, PAUL A ALGATE, TONY N FRUDAKIS PC
C12N1/09, A61K31/7115, A61K35/14, A61K35/76, A61K39/00, A61K39/395, PC
A61K39/395,
PC A61K48/00, A61P35/00, A61P37/04, C07K14/82, C07K19/00, C12N1/15, PC
C12N1/19,

CI2N1/21, CI2N5/06, CI2N5/10, CI2Q1/68, G01N33/53, G01N33/53, G01N33/PC
566,
PC G01N33/574, G01N33/577, CI2N5/00, CI2N5/00, CI2N5/00 CC
Compositions and methods for the therapy and diagnosis of CC
ovarian cancer

source	FT	FT
1. .1567		
/organism='Homo sapiens (human)'		

```

FEATURES
source
1. 1567
location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

```

ORIGIN

Query Match	97.3%;	Score 866;	DB 6;	Length 1567;
Best local similarity	99.8%;	Pred. No. 9	3e-25;	
Matches 888;	Conservative	0;	Mismatches	0;
			Indels	2;
			Gaps	2;

Qy	1	CAAGCTGAGGGCTTCCCTTTCATCTCTGGGAGACAGCTAAGACCTCACTGTTTTCATA	60
Db	679	CAAGCTCTGAGGCTTCTCTTCCATCTCTCGTGGAGACCTCAAGACTCACTGTTTTCATA	738
Qy	61	GCATCTGAGACAGTGGGACTCAGCTGGGGTGATTTCCGCCCCATCTCCGGGGAAATGTC	120
Db	739	GCATCTGAGCAGTGGGACTCAGCTGGGGTGATTTCCGCCCCATCTCCGGGGAAATGTC	798
Qy	121	TGAAGCAATTTTGGTTACTCTCAATGAGGAGTGGAGGAGATACAGTGTCTATCCAAC	180
Db	799	TGAAGCAATTTT-GTTACTCAATGAGGAGTGGAGGAGATACAGTGTCTATCCAAC	857
Qy	181	TAGTGGATTAAGGCAGGGATGCTGCTCAACCTCTACATGTACAGGGACGTCTCCCA	240
Db	858	TAGTGGATTAAGGCAGGGATGCTGCTCAACCTCTACATGTACA-GGACGTCTCCCA	916
Qy	241	TTTCAACTATCCCAATCCGAGTGTCACTGTGTGACGACCTAAGAAACCTGAGTTTGTAGT	300
Db	917	TTTCAACTATCCCAATCCGAGTGTCACTGTGTGACGACCTAAGAAACCTGAGTTTGTAGT	976
Qy	301	AGAAAAGGGCTGCGAAAGAGGGAGCCAAACAATCTGTCTGCTTCCCTCATTAGTATT	360
Db	977	AGAAAAGGGCTGCGAAAGAGGGAGCCAAACAATCTGTCTGCTTCCCTCATTAGTATT	1036
Qy	361	GGCAAAATPAGCAATCTGTCTCTTTGGCTGTGCTCAGCAGAGAGGCCAAACTATTC	420
Db	1037	GGCAAAATPAGCAATCTGTCTCTTTGGCTGTGCTCAGCAGAGAGGCCAAACTATTC	1096
Qy	421	GGGACCCAGATACATCTTCACTGTAACAGAGTTGCAAGGCGCTATGGGAAATGCTTGA	480

Db 1097 GGGCACCGAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTAAGGAAATGCTTGA 1156
Qy 481 TGGGATTAATCTTCAAGCTTGTAGAGCTTAAAGTTTCTTCCCTGATTCACCTGCAAG 540
Db 1157 TGGGATTAATCTTCAAGCTTGTAGAGCTTAAAGTTTCTTCCCTGATTCACCTGCAAG 1216
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 1276
Qy 601 TCTCCAGACCTTCTGCGCCCAATTCATTAAGGCAACAAACATATACCTTCCATGA 660
Db 1277 TCTCCAGACCTTCTGCGCCCAATTCATTAAGGCAACAAACATATACCTTCCATGA 1336
Qy 661 GCACACAGAGCTTTTGAAGCAAGACATGACTCTTGAATGAGGCTTGAAGGATG 720
Db 1337 GCACACAGAGCTTTTGAAGCAAGACATGACTCTTGAATGAGGCTTGAAGGATG 1396
Qy 721 AGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCTTCCACACTCTTCAATGTGA 780
Db 1397 AGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCTTCCACACTCTTCAATGTGA 1456
Qy 781 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTGAAGAAAC 840
Db 1457 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTGAAGAAAC 1516
Qy 841 TGATTTAAGATTCATGATGTTCAAGAGATGATTAATATACATTTCT 890
Db 1517 TGATTTAAGATTCATGATGTTCAAGAGATGATTAATATACATTTCT 1566

RESULT 12
AR238092 1567 bp DNA linear PAT 20-DEC-2002
LOCUS AR238092
DEFINITION Sequence 74 from patent US 648546.
ACCESSION AR238092 GI:27283056
VERSION AR238092.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., King,G.E. and Algate,P.A.
TITLES Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 648546-A 74 22-OCT-2002;
FEATURES Location/Qualifiers
source 1..1567
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 97.3%; Score 866; DB 6; Length 1567;
Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 1 CAAAGCTGAGGCTTCTCTTCCATCTGCGGACAGCTAAGACCTGATTTCAATA 60
Db 679 CAAAGCTGAGGCTTCTCTTCCATCTGCGGACAGCTAAGACCTGATTTCAATA 738
Qy 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTGCCCCCATCTCCGGGGAAATGTC 120
Db 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGATGATTTGCCCCCATCTCCGGGGAAATGTC 798
Qy 121 TGAAGCAATTTTGGTTACTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC 180
Db 799 TGAAGCAATTTT-GTTACTCTAATAGAGAGTGGAGAGATACAGTGTACTACCAAC 857
Qy 181 TAGTGATTAAGGCGAGGATGCTGCTCAACCTCCTACATGTAAGGAGGAGCTCCCA 240
Db 858 TAGTGATTAAGGCGAGGATGCTGCTCAACCTCCTACATGTAAGGAGGAGCTCCCA 916
Qy 241 TTACAATACCAATCCGAATGCAATGTCTCAAGACTTAAGAAACCTGTGTTTGAAT 300

Db 917 TTACAATACCAATCCGAATGCAATGTCTCAAGACTTAAGAAACCTGTGTTTGAAT 976
Qy 301 AGAAAGGCGCTGGAAGAGGGGAGCCAAACAAATCTGTGCTCTCCACATTAATCAAT 360
Db 977 AGAAAGGCGCTGGAAGAGGGGAGCCAAACAAATCTGTGCTCTCCACATTAATCAAT 1036
Qy 361 GGAATATAGCATTTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
Db 1037 GGAATATAGCATTTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 1096
Qy 421 GGGCACAGAGTAAATCTCTCAGTGAACAGAGTTGACAAAGGCTTAAGGAAATGCTGA 480
Db 1097 GGGCACAGAGTAAATCTCTCAGTGAACAGAGTTGACAAAGGCTTAAGGAAATGCTGA 1156
Qy 481 TGGGATTAATCTTCAAGCTTGTAGAGCTTAAAGTTCTTTCCTTCAATTCACCTGCAAG 540
Db 1157 TGGGATTAATCTTCAAGCTTGTAGAGCTTAAAGTTCTTTCCTTCAATTCACCTGCAAG 1216
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 1276
Qy 601 TCTCCAGACCTTCTGCGCCCAATTCATTAAGGCAACAAACATATACCTTCCATGA 660
Db 1277 TCTCCAGACCTTCTGCGCCCAATTCATTAAGGCAACAAACATATACCTTCCATGA 1336
Qy 661 GCACACAGAGCTTTTGAAGCAAGACATGACTCTTGAATGAGGCTTGAAGGATG 720
Db 1337 GCACACAGAGCTTTTGAAGCAAGACATGACTCTTGAATGAGGCTTGAAGGATG 1396
Qy 721 AGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCTTCCACACTCTTCAATGTGA 780
Db 1397 AGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCTTCCACACTCTTCAATGTGA 1456
Qy 781 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTGAAGAAAC 840
Db 1457 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTGAAGAAAC 1516
Qy 841 TGATTTAAGATTCATGATGTTCAAGAGATGATTAATATACATTTCT 890
Db 1517 TGATTTAAGATTCATGATGTTCAAGAGATGATTAATATACATTTCT 1566

RESULT 13
AR257633 1567 bp DNA linear PAT 20-DEC-2002
LOCUS AR257633
DEFINITION Sequence 74 from patent US 6488931.
ACCESSION AR257633
VERSION AR257633.1 GI:27307708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLES Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6488931-A 74 03-DEC-2002;
FEATURES Location/Qualifiers
source 1..1567
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 97.3%; Score 866; DB 6; Length 1567;
Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 1 CAAAGCTGAGGCTTCTCTTCCATCTGCGGACAGCTAAGACCTGATTTCAATA 60
Db 679 CAAAGCTGAGGCTTCTCTTCCATCTGCGGACAGCTAAGACCTGATTTCAATA 738

QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 120
| | | | |
DB 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGACATTTTGGTTTACTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 180
| | | | |
DB 799 TGAAGACATTTT-GTTACTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 857
QY 181 TAGTGAATAAAGCCAGGAGTGTCTCAACCTCTCACTGATACAGGAGCTGTCCCA 240
| | | | |
DB 858 TAGTGAATAAAGCCAGGAGTGTCTCAACCTCTCACTGATACAGGAGCTGTCCCA 916
QY 241 TTCAACTACCAATCCGAAGTGTCACTGTGACAGACTAAGAAACCTGGTTTGTAGT 300
| | | | |
DB 917 TTCAACTACCAATCCGAAGTGTCACTGTGACAGACTAAGAAACCTGGTTTGTAGT 976
QY 301 AGAAAGGCGCTGGAAAGAGGGAGCCAAATCTGTCTCTTCCATTAATGTCAT 360
| | | | |
DB 977 AGAAAGGCGCTGGAAAGAGGGAGCCAAATCTGTCTCTTCCATTAATGTCAT 1036
QY 361 GGGAAATTAAGCATTTCTCTTTGGTGTCTGCTGCTGACAGACAGAGCCGAATCTATC 420
| | | | |
DB 1037 GGGAAATTAAGCATTTCTCTTTGGTGTCTGCTGCTGACAGACAGAGCCGAATCTATC 1096
QY 421 GGGACACAGATTAACATCTCTCAGTGAACAGAGTTCAGAGCCCTATGGGAAATGCTGA 480
| | | | |
DB 1097 GGGACACAGATTAACATCTCTCAGTGAACAGAGTTCAGAGCCCTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTCACTGCAAG 540
| | | | |
DB 1157 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTCACTGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 600
| | | | |
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 1276
QY 601 TCTCCAGACCCCTCTGAGCCACAAATTCAAATTAAGGCAACAAATTAATCTTCCATGAA 660
| | | | |
DB 1277 TCTCCAGACCCCTCTGAGCCACAAATTCAAATTAAGGCAACAAATTAATCTTCCATGAA 1336
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTTAGAGCCTTGAAGATG 720
| | | | |
DB 1337 GCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTTAGAGCCTTGAAGATG 1396
QY 721 AACCTTTGAAGAAAGAAATTAATTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 780
| | | | |
DB 1397 AACCTTTGAAGAAAGAAATTAATTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 1456
QY 781 ACCACTGCTTCTCTGAGCCTTGGAGCCAGGTGCTGATTAATGTTATAGAAAC 840
| | | | |
DB 1457 ACCACTGCTTCTCTGAGCCTTGGAGCCAGGTGCTGATTAATGTTATAGAAAC 1516
QY 841 TGAATTTAGAGTTCTGATCTGTTCAAGAGATGATTAATTAATTAATTTCT 890
| | | | |
DB 1517 TGAATTTAGAGTTCTGATCTGTTCAAGAGATGATTAATTAATTAATTTCT 1566

RESULT 14
AR283679 1567 bp DNA linear PAT 10-APR-2003
LOCUS AR283679 Sequence 74 from patent US 6528253.
DEFINITION AR283679
ACCESSION AR283679
VERSION AR283679.1 GI:29720576
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Fridakis,T.N. and King,G.E.
TITLES Compositions and methods for diagnosis of ovarian cancer
JOURNAL Patent: US 6528253-A 74 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..1567

ORIGIN /organism="unknown"
/mol_type="genomic DNA"
Query Match 97.3%; Score 866; DB 6; Length 1567;
Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 CAAGCTCTGAGGCTTCTCTTTCATCTGCTGAGACAGTAAAGACTCAGTTTCAATA 60
| | | | |
DB 679 CAAGCTCTGAGGCTTCTCTTTCATCTGCTGAGACAGTAAAGACTCAGTTTCAATA 738
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 120
| | | | |
DB 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGACATTTTGGTTTACTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 180
| | | | |
DB 799 TGAAGACATTTT-GTTACTCAATGAGGAGTGGAGAGATACAGTGTCTACTACCAAC 857
QY 181 TAGTGAATAAAGCCAGGAGTGTCTCAACCTCTCACTGATACAGGAGCTGTCCCA 240
| | | | |
DB 977 TAGTGAATAAAGCCAGGAGTGTCTCAACCTCTCACTGATACAGGAGCTGTCCCA 916
QY 241 TTCAACTACCAATCCGAAGTGTCACTGTGACAGACTAAGAAACCTGGTTTGTAGT 300
| | | | |
DB 917 TTCAACTACCAATCCGAAGTGTCACTGTGACAGACTAAGAAACCTGGTTTGTAGT 976
QY 301 AGAAAGGCGCTGGAAAGAGGGAGCCAAATCTGTCTGCTTCCCTCAATTAATGTCAT 360
| | | | |
DB 977 AGAAAGGCGCTGGAAAGAGGGAGCCAAATCTGTCTGCTTCCCTCAATTAATGTCAT 1036
QY 361 GGGAAATTAAGCATTTCTCTTTGGTGTCTGCTGCTGACAGACAGAGCCGAATCTATC 420
| | | | |
DB 1037 GGGAAATTAAGCATTTCTCTTTGGTGTCTGCTGCTGACAGACAGAGCCGAATCTATC 1096
QY 421 GGGACACAGATTAACATCTCTCAGTGAACAGAGTTCAGAGCCCTATGGGAAATGCTGA 480
| | | | |
DB 1097 GGGACACAGATTAACATCTCTCAGTGAACAGAGTTCAGAGCCCTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTCACTGCAAG 540
| | | | |
DB 1157 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATCTCACTGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 600
| | | | |
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTTAGA 1276
QY 601 TCTCCAGACCCCTCTGAGCCACAAATTCAAATTAAGGCAACAAATTAATCTTCCATGAA 660
| | | | |
DB 1277 TCTCCAGACCCCTCTGAGCCACAAATTCAAATTAAGGCAACAAATTAATCTTCCATGAA 1336
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTTAGAGCCTTGAAGATG 720
| | | | |
DB 1337 GCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTTAGAGCCTTGAAGATG 1396
QY 721 AACCTTTGAAGAAAGAAATTAATTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 780
| | | | |
DB 1397 AACCTTTGAAGAAAGAAATTAATTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTGTA 1456
QY 781 ACCACTGCTTCTCTGAGCCTTGGAGCCAGGTGCTGATTAATGTTATAGAAAC 840
| | | | |
DB 1457 ACCACTGCTTCTCTGAGCCTTGGAGCCAGGTGCTGATTAATGTTATAGAAAC 1516
QY 841 TGAATTTAGAGTTCTGATCTGTTCAAGAGATGATTAATTAATTAATTTCT 890
| | | | |
DB 1517 TGAATTTAGAGTTCTGATCTGTTCAAGAGATGATTAATTAATTAATTTCT 1566

RESULT 15
AR443353 1567 bp DNA linear PAT 20-FEB-2004
LOCUS AR443353 Sequence 74 from patent US 6670463.
DEFINITION

ACCESSION AR443353
VERSION AR443353.1 GI:42671132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLE Compositions and methods for therapy of ovarian cancer
JOURNAL Patent: US 6670463-A 74 30-DEC-2003;
FEATURES
Location/Qualifiers
1..1567
source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 97.3%; Score 866; DB 6; Length 1567;
Best Local Similarity 99.8%; Pred. No. 9.3e-255;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
QY 1 CAAGCTTGAGGCTTCTCTTCATCTGCGTGAACAGTAAAGCTCAGTTTCAATA 60
Db 679 CAAGCTTGAGGCTTCTCTTCATCTGCGTGAACAGTAAAGCTCAGTTTCAATA 738
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCATCTCGGGGAATGTC 120
Db 739 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCATCTCGGGGAATGTC 798
QY 121 TGAAGCAATTTTGGTTACTCATAGGAGTGGAGAGATACGTCTACTACCAAC 180
Db 799 TGAAGCAATTTT-GTTACTCATAGGAGTGGAGAGATACGTCTACTACCAAC 857
QY 181 TAGTGATTAAGGCGCAGGGATGCTGCTCAACCTTACCATGACAGGAGCTCCCA 240
Db 858 TAGTGATTAAGGCGCAGGGATGCTGCTCAACCTTACCATGACAGGAGCTCCCA 916
QY 241 TTACAACTACCCAACTCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 300
Db 917 TTACAACTACCCAACTCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 976
QY 301 AGAAAAGGCGCTGGAAAAGGGGAGCCAAATCTGTCTGCTTCTCATTAGTCATT 360
Db 977 AGAAAAGGCGCTGGAAAAGGGGAGCCAAATCTGTCTGCTTCTCATTAGTCATT 1036
QY 361 GGGAAATAAGCATTCTGTCTTGGCTGTGCTCAGCAAGAGGCCAAGCTCTATC 420
Db 1037 GGGAAATAAGCATTCTGTCTTGGCTGTGCTCAGCAAGAGGCCAAGCTCTATC 1096
QY 421 GGGCACAGGATTAACATCTCTCAGTAAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 480
Db 1097 GGGCACAGGATTAACATCTCTCAGTAAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTACCTGCAAG 540
Db 1157 TGGGATTAATCTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTACCTGCAAG 1216
QY 541 CCAAGTTCGTAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTGGAATTAGA 600
Db 1217 CCAAGTTCGTAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTGGAATTAGA 1276
QY 601 TCTCCAGACCTTCTGTGCCACAATTCAAATTAAGCAACAAACATATACCTTCATGAA 660
Db 1277 TCTCCAGACCTTCTGTGCCACAATTCAAATTAAGCAACAAACATATACCTTCATGAA 1336
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTGAGGCTTGAAGAAATG 720
Db 1337 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTGAGGCTTGAAGAAATG 1396
QY 721 AAGCTTTGAAGAAAGAAATACTTTGTTTCAGCCCCCTCCACACTCTTCATGTGTTA 780
Db 1397 AAGCTTTGAAGAAAGAAATACTTTGTTTCAGCCCCCTCCACACTCTTCATGTGTTA 1456
QY 781 ACCACTGCTTCTTGAGACTTGGAGCCACGGTGACTGTATTAATCATGTGTATAGAAAAC 840
```

```
Db 1457 ACCACTGCTTCTTGAGACTTGGAGCCACGGTGACTGTATTAATCATGTGTATAGAAAAC 1516
QY 841 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCTCT 890
Db 1517 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCTCT 1566
```

Search completed: May 30, 2005, 17:54:05
Job time : 4108.01 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 05:15:03 ; Search time 545.854 Seconds

(without alignments)
9651.969 Million cell updates/sec

Title: US-09-763-978B-11

Perfect score: 890

Sequence: 1 caagctctgagctctcct.....tgatataacatacttctcc 890

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	890	100.0	890	AAZ90480	Aaz90480 Cancer sp
2	886.8	99.6	1020	AAAS4133	Aaas4133 Breast ca
3	878	98.7	893	AA59821	Aax59821 Consensus
4	878	98.7	893	AA59820	Aax59820 DNA seque
5	878	98.7	893	ABL57349	ABL57349 Breast BS
6	878	98.7	893	ABL57350	ABL57350 Breast BS
7	878	100.4	12	ADH50891	Adh50891 Breast an
8	878	98.7	2627	AAA70077	Aaa70077 Human ova
9	878	98.7	2627	AAH55681	Aah55681 Human ova
10	878	98.7	2627	ABN72971	Abn72971 Ovarian c
11	878	98.7	2627	ADA08544	Ada08544 Human ova
12	878	98.7	2627	ADFO8887	Adfo8887 cDNA enco
13	878	98.7	2627	ADG46174	Adg46174 Human ova
14	878	98.7	2627	ADN40452	Adn40452 Human bre
15	878	98.7	2627	ADP81075	Adp81075 Human ova
16	878	98.7	3357	AAAD2519	Aad3519 Human B7-
17	877.6	98.6	2603	AAAD29253	Aad29253 Human B7-
18	876.4	98.6	2626	ABL56582	Ab156582 Complete
19	867	97.4	2591	ABL57354	Ab157354 Breast BS
20	866	97.3	1567	AA659764	Aaa659764 Human ova

21	866	97.3	1567	6	ABN72658	Abn72658 Ovarian c
22	866	97.3	1567	9	ADA08823	Ada08823 Human ova
23	866	97.3	1567	10	ADP08570	Adp08570 cDNA enco
24	866	97.3	1567	10	ADG46318	Adg46318 Human ova
25	866	97.3	2587	3	AAZ90470	Aaz90470 Cancer sp
26	856.6	96.2	2626	4	AAZ6593	Aaz6593 DNA enco
27	856.6	96.2	2626	6	AAZ32526	Aad32526 Human B7-
28	807	90.7	846	5	ADL63234	Adl63234 Human ova
29	804.4	90.4	836	4	AAFA4856	Aafa4856 Human bre
30	711	79.9	725	6	ABL57361	Ab157361 Breast BS
31	629.2	70.7	1808	12	ADH50892	Adh50892 Breast an
32	629.2	70.7	1898	12	ADH50893	Adh50893 Breast an
33	626.2	70.4	1811	6	ABST6536	Abst6536 cDNA enco
34	626.2	70.4	1811	6	ABST6420	Abst6420 cDNA enco
35	626.2	70.4	1811	8	ACCS0158	Accs0158 Breast ca
36	626.2	70.4	1811	10	ADH80507	Adh80507 Ovarian c
37	626.2	70.4	1811	12	ADP81074	Adp81074 Human ova
38	552	62.0	563	6	ABL80970	Ab180970 Human ova
39	544	61.1	555	6	AA561836	Aa561836 Lung smal
40	517	58.1	1596	11	ACN92433	Acn92433 Breast ca
41	494.6	55.6	538	6	ABT09900	Abt09900 Human bre
42	494.6	55.6	538	6	ABL78520	Ab178520 Human ova
43	494.6	55.5	524	6	ABL79323	Ab179323 Human ova
44	487.8	54.8	578	5	ADL43792	Adl43792 Human ova
45	480	53.9	491	2	AA59818	Aax59818 DNA seque

ALIGNMENTS

RESULT 1
AAZ90480
ID AAZ90480 standard; cDNA; 890 BP.
AC
XX
AC AAZ90480;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cancer specific gene (clone ID 16656542) fragment #11.
XX
KW CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KM endometrial; uterine; lung; cytotoxic; ss.
XX
OS Homo sapiens.
XX
XX
PN WO200012758-A1.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US019655.
XX
PR 02-SEP-1998; 98US-0098880P.
XX
PA (DIAD-) DIADEXUS LLC.
PI Salceda S, Sun Y, Recipon H, Cafterkey R;
DR WPI; 2000-256657/22.
XX
PT Diagnosing, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer.
PT involves measuring cancer specific gene levels in cells and body fluids.
XX
XX
PS Claim 9; Page 51; 58pp; English.
XX
XX The invention relates to detecting, diagnosing metastasis and staging
XX cancer by measuring levels of cancer specific genes (CSG) in cells,
XX tissues or body fluids. Their remission and progression, decreases and
XX increases in CSG levels, is also monitored, by periodic sample analysis.
XX The methods are useful for detecting cancers, especially gynecologic
XX cancers which include ovarian, breast, endometrial and uterine cancer and
XX lung cancer. Antibodies against the CSGs labeled with paramagnetic ions
XX or a radioisotope is useful for imaging cancer and when conjugated with a

CC cytotoxic agent are useful for treating cancer. The present sequence
 XX represents a CSG (clone ID: 16656542 and gene ID: 234617) fragment
 SQ Sequence 890 BP; 242 A; 213 C; 194 G; 241 T; 0 U; 0 Other;

Query Match 100.0%; Score 890; DB 3; Length 890;
 Best Local Similarity 100.0%; Pred. No. 1.5e-288;
 Matches 890; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCCGGAGCACTTAAGACTCAGTTTCAATA 60
 DB 1 CAAGCTCTGAGGCTTCTCTTCCATCCCGGAGCACTTAAGACTCAGTTTCAATA 60
 QY 61 GCATCTAGAGCACTGAGGAGTGTGCTCAACCTCCATGATGAGGAGGAGTATGTC 120
 DB 61 GCATCTAGAGCACTGAGGAGTGTGCTCAACCTCCATGATGAGGAGGAGTATGTC 120
 QY 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
 DB 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
 QY 181 TAGTGATTAAGGCGCAGGAGTGTGCTCAACCTCCATGATGAGGAGGAGTATGTC 240
 DB 181 TAGTGATTAAGGCGCAGGAGTGTGCTCAACCTCCATGATGAGGAGGAGTATGTC 240
 QY 241 TTAACAATACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCCTGTTTGAAT 300
 DB 241 TTAACAATACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCCTGTTTGAAT 300
 QY 301 AGAAAAGGCGCTGGAAGAGGAGGAGCAAAATCTGTCTCTCTCTCAATTAATGTCATT 360
 DB 301 AGAAAAGGCGCTGGAAGAGGAGGAGCAAAATCTGTCTCTCTCTCAATTAATGTCATT 360
 QY 361 GGAATAATAGCAATCTCTCTTGGCTGTGCTGCTAGAGCAAGAGCCAGAACTCTATC 420
 DB 361 GGAATAATAGCAATCTCTCTTGGCTGTGCTGCTAGAGCAAGAGCCAGAACTCTATC 420
 QY 421 GGGACACGAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTGGAAATGCTGA 480
 DB 421 GGGACACGAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTGGAAATGCTGA 480
 QY 481 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTCTTTCCCTTCATCTACCTGCAAG 540
 DB 481 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTCTTTCCCTTCATCTACCTGCAAG 540
 QY 541 CGAAGTCTGTAGAAGAAATGCTGAGTCTAGCTAGGTTTCTTACTCTGAATTAGA 600
 DB 541 CGAAGTCTGTAGAAGAAATGCTGAGTCTAGCTAGGTTTCTTACTCTGAATTAGA 600
 QY 601 TCTCCAGACCCCTTCGCGCACAATTCAAATTAAAGCAACAAATATACCTTCCATGAA 660
 DB 601 TCTCCAGACCCCTTCGCGCACAATTCAAATTAAAGCAACAAATATACCTTCCATGAA 660
 QY 661 GCACACACAGACTTTGAAAGCAAGCAATGACTCTGTAATTGAGGCGCTTGAAGAAAG 720
 DB 661 GCACACACAGACTTTGAAAGCAAGCAATGACTCTGTAATTGAGGCGCTTGAAGAAAG 720
 QY 721 AAGCTTGAAGAAAGAAATACCTTGTTCACGCCCTTCCACACTCTCAATGAGTGA 780
 DB 721 AAGCTTGAAGAAAGAAATACCTTGTTCACGCCCTTCCACACTCTCAATGAGTGA 780
 QY 781 ACCACTGCGCTTCTCTGAGCCTTGAGGACAGGTAAGTATTAATGATTTATAGAAAC 840
 DB 781 ACCACTGCGCTTCTCTGAGCCTTGAGGACAGGTAAGTATTAATGATTTATAGAAAC 840
 QY 841 TGAATTTAAGATTCTGATGCTTCAAGAGAAATGAATTAATATACATTTCT 890
 DB 841 TGAATTTAAGATTCTGATGCTTCAAGAGAAATGAATTAATATACATTTCT 890

RESULT 2
 AAAS4133
 ID AAAS4133 standard; DNA; 1020 BP.

XX AC AAAS4133;
 XX DT 08-FEB-2001 (first entry)
 DE Breast cancer protein BCU7 coding sequence.
 KW Breast cancer; diagnosis; prognosis; detection; screening; antibody;
 KW oestrogen receptor; anti-oestrogen; immune response; lymph node;
 KW metastases; tumour; BCR3; BC08; BC05; BCH1; BCN1; BCN2; BCN5; BC02; BCX2;
 KW BCX3; BC42; BCR2; BCU7; BCY3; human; ds.
 XX OS Homo sapiens.
 XX PN WO200055629-A2.
 XX PD 21-SEP-2000.
 XX PF 15-MAR-2000; 2000WO-US006952.
 XX PR 15-MAR-1999; 99US-00268865.
 XX PR 12-NOV-1999; 99US-00439878.
 XX PR 12-NOV-1999; 99US-00440370.
 XX PR 15-NOV-1999; 99US-00440493.
 XX PR 16-NOV-1999; 99US-00440676.
 XX PR 16-NOV-1999; 99US-00440677.
 XX PR 29-NOV-1999; 99US-00450810.
 XX PR 02-DEC-1999; 99US-00453137.
 XX PR 08-MAR-2000; 2000US-00453137.
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX PI Mack D, Gish KC;
 XX DR WPI; 2000-638216/61.
 XX PT Screening drug candidates for their ability to modulate breast cancer by
 PT contacting the drug to a cell expressing an expression profile gene and
 XX determining modulation of expression of the gene.
 XX PS Disclosure; Fig 72; 258pp; English.
 XX XS
 CC New methods for screening drug candidates are described which comprise
 CC adding a drug candidate to a cell that expresses a protein selected from
 CC BCH1, BC42, BCU7, BCN1, BCN5, BC02, BC05, BCR2, BCX2 and BCY3 or their
 CC fragments and determining the effect of the drug on the expression of
 CC those proteins. Antibodies to breast cancer genes (specifically BCH1 or
 CC its fragment (BCH1p1 or BCH1p2)) are useful for inhibiting and treating
 CC breast cancer in individuals who are non-responsive to anti-oestrogen and
 CC positive for oestrogen receptor. Compositions comprising BCH1 or a
 CC nucleic acid encoding BCH1 are useful for eliciting an immune response in
 CC an individual. The antibodies are also useful for the diagnosis and
 CC prognosis of breast cancer and for screening compositions which modulate
 CC the breast cancer phenotype. The method allows rapid and simple detection
 CC of lymph node metastases
 XX SQ Sequence 1020 BP; 287 A; 237 C; 215 G; 280 T; 0 U; 1 Other;
 Query Match 99.6%; Score 886.8; DB 3; Length 1020;
 Best Local Similarity 99.8%; Pred. No. 1.9e-287;
 Matches 888; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCCGGAGCACTTAAGACTCAGTTTCAATA 60
 DB 106 CAAGCTCTGAGGCTTCTCTTCCATCCCGGAGCACTTAAGACTCAGTTTCAATA 165
 QY 61 GCATCTAGAGCACTGAGGAGTGTGCTCAACCTCCATGATGAGGAGGAGTATGTC 120
 DB 166 GCATCTAGAGCACTGAGGAGTGTGCTCAACCTCCATGATGAGGAGGAGTATGTC 225
 QY 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAAGAGATTAAGGCTACTACCAAC 180
 DB 226 TGAAGCAATTTGGTTACCTCAATGAGGAGTGAAGAGATTAAGGCTACTACCAAC 285


```
QY 601 TCTCCAGACCCCTTCTGGCACAATTCAATTAAAGGCAACAAATATATCTTCCATGAA 660
DB 600 TCTCCAGACCCCTTCTGGCACAATTCAATTAAAGGCAACAAATATATCTTCCATGAA 659
QY 661 GCACACACAGACTTTTGAAGAGCAATGACTGCTTGAATTGAAGGCTTGAGGAATG 720
DB 660 GCACACACAGACTTTTGAAGAGCAATGACTGCTTGAATTGAAGGCTTGAGGAATG 719
QY 721 AAGCTTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 780
DB 720 AAGCTTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 779
QY 781 ACCACGCTCTCCCTGGACCTGGAGCAGGTAAGTATGATTAATATATATCAATTTCT 840
DB 780 ACCACGCTCTCTCCCTGGACCTGGAGCAGGTAAGTATGATTAATATATATCAATTTCT 839
QY 841 TGAATTTAGAGTTCTGATCGTTTCAGAGATGATTAATATATATCAATTTCT 890
DB 840 TGAATTTAGAGTTCTGATCGTTTCAGAGATGATTAATATATATCAATTTCT 889
```

RESULT 4
AAK59820
ID AAK59820 standard; DNA; 893 BP.

AAK59820;

28-JUL-1999 (first entry)

DNA sequence of BS265 clone 3090742inh.

BS265: marker; breast disease; cancer; metastasis; atypical hyperplasia;
fibroadenoma; cyst; therapeutic antagonist; antibody;
chromosomal anomaly; genetic immunization; ss.

Homo sapiens.

MO9925877-A1.

27-MAY-1999.

18-NOV-1998; 98WO-US024620.

18-NOV-1997; 97US-00972376.

(ABBO) ABBOTT LAB.

Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
Grandos EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L,
Russell JC, Stroupe SD;
WPI; 1999-347495/29.

BS265 nucleic acid; marker for breast disease.

Claim 1; Page 95; 102pp; English.

AAK5816-20 represent clones used to derive the consensus sequence of
nucleic acid designated BS265. BS265 is a marker of breast disease,
particularly cancer and its metastases, but also atypical hyperplasia,
fibroadenoma and cysts, so detection/quantification of BS265, encoded
polypeptides and antibodies is used for diagnosis, staging, monitoring,
prognosis, in vivo imaging of, and determining predisposition to these
diseases. The antibodies are useful as therapeutic antagonists
(optionally coupled to a cytotoxin), as immunoassay reagents and in
competitive drug screens. The polynucleotide and its fragments, are used
as probes and primers (in diagnostic assays, for quantifying gene
expression), for detecting chromosomal anomalies and to isolate related
sequences), for genetic immunization, as a source of therapeutic
antibense, triplex-forming and ribozyme sequences, and for recombinant
production of the protein

Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other;
Query Match 98.7%; Score 878; DB 2; Length 893;
Best Local Similarity 99.9%; Pred. No. 1.7e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 CAAGCTTGAGGCTTCTCTTTCATCTGCTGAGACAGTAAGACCTTCAATTA 60
DB 1 CAAGCTTGAGGCTTCTCTTTCATCTGCTGAGACAGTAAGACCTTCAATTA 60
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCACTCTCGGGGGATGTC 120
DB 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGGCCCCCACTCTCGGGGGATGTC 120
QY 121 TGAAGACAATTTGGTTACCTCAATGAGGAGTGAAGAGATAGAGTCTACTCAAC 180
DB 121 TGAAGACAATTTGGTTACCTCAATGAGGAGTGAAGAGATAGAGTCTACTCAAC 180
QY 181 TAGTGATTAAGGCCAGGATGCTGCTCAACCTCTCAATGATAGAGGACGTCTCCCA 240
DB 181 TAGTGATTAAGGCCAGGATGCTGCTCAACCTCTCAATGATAGAGGACGTCTCCCA 240
QY 241 TTACAACTAACCAGTCCGAAAGTGTCACTGTGTGAGACTAAGAAACCTGTGTTGAGT 300
DB 240 TTACAACTAACCAGTCCGAAAGTGTCACTGTGTGAGACTAAGAAACCTGTGTTGAGT 299
QY 301 AGAAAAAGGCTGGAAGAGGGGAGCCAAACAATCTGTCTGCTCTCAATTAATGTCATT 360
DB 300 AGAAAAAGGCTGGAAGAGGGGAGCCAAACAATCTGTCTGCTCTCAATTAATGTCATT 359
QY 361 GGCAAATTAAGACTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTGTATC 420
DB 360 GGCAAATTAAGACTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTGTATC 419
QY 421 GGGCACAGAGTAACATCTCTGAGGAACAGAGTTGACAGAGCCATAGGAAATGCCCTGA 480
DB 420 GGGCACAGAGTAACATCTCTGAGGAACAGAGTTGACAGAGCCATAGGAAATGCCCTGA 479
QY 481 TGGGATTAATCTCAGCTTGTGAGGCTCTAAGTCTCTTCCCTCATTTCACTGACGACAG 540
DB 480 TGGGATTAATCTCAGCTTGTGAGGCTCTAAGTCTCTTCCCTCATTTCACTGACGACAG 539
QY 541 CCAAGTCTGTAAGAAATGCTGATCTAAGTCTGAGGTTTCTTACTCTGAAATTTAGA 600
DB 540 CCAAGTCTGTAAGAAATGCTGATCTAAGTCTGAGGTTTCTTACTCTGAAATTTAGA 599
QY 601 TCTCCAGACCCCTTCTGGCACAATTCAATTAAAGGCAACAAATATATCTTCCATGAA 660
DB 600 TCTCCAGACCCCTTCTGGCACAATTCAATTAAAGGCAACAAATATATCTTCCATGAA 659
QY 661 GCACACACAGACTTTTGAAGAGCAATGACTGCTTGAATTGAAGGCTTGAGGAATG 720
DB 660 GCACACACAGACTTTTGAAGAGCAATGACTGCTTGAATTGAAGGCTTGAGGAATG 719
QY 721 AAGCTTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 780
DB 720 AAGCTTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 779
QY 781 ACCACGCTCTCTCCCTGGACCTGGAGCAGGTAAGTATGATTAATATATATCAATTTCT 840
DB 780 ACCACGCTCTCTCCCTGGACCTGGAGCAGGTAAGTATGATTAATATATATCAATTTCT 839
QY 841 TGAATTTAGAGTTCTGATCGTTTCAGAGATGATTAATATATATCAATTTCT 890
DB 840 TGAATTTAGAGTTCTGATCGTTTCAGAGATGATTAATATATATCAATTTCT 889
```

RESULT 5
ABL57349
ID ABL57349 standard; cDNA; 893 BP.
AC ABL57349;
XX

DT 12-AUG-2002 (first entry)
 XX DE Breast BS265 gene EST clone 3090742H1.
 XX KW BS265; human; breast; cancer; tumour; metastasis; diagnosis;
 XX gene therapy; expressed sequence tag; EST; ss.
 XX OS Homo sapiens.
 XX US2002034749-A1.
 PN 21-MAR-2002.
 PD 07-MAY-2001; 2001US-00850178.
 PF 18-NOV-1997; 97US-00972376.
 PR 18-NOV-1998; 98US-00193944.
 XX (BIL/) BILLINGEL P A.
 PA (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (GRAN/) GRANADOS E N.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L A.
 PA (RUSS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 XX Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, KLAS MR, Kratochvil JD, Roberts-Rapp LA;
 PI Russell JC, Stroupe SD;
 DR WPI; 2002-403712/43.
 XX
 PT New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
 PT staging, monitoring, prognosticating, in vivo imaging, preventing,
 PT treating, or determining the predisposition of an individual to breast
 PT cancer.
 XX
 XX Claim 1; Page 37; 52pp; English.
 XX
 CC The present sequence is of BS265 gene expressed sequence tag (EST) full-
 CC length sequence clone 3090742H1 (ATCC 98683). ESTs were derived from cDNA
 CC libraries made from breast tumour tissues, breast non-tumour tissues and
 CC numerous other tissues, and entered into a database as gene transcript
 CC images. They were then evaluated to identify EST sequences that were
 CC representative primarily of the breast tissue libraries, and were ranked
 CC according to their abundance in target libraries and absence from
 CC background libraries. Partial clones 3090742H1, 991752, 92058967 and
 CC 9161448 (see ABL57345-48) represent the minimum number of clones that,
 CC together with the present full-length sequence of clone 3090752H1, were
 CC needed to form a contig and from which a consensus sequence (see
 CC ABL57350) was derived. ESTs corresponding to the consensus sequence of
 CC BS265 were found in 33.3% (9/27) of breast tissue libraries, and in 0.6%
 CC (3/476) of non-breast libraries. This set of contiguous and partially
 CC overlapping cDNA sequences, designated as BS265 and transcribed from
 CC breast tissue, and the polypeptides encoded by them, are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
 CC imaging, preventing, treating, or determining the predisposition of an
 CC individual to diseases and conditions of the breast, such as breast
 CC cancer. Also provided are antibodies which specifically bind to BS265
 CC proteins, and agonists or inhibitors which prevent action of the
 CC proteins, and which are useful for treatment of breast disease,
 CC especially tumours and metastases
 CC
 SO Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 6; Length 893;
 Best Local Similarity 99.9%; Pred. No. 1,7e-284;
 Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAAGCTCTGAGGCTTCTCTCCCTTTCATCTGCGTGAAGCTAGACCTGATTTTCATA 60
 DB 1 CAAAGCTCTGAGGCTTCTCTCCCTTTCATCTGCGTGAAGCTAGACCTGATTTTCATA 60
 QY 61 GCATCTTAGAGCAGTGGAGTCACTGAGGAGATTTGGCCCCCATCTCCGGGGAATGTC 120
 DB 61 GCATCTTAGAGCAGTGGAGTCACTGAGGAGATTTGGCCCCCATCTCCGGGGAATGTC 120
 QY 121 TGAAGACATTTTGGTTTACTCTCAATGAGGAGTGAAGAGATTAAGTGTACTACCAAC 180
 DB 121 TGAAGACATTTTGGTTTACTCTCAATGAGGAGTGAAGAGATTAAGTGTACTACCAAC 180
 QY 181 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCCTCACTGATACAGGAGCTGCCCA 240
 DB 181 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCCTCACTGATACAGGAGCTGCCCA 240
 QY 241 TTACAACCTACCCATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGTGTTGAGT 300
 DB 241 TTACAACCTACCCATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGTGTTGAGT 300
 QY 301 AGAAAAGGCGCTGAAAAGAGGAGCCCAACAAATCTGTCTCTTCTTCACTTAGTCATT 360
 DB 301 AGAAAAGGCGCTGAAAAGAGGAGCCCAACAAATCTGTCTCTTCTTCACTTAGTCATT 360
 QY 361 GGGAAATTAAGCATTTCTCTCTTTGGCTGTGCTGTGCTGAGCAGAGAGCCGAATCTATC 420
 DB 361 GGGAAATTAAGCATTTCTCTCTTTGGCTGTGCTGTGCTGAGCAGAGAGCCGAATCTATC 420
 QY 421 GGGCACCAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 480
 DB 421 GGGCACCAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 480
 QY 481 TGGGATTAATCTCAGCTTGTGAGCTTCTTCAAGTTCTTTCCTTCAATTTACCTGCAAG 540
 DB 481 TGGGATTAATCTCAGCTTGTGAGCTTCTTCAAGTTCTTTCCTTCAATTTACCTGCAAG 540
 QY 541 CCAAGTCTGTGAAGAAATAGCTGAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 600
 DB 541 CCAAGTCTGTGAAGAAATAGCTGAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 600
 QY 601 TCTCCAGACCCCTTCTGAGCCACAAATTCATTAAGGCAACAAATATACCTTCCATGAA 660
 DB 601 TCTCCAGACCCCTTCTGAGCCACAAATTCATTAAGGCAACAAATATACCTTCCATGAA 660
 QY 661 GCACACACAGATTTTGAAGCAAGGACATGACTGTTGAATGAGGCTTGAAGAAATG 720
 DB 661 GCACACACAGATTTTGAAGCAAGGACATGACTGTTGAATGAGGCTTGAAGAAATG 720
 QY 721 AAGCTTTGAAGAAAGAAATATCTTTTTCAGAGCCCTTCCACACTCTTCAATGTGTTA 780
 DB 721 AAGCTTTGAAGAAAGAAATATCTTTTTCAGAGCCCTTCCACACTCTTCAATGTGTTA 780
 QY 781 ACCACTGCTTCTGAGACCTTGAAGCAGGAGCTGATGATTAATGATGTTGTTAAGAAAC 840
 DB 781 ACCACTGCTTCTGAGACCTTGAAGCAGGAGCTGATGATTAATGATGTTGTTAAGAAAC 840
 QY 841 TGAATTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 890
 DB 841 TGAATTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 890
 RESULT 6
 ABL57350
 ID ABL57350 standard; cDNA; 893 BP.
 XX ABL57350;
 AC
 XX
 DT 12-AUG-2002 (first entry)
 XX DE Breast BS265 gene consensus sequence.
 XX KW BS265; human; breast; cancer; tumour; metastasis; diagnosis;

KW gene therapy; expressed sequence tag; EST; gene; ss.
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..123
FT /tag= a
FT /product= "BS265"
FT /partial
FT /note= "the CDS does not include a start codon"
XX
XX US2002034749-A1.
XX
XX PD 21-MAR-2002.
XX
XX PF 07-MAY-2001; 2001US-00850178.
XX
XX PR 18-NOV-1997; 97US-00972376.
XX PR 18-NOV-1998; 98US-00193944.
XX
XX PA (BILL/) BILLINGEL P A.
XX PA (COHE/) COHEN M.
XX PA (COLE/) COLETTIS T L.
XX PA (FRIE/) FRIEDMAN P N.
XX PA (GORD/) GORDON J.
XX PA (GRAN/) GRANADOS E N.
XX PA (HODG/) HODGES S C.
XX PA (KIAS/) KIAS M R.
XX PA (KRAT/) KRATOCHVIL J D.
XX PA (ROBE/) ROBERTS-RAEP L A.
XX PA (RUS/) RUSSELL J C.
XX PA (STRO/) STROUPE S D.
XX
XX PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
XX PI Granados EN, Hodges SC, Kias MR, Kratochvil JD, Roberts-Rapp LA,
XX PI Russell JC, Strophe SD;
XX
XX DR P-PSDB; ABB76272.
XX
XX PT MPI; 2002-403712/43.
XX
XX PT New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
XX PT staging, monitoring, prognosticating, in vivo imaging, preventing,
XX PT treating, or determining the predisposition of an individual to breast
XX PT cancer.
XX
XX PS Claim 1; Page 38; 52pp; English.
XX
XX CC The present sequence is a consensus sequence of the human breast BS265
XX CC gene. Expressed sequence tags (ESTs) were derived from cDNA libraries
XX CC made from breast tumour tissues, breast non-tumour tissues and numerous
XX CC other tissues, and entered into a database as gene transcript images.
XX CC They were then evaluated to identify EST sequences that were
XX CC representative primarily of the breast tissue libraries, and were ranked
XX CC according to their abundance in target libraries and absence from
XX CC background libraries. 4 Overlapping EST clones, together with a full-
XX CC length sequence (see ABL57345-49), were used to form a contig from which
XX CC the present consensus sequence was derived. ESTs corresponding to the
XX CC consensus sequence were found in 33.3% (9/27) of breast tissue libraries,
XX CC and in 0.6% (3/476) of non-breast libraries. The set of contiguous and
XX CC partially overlapping cDNA sequences, designated as BS265 and transcribed
XX CC from breast tissue, and the polypeptides encoded by them, are useful for
XX CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
XX CC imaging, preventing, treating, or determining the predisposition of an
XX CC individual to diseases and conditions of the breast, such as breast
XX CC cancer. Also provided are antibodies which specifically bind to BS265
XX CC proteins, and agonists or inhibitors which prevent action of the
XX CC proteins, and which are useful for treatment of breast disease,
XX CC especially tumours and metastases
XX
XX SQ Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 6; Length 893;
Best Local Similarity 99.9%; Pred. No. 1.7e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CAAGCTTGAAGGCTTCTCTTCCATCTCGGTGAGACAGTAAAGACTCAGTTTCAATA 60
DB 1 CAAGCTTGAAGGCTTCTCTTCCATCTCGGTGAGACAGTAAAGACTCAGTTTCAATA 60
QY 61 GCATCTAAGACAGTGGGACTCAGCTGGGGTGATTTTGGCCCCCATCTCCGGGGGAATGTC 120
DB 61 GCATCTAAGACAGTGGGACTCAGCTGGGGTGATTTTGGCCCCCATCTCCGGGGGAATGTC 120
QY 121 TGAAGACAATTTGGTTACCTCAATGAGAGAGTGAAGAGATAGAGTCTACTACCAAC 180
DB 121 TGAAGACAATTTGGTTACCTCAATGAGAGAGTGAAGAGATAGAGTCTACTACCAAC 180
QY 181 TAGTGATTAAGAGCCAGGAGATGCTGCTCAACTCTTACCATATGACAGGAGCTGCCCA 240
DB 181 TAGTGATTAAGAGCCAGGAGATGCTGCTCAACTCTTACCATATGACAGGAGCTGCCCA 240
QY 241 TTACAACTAACCAGATCCGAAAGTGTCACTGTCTCAGACTAAGAAACCTGTGTTGAGT 300
DB 241 TTACAACTAACCAGATCCGAAAGTGTCACTGTCTCAGACTAAGAAACCTGTGTTGAGT 300
QY 301 AGAAAAAGGCGCTGGAAGAGGGGAGCCAAATCTGTCGCTCTGCACATTAGTCATT 360
DB 301 AGAAAAAGGCGCTGGAAGAGGGGAGCCAAATCTGTCGCTCTGCACATTAGTCATT 360
QY 361 GGCAGTAATAGCATCTCTCTTTGGCTGCTGCTCAGACAGAGAGGAGGAGGAGTATC 420
DB 361 GGCAGTAATAGCATCTCTCTTTGGCTGCTGCTCAGACAGAGAGGAGGAGGAGTATC 420
QY 421 GGGACACAGAGATACATCTCTGAGTGAACAGAGTTGACAGAGGCTTATGGAAATGCTTGA 480
DB 421 GGGACACAGAGATACATCTCTGAGTGAACAGAGTTGACAGAGGCTTATGGAAATGCTTGA 480
QY 481 TGGGATTAATCTTCACTTGTGAGTGTGAGTTTCTTCCCTTCAATTCACCTGCAAG 540
DB 481 TGGGATTAATCTTCACTTGTGAGTGTGAGTTTCTTCCCTTCAATTCACCTGCAAG 540
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAAATTAGA 600
DB 541 CCAAGTTCTGTAAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAAATTAGA 600
QY 540 CCAAGTTCTGTAAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAAATTAGA 599
DB 540 CCAAGTTCTGTAAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAAATTAGA 599
QY 601 TCTCCAGACCTTCTGCGCACATTCAAATTAAAGCAACAACATATACCTTCCATGAA 660
DB 601 TCTCCAGACCTTCTGCGCACATTCAAATTAAAGCAACAACATATACCTTCCATGAA 660
QY 600 TCTCCAGACCTTCTGCGCACATTCAAATTAAAGCAACAACATATACCTTCCATGAA 659
DB 600 TCTCCAGACCTTCTGCGCACATTCAAATTAAAGCAACAACATATACCTTCCATGAA 659
QY 661 GCACACACAGACTTTTGAAGAGAGACATGACTGTGAATTGAGGCTTGAGGAATG 720
DB 661 GCACACACAGACTTTTGAAGAGAGACATGACTGTGAATTGAGGCTTGAGGAATG 720
QY 660 GCACACACAGACTTTTGAAGAGAGACATGACTGTGAATTGAGGCTTGAGGAATG 719
DB 660 GCACACACAGACTTTTGAAGAGAGACATGACTGTGAATTGAGGCTTGAGGAATG 719
QY 721 AAGCTTTGAAGAAAGAAATACCTTGTCCAGCCCCCTTCCACACTCTTCATGTGTTA 780
DB 721 AAGCTTTGAAGAAAGAAATACCTTGTCCAGCCCCCTTCCACACTCTTCATGTGTTA 780
QY 720 AAGCTTTGAAGAAAGAAATACCTTGTCCAGCCCCCTTCCACACTCTTCATGTGTTA 779
DB 720 AAGCTTTGAAGAAAGAAATACCTTGTCCAGCCCCCTTCCACACTCTTCATGTGTTA 779
QY 781 ACCACTGCTTCTGAGACCTTGGAGCCAGGCTGATTTATCATGTTGTTATGAAGAC 840
DB 781 ACCACTGCTTCTGAGACCTTGGAGCCAGGCTGATTTATCATGTTGTTATGAAGAC 840
QY 780 ACCACTGCTTCTGAGACCTTGGAGCCAGGCTGATTTATCATGTTGTTATGAAGAC 839
DB 780 ACCACTGCTTCTGAGACCTTGGAGCCAGGCTGATTTATCATGTTGTTATGAAGAC 839
QY 841 TGAATTTAGAGTTCGATGCTTCAAGAGAAATGATTAATATCATTTCTCT 890
DB 841 TGAATTTAGAGTTCGATGCTTCAAGAGAAATGATTAATATCATTTCTCT 889
DB 840 TGAATTTAGAGTTCGATGCTTCAAGAGAAATGATTAATATCATTTCTCT 889
RESULT 7
ADH50891
ID ADH50891 standard; DNA; 1004 BP.
AC ADH50891;
XX
XX
DT 25-MAR-2004 (first entry)
XX
XX Breast and endothelium cancer-linked gene.
XX

CC The present invention describes an isolated polypeptide comprising an
 CC immunogenic portion of an ovarian carcinoma protein (or its variants).
 CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
 CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
 CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
 CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
 CC cancer. AA69691 to AA70077 and AA12552 to AA12557 represent human
 CC ovarian carcinoma polynucleotides and proteins used in the
 CC exemplification of the present invention
 CC

XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 3; Length 2627;

Best Local Similarity 99.9%; Pred. No. 3.1e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTAAGACTGATTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTAAGACTGATTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGATTTGCCCCCATCTCCGGGGAAATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGATTTGCCCCCATCTCCGGGGAAATGTC 1840
 QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
 DB 1841 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
 QY 181 TAGTGATTAAGGCGCAGGGATGCTGCTCACTCTTCAATGATGAGGAGAGCTCTCCCA 240
 DB 1901 TAGTGATTAAGGCGCAGGGATGCTGCTCACTCTTCAATGATGAGGAGAGCTCTCCCA 1959
 QY 241 TTACACTCTCCCACTCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGGTTTGAAT 300
 DB 1960 TTACACTCTCCCACTCCGAAGTGTGTCAACTGTGTGAGAGCTAAGAAACCTGGTTTGAAT 2019
 QY 301 AGAAAAAGGCGCTGGAAGAGGGAGCCAACTGTCTGCTTCTCTCAATTAGTCATT 360
 DB 2020 AGAAAAAGGCGCTGGAAGAGGGAGCCAACTGTGTCTGCTTCTCTCAATTAGTCATT 2079
 QY 361 GGGAAATTAAGCATTTCTGCTTTGGCTGTGCTCTAGCAAGAGAGCCAGAACTTATC 420
 DB 2080 GGGAAATTAAGCATTTCTGCTTTGGCTGTGCTCTAGCAAGAGAGCCAGAACTTATC 2139
 QY 421 GGGCAGCAGGATTAACATCTCTGAGTGAACAGATGTGAAGAGGCTATGGAAATGCTGA 480
 DB 2140 GGGCAGCAGGATTAACATCTCTGAGTGAACAGATGTGAAGAGGCTATGGAAATGCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTGAAGTTCTTTCCTTCAATCTACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTGAAGTTCTTTCCTTCAATCTACCTGCAAG 2259
 QY 541 CCAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTGTAATTAA 600
 DB 2260 CCAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTGTAATTAA 2319
 QY 601 TCTCCAGACCTCTTGGCCACAATTCATTAAGGCAACAACATATACCTTCCATGA 660
 DB 2320 TCTCCAGACCTCTTGGCCACAATTCATTAAGGCAACAACATATACCTTCCATGA 2379
 QY 661 GCACACACAGATTTGAAAGCAAGACAATGACTCTTGAATTAAGGCGCTTGAAGAAATG 720
 DB 2380 GCACACACAGATTTGAAAGCAAGACAATGACTCTTGAATTAAGGCGCTTGAAGAAATG 2439
 QY 721 AAGCTTTGAAGAAAAAATACTTTTGTTCAGCCCCCTTCCACACTCTTCAATGTGTA 780
 DB 2440 AAGCTTTGAAGAAAAAATACTTTTGTTCAGCCCCCTTCCACACTCTTCAATGTGTA 2499
 QY 781 ACCACTGCGCTTCTGAGACCTTGAGGCAAGGAGTGTATTAATGTTGTTAAGAAAC 840
 DB 2500 ACCACTGCGCTTCTGAGACCTTGAGGCAAGGAGTGTATTAATGTTGTTAAGAAAC 2559
 QY 841 TGATTTAGAGTTCTGATGTTTCAGAGATGATTAATATACATTTCT 890

DB 2560 TGATTTAGAGTTCTGATGTTTCAGAGATGATTAATATACATTTCT 2609

RESULT 9

AAH55681

ID AAH55681 standard; DNA; 2627 BP.

AAH55681;

04-SEP-2001 (first entry)

Human ovarian tumour-derived antigen OBE DNA sequence.

Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;

antigen; OBE; ds.

Homo sapiens.

WO200140269-A2.

07-JUN-2001.

29-NOV-2000; 2000MO-US032520.

30-NOV-1999; 99US-00451651.

22-FEB-2000; 2000US-00510662.

10-MAR-2000; 2000US-00523586.

07-APR-2000; 2000US-00545068.

15-MAY-2000; 2000US-00571025.

(CORI-) CORIXA CORP.

Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;

WPI; 2001-356154/37.

N-PSDB; AAB99204; AAB99205.

Breast tumor polypeptides and the nucleic acids that encode them, useful

for the prevention, diagnosis and treatment of breast cancer.

Claim 24; Page 189; 221pp; English.

The present invention relates to human breast tumour protein coding

sequences (see AAH5479-AAH5513, AAH5517-AAH55679 and AAH55682-

AAH55762). The breast tumour protein DNA sequences may be used in the

prevention, diagnosis and treatment of diseases associated with

CC inappropriate expression of the breast tumour protein e.g. breast cancer.

CC The present sequence is a human ovarian tumour-derived antigen coding

sequence, which was used in an example from the present invention

XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 4; Length 2627;

Best Local Similarity 99.9%; Pred. No. 3.1e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTAAGACTGATTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTAAGACTGATTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGATTTGCCCCCATCTCCGGGGAAATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGATTTGCCCCCATCTCCGGGGAAATGTC 1840
 QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATTAAGTCTACTACCAAC 180
 DB 1841 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATTAAGTCTACTACCAAC 1900
 QY 181 TAGTGATTAAGGCGCAGGGATGCTGCTCACTCTTCAATGATGAGGAGAGCTCTCCCA 240
 DB 1901 TAGTGATTAAGGCGCAGGGATGCTGCTCACTCTTCAATGATGAGGAGAGCTCTCCCA 1959

QY 241 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 300
 DB 1960 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 2019
 QY 301 AGAAAGGCGCTGGAAAGAGGGAGCAACAATCTGTCTGCTTCTCACTAATGATCAT 360
 DB 2020 AGAAAGGCGCTGGAAAGAGGGAGCAACAATCTGTCTGCTTCTCACTAATGATCAT 2079
 QY 361 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGCTGCAAGAGAGCCGAAGCTCATC 420
 DB 2080 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGCTGCAAGAGAGCCGAAGCTCATC 2139
 QY 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTATGGAAATGCTCGA 480
 DB 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTATGGAAATGCTCGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 2259
 QY 541 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 600
 DB 2260 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 2319
 QY 601 TCTCCAGAACCTTCTCTGCGCAATTCAAATTAAGCAACAATATACCTTCCATGAA 660
 DB 2320 TCTCCAGAACCTTCTCTGCGCAATTCAAATTAAGCAACAATATACCTTCCATGAA 2379
 QY 661 GCACACACAGACTTTTGAAGAGCAAGCAATGACTGCTTGAATTTAGAGCTTGAAGAG 720
 DB 2380 GCACACACAGACTTTTGAAGAGCAAGCAATGACTGCTTGAATTTAGAGCTTGAAGAG 2439
 QY 721 AACCTTGAAGAGAAAGAAATATCTTGTGTTCCAGCCCCCTTCCACATCTTCCATGTTA 780
 DB 2440 AACCTTGAAGAGAAAGAAATATCTTGTGTTCCAGCCCCCTTCCACATCTTCCATGTTA 2499
 QY 781 ACCACTGCTTCTCTGAGCTTGGAGCCAGGTGACTGTATTAATGTTGTTATAGAAAC 840
 DB 2500 ACCACTGCTTCTCTGAGCTTGGAGCCAGGTGACTGTATTAATGTTGTTATAGAAAC 2559
 QY 841 TGAATTTAGAGTTCTGATGCTTCAAGAAATGATTAATATACATTTCT 890
 DB 2560 TGAATTTAGAGTTCTGATGCTTCAAGAAATGATTAATATACATTTCT 2609
 RESULT 10
 ABN72971
 ID ABN72971 standard; DNA; 2627 BP.
 AC ABN72971;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Ovarian carcinoma polynucleotide O8E.
 XX
 KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
 OS Homo sapiens.
 XX
 PN WO200206317-A2.
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001MO-US022635.
 XX
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00844441.
 XX
 PA (CORI-) CORIXA CORP.
 XX

PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
 PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
 DR WPI; 2002-164781/21.
 DR P-PSDB; ABP30900, ABP30901.
 XX
 PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
 PT protein or its variants, useful for stimulating an immune response in a
 PT patient and treating ovarian cancer.
 XX
 PS Example 2; Page 319-320; 408bp; English.
 XX
 CC This invention relates to polypeptides comprising an immunogenic portion
 CC of an ovarian carcinoma protein which acts as an immunostimulant and is
 CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations and antigen presenting cells that express
 CC the polypeptides are useful for stimulating an immune response in a
 CC patient and treating ovarian cancer. This sequence represents DNA related
 CC to the invention
 XX
 SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
 Query Match 98.7%; Score 878; DB 6; Length 2627;
 Best Local Similarity 99.9%; Pred. No. 3.1e-284;
 Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CAAAGCTGTGAGCTTCTCTTCCATTCCTGCGAGACAGTAAAGACTCACTTTTCAATA 60
 DB 1721 CAAAGCTGTGAGCTTCTCTTCCATTCCTGCGAGACAGTAAAGACTCACTTTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGTCAAGCTGGGGGATTTGGCCCCCATCTCGGGGGAAATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGTCAAGCTGGGGGATTTGGCCCCCATCTCGGGGGAAATGTC 1840
 QY 121 TGAAGCAATTTGTTTACTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
 DB 1841 TGAAGCAATTTGTTTACTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
 QY 181 TAGTGATTAAGGCGCAGGAGTGTCTCAACTCTCTCAATGATGAGGAGCTCTCCCA 240
 DB 1901 TAGTGATTAAGGCGCAGGAGTGTCTCAACTCTCTCAATGATGAGGAGCTCTCCCA 1959
 QY 241 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 300
 DB 1960 TTACAACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGTGTTTGTAGT 2019
 QY 301 AGAAAGGCGCTGGAAAGAGGGAGCAACAATCTGTCTGCTTCTCACTAATGATCAT 360
 DB 2020 AGAAAGGCGCTGGAAAGAGGGAGCAACAATCTGTCTGCTTCTCACTAATGATCAT 2079
 QY 361 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGCTGCAAGAGAGCCGAAGCTCATC 420
 DB 2080 GGGCAATTAAGCAATCTGTCTTGTGCTGCTGCTGCAAGAGAGCCGAAGCTCATC 2139
 QY 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTATGGAAATGCTCGA 480
 DB 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTATGGAAATGCTCGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCAATTCACCTGCAAG 2259
 QY 541 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 600
 DB 2260 CCAAGTTCTGTAAAGAAATGCCGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 2319
 QY 601 TCTCCAGAACCTTCTCTGCGCAATTCAAATTAAGCAACAATATACCTTCCATGAA 660
 DB 2320 TCTCCAGAACCTTCTCTGCGCAATTCAAATTAAGCAACAATATACCTTCCATGAA 2379
 QY 661 GCACACACAGACTTTTGAAGAGCAAGCAATGACTGCTTGAATTTAGAGCTTGAAGAG 720
 DB 2380 GCACACACAGACTTTTGAAGAGCAAGCAATGACTGCTTGAATTTAGAGCTTGAAGAG 2439

```

OY 721 AAGCTTTGAAGAAAAAGATACCTTGTTCAGACCCCTTCCACACTCTTCATGTGTA 780
DB 2440 AAGCTTTGAAGAAAAAGATACCTTGTTCAGACCCCTTCCACACTCTTCATGTGTA 2499
OY 781 ACCACTGCTCTCTGAGACCTTGAGCCAGCTGATGTAATTAATGTTTATAGAAAC 840
DB 2500 ACCACTGCTCTCTGAGACCTTGAGCCAGCTGATGTAATTAATGTTTATAGAAAC 2559
OY 841 TGAATTTAGTTCGATGCTTCAAGAGATGATTAATATACATTTCT 890
DB 2560 TGAATTTAGTTCGATGCTTCAAGAGATGATTAATATACATTTCT 2609

RESULT 11
ADA08544
ID ADA08544 standard; cDNA; 2627 BP.
XX
AC ADA08544;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma polynucleotide OSE.
XX
KW ss; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2003-532352/50.
XX
PT New isolated 0772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
PS Example 2; SEQ ID NO 391; 371pp; English.
XX
CC The invention relates to an isolated 0772P polypeptide, which has the
CC structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen polynucleotide.
XX
SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
XX
Query Match 98.7%; Score 878; DB 9; Length 2627;
Best Local Similarity 99.9%; Pred. No. 3.1e-284;

```

```

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 CAAGCTTGAAGGCTTCTCTCTTCCATCTGCTGAGACAGTAAGACTCAGTTTCAATA 60
DB 1721 CAAGCTTGAAGGCTTCTCTCTTCCATCTGCTGAGACAGTAAGACTCAGTTTCAATA 1780
OY 61 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTCCGCCCCCATCTCCGGGGAAATGTC 120
DB 1781 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTCCGCCCCCATCTCCGGGGAAATGTC 1840
OY 121 TGAAGACAATTTGGTGTACCTCAATGAGGAGTGGAGGATACAGTCTACTACCAAC 180
DB 1841 TGAAGACAATTTGGTGTACCTCAATGAGGAGTGGAGGATACAGTCTACTACCAAC 1900
OY 181 TAGTGATTAAGGCGCAGGAGATGCTGCTCACTCCTTACCATGTAAGGAGCGTCTCCCA 240
DB 1901 TAGTGATTAAGGCGCAGGAGATGCTGCTCACTCCTTACCATGTAAGGAGCGTCTCCCA 1959
OY 241 TTACAACTAACCCAAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 300
DB 1960 TTACAACTAACCCAAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 2019
OY 301 AGAAAAGGCGCTGGAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACAATTAGTCATT 360
DB 2020 AGAAAAGGCGCTGGAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACAATTAGTCATT 2079
OY 361 GGCAAATTAAGCATCTGTCTCTTTGGCTGTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 2080 GGCAAATTAAGCATCTGTCTCTTTGGCTGTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
OY 421 GGGCACCAAGATTAATCATCTCTGATGAACAGAGTTGACAGAGGCTTAAGGAAATGCTTGA 480
DB 2140 GGGCACCAAGATTAATCATCTCTGATGAACAGAGTTGACAGAGGCTTAAGGAAATGCTTGA 2199
OY 481 TGGGATTAATCTTCACTTGTGAGCTTGAAGTTTGAAGTTCTTCCCTTCACTTCACTGCAAG 540
DB 2200 TGGGATTAATCTTCACTTGTGAGCTTGAAGTTTGAAGTTCTTCCCTTCACTTCACTGCAAG 2259
OY 541 CCAAGTTCTGTAAGAAATGCTGATGTTAGTCTCAGGTTTCTTACTCTGAATTAGA 600
DB 2260 CCAAGTTCTGTAAGAAATGCTGATGTTAGTCTCAGGTTTCTTACTCTGAATTAGA 2319
OY 601 TCTCCAGACCTTCTCTGCGCCACAAATTAAGGCAACAACATTAATCTTCCATGAA 660
DB 2320 TCTCCAGACCTTCTCTGCGCCACAAATTAAGGCAACAACATTAATCTTCCATGAA 2379
OY 661 GCACACACAGACTTTGAAGCAAGACAAATGACTGTTGAATTGAGGCTTGAAGAAATG 720
DB 2380 GCACACACAGACTTTGAAGCAAGACAAATGACTGTTGAATTGAGGCTTGAAGAAATG 2439
OY 721 AAGCTTTGAAGAAAAAGATACCTTGTTCAGACCCCTTCCACACTCTTCATGTGTA 780
DB 2440 AAGCTTTGAAGAAAAAGATACCTTGTTCAGACCCCTTCCACACTCTTCATGTGTA 2499
OY 781 ACCACTGCTCTCTGAGACCTTGAGCCAGCTGATGTAATTAATGTTTATAGAAAC 840
DB 2500 ACCACTGCTCTCTGAGACCTTGAGCCAGCTGATGTAATTAATGTTTATAGAAAC 2559
OY 841 TGAATTTAGTTCGATGCTTCAAGAGATGATTAATATACATTTCT 890
DB 2560 TGAATTTAGTTCGATGCTTCAAGAGATGATTAATATACATTTCT 2609

RESULT 12
ADF08887
ID ADF08887 standard; cDNA; 2627 BP.
XX
AC ADF08887;
XX
DT 12-FEB-2004 (first entry)
XX
DE cDNA encoding secreted ovarian carcinoma antigen seqid 391.
XX

```

KM gene therapy; protein therapy; vaccine; antibody inhibition;
 KM breast cancer; restorative therapy; diagnostic agent; immunoassay;
 KM secreted ovarian carcinoma antigen; gene; ss.
 XX Homo sapiens.
 OS US2003124140-A1.
 PN 03-JUL-2003.
 PD 17-JUL-2002; 2002US-00198053.
 PF 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 PR 17-JUL-2001; 2001US-00907969.
 XX (CORI-) CORIXA CORP.
 PA Bangur CS, Retter MW, Fanger GR, Hill P;
 PI WPI; 2003-897152/82.
 DR P-PSDB; ADF08888, ADF08889.
 XX Oncogenic nucleic acids useful for the prevention, diagnosis and
 PT treatment of breast cancer.
 PS Example 2; SEQ ID NO 391; 399bp; English.
 XX The invention describes nucleic acids (I) and the polypeptides (II) they
 CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
 CC treating diseases related to their aberrant expression i.e. breast
 CC cancers. For example, (I) and (II) may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of (II) by expressing
 CC inactive proteins or to supplement the patients own production of (II).
 CC Additionally, (I) may be used to produce (II), by inserting (I) into a
 CC host cell and culturing the cell to express the protein (II). (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. The host cell may also be used as antigens in the production of
 CC antibodies against (II) and in assays to identify modulators of (II)'s
 CC expression and activity. The anti-(II) antibodies, agonists and
 CC antagonists may be used to regulate expression and activity and as
 CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
 CC immunoassay). This sequence represents a polynucleotide encoding a
 CC secreted ovarian carcinoma antigen.
 XX
 XX
 SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
 Query Match 98.7%; Score 878; DB 10; Length 2627;
 Best Local Similarity 99.9%; Pred. No. 3.1e-284;
 Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CAAGCTCTGAGGCTTCCCTTCATCCGCGGAGACAGTAAAGACTGTTTCAAT 60
 DB 1721 CAAGCTCTGAGGCTTCCCTTCATCCGCGGAGACAGTAAAGACTGTTTCAAT 1780
 QY 61 GCATCTAGAGCACTGAGCACTGAGGATGATTTGCCCCCATCTCCGGGGAAATGTC 120
 DB 1781 GCATCTAGAGCACTGAGCACTGAGGATGATTTGCCCCCATCTCCGGGGAAATGTC 1840
 QY 121 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGAGAGAGATACAGTGTACTACCAAC 180
 DB 1841 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGAGAGAGATACAGTGTACTACCAAC 1900

QY 181 TAGGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTACCATGTATACAGGAGCTCCCCA 240
 DB 1901 TAGGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTACCATGTATACAGGAGCTCCCCA 1959
 QY 241 TTACAACTACCCCAATCCGAAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGTGTTGAGT 300
 DB 1960 TTACAACTACCCCAATCCGAAAGTGTCAACTGTGTCAAGACTTAAGAAACCTGTGTTGAGT 2019
 QY 301 AGAAAAAGGCTGTGAAAAGAGGGGAGCCAACTGTGTGTCTCTCTCACTTAATGTCATT 360
 DB 2020 AGAAAAAGGCTGTGAAAAGAGGGGAGCCAACTGTGTGTCTCTCTCACTTAATGTCATT 2079
 QY 361 GGCATAATAGCAATTCGTCTTGTGCTGTGCTGCTGAGCAGACAGAGGCCGAATCTATC 420
 DB 2080 GGCATAATAGCAATTCGTCTTGTGCTGTGCTGCTGAGCAGACAGAGGCCGAATCTATC 2139
 QY 421 GGGCACCAAGATTAACATCTCTCAGTAAAGAGAGTTGACAGGCTATGGGAAATGCTCTGA 480
 DB 2140 GGGCACCAAGATTAACATCTCTCAGTAAAGAGAGTTGACAGGCTATGGGAAATGCTCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCTTCCCTTCAATCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTCTTCTTCCCTTCAATCTGCAAG 2259
 QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTAGA 600
 DB 2260 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTAGA 2319
 QY 601 TCTCCAGACCCCTTCTGCGCACAAATTAATTAAAGCAACAAATATACCTTCAATGAA 660
 DB 2320 TCTCCAGACCCCTTCTGCGCACAAATTAATTAAAGCAACAAATATACCTTCAATGAA 2379
 QY 661 GCACACACAGACTTTGAAAAGCAAGACATGACTCTGTAATGAGCGCTTGAAGATG 720
 DB 2380 GCACACACAGACTTTGAAAAGCAAGACATGACTCTGTAATGAGCGCTTGAAGATG 2439
 QY 721 AAGCTTTGAAGAAAGAAATACCTTGTTCAGGCCCCCTTCCACACTCTTCAATGTTA 780
 DB 2440 AAGCTTTGAAGAAAGAAATACCTTGTTCAGGCCCCCTTCCACACTCTTCAATGTTA 2499
 QY 781 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTCAGTATTAATCATGTTTATAGAAAC 840
 DB 2500 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTCAGTATTAATCATGTTTATAGAAAC 2559
 QY 841 TGATTTTAAGATTCGATGCTTCAAGAGATGATTAATATACATTTCT 890
 DB 2560 TGATTTTAAGATTCGATGCTTCAAGAGATGATTAATATACATTTCT 2609
 RESULT 13
 ADG46174
 ID ADG46174 standard; cDNA; 2627 BP.
 AC ADG46174;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human ovarian carcinoma polynucleotide #387.
 DE Human ovarian carcinoma; gene; ss; 08E; ovarian cancer;
 KM Human; ovarian carcinoma; gene; ss; 08E; ovarian cancer;
 KM secreted tumour antigen; cytosolic; 0772P.
 XX
 OS Homo sapiens.
 PN US2003165504-A1.
 PD 04-SEP-2003.
 PF 04-APR-2001; 2001US-00827271.
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.

PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 XX
 PA (RETT/) BETTER M W.
 PA (FANG/) FANGER G R.
 XX
 PI Retter MM, Fanger GR;
 XX
 DR WPI; 2003-898035/B2.
 XX
 PT New isolated OBE or O772P polypeptides, useful for diagnosing,
 PT preventing, treating and monitoring cancer, e.g. ovarian cancer,
 PT stimulating the immune response in patient.
 XX
 PS Example 2; SEQ ID NO 391; 290pp; English.
 XX
 CC The invention relates to human ovarian carcinoma polypeptides, designated
 CC OBE or O772P, and the polynucleotides encoding them. The invention also
 CC relates to methods for inhibiting the development of cancer, e.g. ovarian
 CC cancer in a patient, methods for stimulating and/or expanding T cells and
 CC methods for identifying secreted tumour antigens. The polypeptides,
 CC compositions, antibodies to the polypeptides and methods are useful for
 CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
 CC cancer. The composition is particularly useful for stimulating an immune
 CC response in patient. This sequence represents a human ovarian carcinoma
 CC polynucleotide of the invention.
 XX
 SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 10; Length 2627;
 Best Local Similarity 99.9%; Pred. No. 3.1e-284;
 Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTTAAGACCTTCAATTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTTAAGACCTTCAATTTCAATA 1780
 QY 61 GGATCTAGAGAGAGTGGAGCTCAAGCTGGGGTGAATTTGGCCCCCATCTCCGGGGGAATGTC 120
 DB 1781 GGATCTAGAGAGAGTGGAGCTCAAGCTGGGGTGAATTTGGCCCCCATCTCCGGGGGAATGTC 1840
 QY 121 TGAAGACAAATTTTGTCTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
 DB 1841 TGAAGACAAATTTTGTCTTACCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
 QY 181 TAGTGATTAAGGCCCGAGGATGCTGCTCAACTCTCAATGATTAACAGGAGCTTCTCCCA 240
 DB 1901 TAGTGATTAAGGCCCGAGGATGCTGCTCAACTCTCAATGATTAACAGGAGCTTCTCCCA 1959
 QY 241 TTACAACCTACCAATCCGAAGTGTCAACTGTGTCAAGAGCTAAGAAAACCTGGTTTGAAT 300
 DB 1960 TTACAACCTACCAATCCGAAGTGTCAACTGTGTCAAGAGCTAAGAAAACCTGGTTTGAAT 2019
 QY 301 AGAAAAAGGCTGGAAGAAGGGGAGCCAAACAATCTGTCTCTCTCAATTAGTCATT 360
 DB 2020 AGAAAAAGGCTGGAAGAAGGGGAGCCAAACAATCTGTCTCTCTCAATTAGTCATT 2079
 QY 361 GGGCAATAAGCAATCTGTCTCTTTGGCTGCTGCTTGAAGACAGAGAGCCAGAACTTATC 420
 DB 2080 GGGCAATAAGCAATCTGTCTCTTTGGCTGCTGCTTGAAGACAGAGAGCCAGAACTTATC 2139
 QY 421 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTGGGAATGCTGA 480
 DB 2140 GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTGAACAAGGCTTGGGAATGCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTTCTTTCCCTTCAATCTTCCGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTTCTTTCCCTTCAATCTTCCGCAAG 2259
 QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTTGAAGTCTCAGGTTTCTTACTCTGAATTTAGA 600

DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
 QY 601 TCTCCAGACCCCTCTGCGCCACCAATTCATAATTAAGCAACAACATATACCTTCCATGAA 660
 DB 2320 TCTCCAGACCCCTCTGCGCCACCAATTCATAATTAAGCAACAACATATACCTTCCATGAA 2379
 QY 661 GCACACACAGACTTTGAAAGCAGACATGACTGCTTGAATTGAGGCTTGAAGGAATG 720
 DB 2380 GCACACACAGACTTTGAAAGCAGACATGACTGCTTGAATTGAGGCTTGAAGGAATG 2439
 QY 721 AAGCTTGAAGGAAGAAATCTTTGTTCCAGCCCCCTGCCACACTCTTCAATGTTA 780
 DB 2440 AAGCTTGAAGGAAGAAATCTTTGTTCCAGCCCCCTGCCACACTCTTCAATGTTA 2499
 QY 781 ACCACTGCTTCTCTGAGCTTGAAGCCAGCGTGAATGATTAATGTTTGAATGAAGAAAC 840
 DB 2500 ACCACTGCTTCTCTGAGCTTGAAGCCAGCGTGAATGATTAATGTTTGAATGAAGAAAC 2559
 QY 841 TGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATATATCTTCT 890
 DB 2560 TGATTTTGAAGTTCTGATGCTTCAAGAGATGATTAATATATATCTTCT 2609
 RESULT 14
 ADN40452
 ID ADN40452 standard; cDNA; 2627 BP.
 XX
 AC ADN40452;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human breast cancer associated cDNA sequence #203.
 XX
 KW Human; breast cancer; T cell; tumour protein; antigen presenting cell;
 KW immune response; CD4+; CD8+; cytostatic; gene therapy; gene; ss.
 OS Homo sapiens.
 XX
 PN US2004101899-A1.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003US-00714389.
 XX
 PR 30-NOV-1999; 99US-00451651.
 PR 22-FEB-2000; 2000US-00510662.
 PR 10-MAR-2000; 2000US-00523586.
 PR 07-APR-2000; 2000US-00545068.
 PR 15-MAY-2000; 2000US-00571025.
 PR 06-FEB-2001; 2001US-00778320.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;
 PI McNeill PD;
 XX
 DR WPI; 2004-399689/37.
 DR P-PSDB; ADN40453, ADN40454.
 XX
 PT New polynucleotides, useful for treating and diagnosing cancer,
 PT particularly breast cancer by stimulating immune response in a patient
 PT and inhibiting the development of cancer.
 XX
 PS Claim 1; SEQ ID NO 207; 151pp; English.
 XX
 CC The present invention relates to polynucleotide and polypeptide sequences
 CC associated with breast cancer. Also disclosed are expression vectors
 CC comprising the polynucleotide sequences of the invention operably linked
 CC to an expression control sequence, host cells comprising the vector,
 CC antibodies (or antigen binding fragments of antibodies) specifically
 CC binding the polypeptides of the invention, fusion proteins comprising at
 CC least one of the polypeptides, stimulating and/or expanding T cells
 CC specific for a tumour protein. The polynucleotide sequences, polypeptide

CC sequences, and antigen presenting cells can be administered
 CC therapeutically/prophylactically to induce an immune response. They can
 CC be included with a physiological carrier/immunostimulant in compositions
 CC such as vaccines, particularly to treat or prevent cancers such as breast
 CC cancer. They can also be used to inhibit the development of cancer by
 CC incubating one or more of them with CD4+ and/or CD8+ T cells isolated
 CC from a patient, such that the T cells proliferate, and administering the
 CC proliferated T cells to the patient. The polynucleotide sequences are
 CC useful for detecting cancer in a patient, producing fusion proteins,
 CC producing T cell populations and antigen presenting cells. The present
 CC sequence represents a polynucleotide sequence of the invention.

XX Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 12; Length 2627;

Best Local Similarity 99.9%; Pred. No. 3,1e-284;

Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTCGTGGACAGCTAAGACCTCAGTTTCAATA 60
 DB 1721 CAAGCTCTGAGGCTTCTCTTCCATCTCGTGGACAGCTAAGACCTCAGTTTCAATA 1780
 QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGGATGTC 120
 DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGGATGTC 1840
 QY 121 TGAAGCAATTTTGTTTCTCAATGAGGAGTGGAGAGATGCTACTACCAAC 180
 DB 1841 TGAAGCAATTTTGTTTCTCAATGAGGAGTGGAGAGATGCTACTACCAAC 1900
 QY 181 TAGTGTATAAGGCGCAGGAGTGTCTCAACCTCTCACTACATGACAGGAGCTGCCCA 240
 DB 1901 TAGTGTATAAGGCGCAGGAGTGTCTCAACCTCTCACTACATGACAGGAGCTGCCCA 1959
 QY 241 TTACAACTACCCCAATCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTTGTTTGAAT 300
 DB 1960 TTACAACTACCCCAATCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTTGTTTGAAT 2019
 QY 301 AGAAAGGCGCTGGAAAGAGGAGCCCAACAATCTGTCTCTTCCATTAATGATAT 360
 DB 2020 AGAAAGGCGCTGGAAAGAGGAGCCCAACAATCTGTCTCTTCCATTAATGATAT 2079
 QY 361 GGCATAATAGCATTTCTCTTGTGCTGCTCAGCAAGAGAGCCAGAACTATAC 420
 DB 2080 GGCATAATAGCATTTCTCTTGTGCTGCTCAGCAAGAGAGCCAGAACTATATC 2139
 QY 421 GGGCACCAGATTAACATCTCTCAGTGAACAGATTTGCAAGGCGCTATGGAAATGCTCTGA 480
 DB 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGATTTGCAAGGCGCTATGGAAATGCTCTGA 2199
 QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTTCTTCCCTTCAATTCACCTGCAAG 540
 DB 2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTTAAGTTTCTTCCCTTCAATTCACCTGCAAG 2259
 QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
 DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
 QY 601 TCTCCAGACCCCTTCTGCGCACAATTCAAATTAAGCAACAAATATACCTTCCATGAA 660
 DB 2320 TCTCCAGACCCCTTCTGCGCACAATTCAAATTAAGCAACAAATATACCTTCCATGAA 2379
 QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTTGAGGCGCTTGAAGAGATG 720
 DB 2380 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTGAATTTGAGGCGCTTGAAGAGATG 2439
 QY 721 AAGCTTGAAGAAAGAAATACCTTTGTTTCCAGCCCTCCACACTCTTCATGAGTTA 780
 DB 2440 AAGCTTGAAGAAAGAAATACCTTTGTTTCCAGCCCTCCACACTCTTCATGAGTTA 2499
 QY 781 ACCACTGCTTCTCTGAGCACTTGGAGCAGGTAAGTATTAATGTTTGTATAGAAAC 840
 DB 2500 ACCACTGCTTCTCTGAGCACTTGGAGCAGGTAAGTATTAATGTTTGTATAGAAAC 2559

QY 841 TGAATTTAGAGTTCTGTAGCTTCAAGAGATGATTAATATACATTTTCT 890
 DB 2560 TGAATTTAGAGTTCTGTAGCTTCAAGAGATGATTAATATACATTTTCT 2609

RESULT 15

ADP81075
 ID ADP81075 standard; DNA; 2690 BP.

XX ADP81075;

XX 09-SEP-2004 (first entry)

DE Human ovarian specific gene, SEQ ID NO 109.

XX normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
 KW metastatic; cancer; vaccine; cytotatic; human; gene; ds.

XX Homo sapiens.

PN W02004053079-A2.

XX 24-JUN-2004.

PF 08-DEC-2003; 2003MO-US038855.

XX 06-DEC-2002; 2002US-0431301P.

PR 06-DEC-2002; 2002US-0431321P.

PR 30-JUN-2003; 2003US-0484584P.

PR 07-NOV-2003; 2003US-0518607P.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Turner LR, Sun Y, Liu S, Chen H;

XX WPI; 2004-468850/44.

DR P-P-SDB; ADP81235, ADP81236.

PT New ovarian specific nucleic acid molecules and polypeptides useful for
 PS diagnosing, preventing or treating ovarian cancer, for producing
 XX transgenic animals or cells, or for research purposes.

XX Claim 1; SEQ ID NO 109; 754bp; English.

CC The invention relates to novel isolated nucleic acid molecules and
 CC polypeptides present in normal and neoplastic ovarian cells. These
 CC comprise a nucleic acid sequence encoding any of the 167 amino acid
 CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
 CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
 CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
 CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
 CC further comprises: a method for determining the presence of a ovarian
 CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
 CC nucleic acid molecule; a host cell comprising the vector; a method for
 CC producing a polypeptide encoded by the above nucleic acid molecule; a
 CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
 CC or its fragment that specifically binds to the above polypeptide; a
 CC method for determining the presence of an ovarian specific protein in a
 CC sample; a method for diagnosing or monitoring the presence and metastases
 CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
 CC presence of cancer in a patient; the kit comprising a means for
 CC determining the presence of the above nucleic acid molecule or
 CC polypeptide; a method of treating a patient with ovarian cancer; and a
 CC vaccine comprising the above polypeptide or nucleic acid encoding the
 CC polypeptide. The isolated nucleic acid molecules and polypeptides have
 CC cytotatic activity. The isolated polypeptides may be used to create a
 CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
 CC for diagnosing or monitoring the presence and metastases of ovarian
 CC cancer and treating ovarian cancer. This polynucleotide sequence
 CC represents an ovarian specific gene of the invention.

XX Sequence 2690 BP; 760 A; 611 C; 603 G; 716 T; 0 U; 0 Other;

Query Match 98.7%; Score 878; DB 12; Length 2690;
Best Local Similarity 99.9%; Pred. No. 3.2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY      1 CAAGCTCTGAGGCTTCTCTTTCATCTGCGTGGACAGCTAAGACCTCAGTTTCAATA 60
      |||
DB      1801 CAAGCTCTGAGGCTTCTCTTTCATCTGCGTGGACAGCTAAGACCTCAGTTTCAATA 1860
      |||

QY      61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 120
      |||
DB      1861 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 1920
      |||

QY      121 TGAAGCAATTTTGTGTTACTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 180
      |||
DB      1921 TGAAGCAATTTTGTGTTACTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1980
      |||

QY      181 TAGTGATTAAGGCCAGGGATGCTGCTCAACTCTTACCATGTACAGGAGCTTCCCA 240
      |||
DB      1981 TAGTGATTAAGGCCAGGGATGCTGCTCAACTCTTACCATGTACA-GGACGTTCCCA 2039
      |||

QY      241 TTACAACTCCCAATCCGAAGTGTCAACTGTGTGAGAGCACTAAGAAACCCGTTTGAAT 300
      |||
DB      2040 TTACAACTCCCAATCCGAAGTGTCAACTGTGTGAGAGCACTAAGAAACCCGTTTGAAT 2099
      |||

QY      301 AGAAAAGGCGCTGGAAGAAGGGAGCCAACAAACTGTCTGTCTCTCAATTAGTCATT 360
      |||
DB      2100 AGAAAAGGCGCTGGAAGAAGGGAGCCAACAAACTGTCTGTCTCTCAATTAGTCATT 2159
      |||

QY      361 GGCAAATAAGCATTTCTGTCTTTGGCTGTGCTCAGACACAGAGGCCAAGACTTATC 420
      |||
DB      2160 GGCAAATAAGCATTTCTGTCTTTGGCTGTGCTCAGACACAGAGGCCAAGACTTATC 2219
      |||

QY      421 GGGCACAGAGATTAACATCTCTCAGTAAACAGAGTTGACAAGGCCCTATGGGAAATGCTGA 480
      |||
DB      2220 GGGCACAGAGATTAACATCTCTCAGTAAACAGAGTTGACAAGGCCCTATGGGAAATGCTGA 2279
      |||

QY      481 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTTCTTCCCTCAATCTACCTGCAAG 540
      |||
DB      2280 TGGGATTAATCTTCAGCTTGTGAGCTTGAAGTTTCTTCCCTCAATCTACCTGCAAG 2339
      |||

QY      541 CCAAGTTCTGTAAAGAGAAATGCTGAGTTTCTAGCTCAGGTTTCTTACTGTGAATTAGA 600
      |||
DB      2340 CCAAGTTCTGTAAAGAGAAATGCTGAGTTTCTAGCTCAGGTTTCTTACTGTGAATTAGA 2399
      |||

QY      601 TCTCCAGACCTTCCCTGGCCACAATTCAATTAAAGGCAACAACATATACCTTCATGAA 660
      |||
DB      2400 TCTCCAGACCTTCCCTGGCCACAATTCAATTAAAGGCAACAACATATACCTTCATGAA 2459
      |||

QY      661 GCACACACAGACTTTTGAAGAAGCAATGACTGCTGAATTGAGGCTTGAGGAATG 720
      |||
DB      2460 GCACACACAGACTTTTGAAGAAGCAATGACTGCTGAATTGAGGCTTGAGGAATG 2519
      |||

QY      721 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCCACTCTTCATGTGTTA 780
      |||
DB      2520 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCCACTCTTCATGTGTTA 2579
      |||

QY      781 ACCACTGCTTCTCTGAGCCTTGAGGCCAGGTGACTGTATTAATGTTGTTATAGAAAC 840
      |||
DB      2580 ACCACTGCTTCTCTGAGCCTTGAGGCCAGGTGACTGTATTAATGTTGTTATAGAAAC 2639
      |||

QY      841 TGAATTTAGAGTTCTGATGTTCAAGAGATGATTAATAATACATTTCCCT 890
      |||
DB      2640 TGAATTTAGAGTTCTGATGTTCAAGAGATGATTAATAATACATTTCCCT 2689
      |||
```

Search completed: May 30, 2005, 10:27:11
Job time : 548.854 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 ; Search time 164.951 Seconds
(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-11

Perfect score: 890

Sequence: 1 caagctctgagctctctcct.....tgatataatcatctcct 890

Scoring table: IDENTITY_NUC

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	878	98.7	2627	3	US-09-404-879A-391
2	878	98.7	2627	4	US-09-667-857-391
3	866	97.3	1567	3	US-09-404-879A-74
4	866	97.3	1567	4	US-09-338-933-74
5	866	97.3	1567	4	US-09-215-681-74
6	866	97.3	1567	4	US-09-216-003A-74
7	866	97.3	1567	4	US-09-667-857-74
8	448.2	50.4	461	3	US-09-404-879A-27
9	448.2	50.4	461	4	US-09-338-933-27
10	448.2	50.4	461	4	US-09-215-681-27
11	448.2	50.4	461	4	US-09-216-003A-27
12	448.2	50.4	461	4	US-09-667-857-27
13	433.8	48.7	695	3	US-09-040-984-15
14	433.8	48.7	695	3	US-09-123-912-15
15	433.8	48.7	695	3	US-09-643-597-15
16	433.8	48.7	695	4	US-09-480-884A-15
17	433.8	48.7	695	4	US-09-542-615A-15
18	433.8	48.7	695	4	US-09-606-421B-15
19	433.8	48.7	695	4	US-09-221-107-15
20	433.8	48.7	695	4	US-09-466-396A-15
21	433.8	48.7	695	4	US-09-476-496A-15
22	433.8	48.7	695	4	US-09-630-940B-15
23	433.8	48.7	695	4	US-09-285-479-15
24	75.8	8.5	132438	4	US-09-949-016-14349
25	75.8	8.5	132438	4	US-09-949-016-14350
26	75.8	8.5	151089	4	US-09-949-016-14348
27	75.8	8.5	524032	4	US-09-949-016-16928

C 28	75.8	8.5	524032	4	US-09-949-016-16929	Sequence 16929, A
C 29	75.8	8.5	524032	4	US-09-949-016-16930	Sequence 16930, A
C 30	75.8	8.5	524032	4	US-09-949-016-16931	Sequence 16931, A
C 31	75.8	8.5	529885	4	US-09-949-016-14340	Sequence 14340, A
C 32	75.8	8.5	529885	4	US-09-949-016-14341	Sequence 14341, A
C 33	75.8	8.5	529885	4	US-09-949-016-14342	Sequence 14342, A
C 34	75.8	8.5	529885	4	US-09-949-016-14343	Sequence 14343, A
C 35	75.8	8.5	529885	4	US-09-949-016-14344	Sequence 14344, A
C 36	75.8	8.5	529885	4	US-09-949-016-14345	Sequence 14345, A
C 37	75.8	8.5	529885	4	US-09-949-016-14346	Sequence 14346, A
C 38	75.8	8.5	529885	4	US-09-949-016-14347	Sequence 14347, A
C 39	73.2	8.2	601	4	US-09-949-016-184694	Sequence 184694, A
C 40	73.2	8.2	88557	4	US-09-949-016-17028	Sequence 17028, A
C 41	72.6	8.2	247299	4	US-09-949-016-17590	Sequence 17590, A
C 42	72	8.1	601	4	US-09-949-016-73026	Sequence 73026, A
C 43	72	8.1	601	4	US-09-949-016-73027	Sequence 73027, A
C 44	72	8.1	221545	4	US-09-949-016-13875	Sequence 13875, A
C 45	67	7.5	218	4	US-09-573-080A-317	Sequence 317, App

ALIGNMENTS

RESULT 1						
US-09-404-879A-391						
; Sequence 391, Application US/09404879A						
; Patent No. 6468546						
; GENERAL INFORMATION:						
; APPLICANT: Mitcham, Jennifer L.						
; APPLICANT: King, Gordon E.						
; APPLICANT: Algate, Paul A.						
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND						
; FILE REFERENCE: 210121.462C2						
; CURRENT APPLICATION NUMBER: US/09/404, 879A						
; CURRENT FILING DATE: 1999-09-24						
; NUMBER OF SEQ ID NOS: 393						
; SOFTWARE: FastSeq for Windows Version 3.0						
; SEQ ID NO 391						
; LENGTH: 2627						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
US-09-404-879A-391						
Query Match 98.7%; Score 878; DB 3; Length 2627;						
Best Local Similarity 99.9%; Pred. No. 8.9e-267;						
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;						
QY	1	CAAGCTGAGGCTTCCTTCCTTCATCTGCGGAGAGCTAGAGCTGAGTTTCATTA	60			
DB	1721	CAAGCTGAGGCTTCCTTCCTTCATCTGCGGAGAGCTAGAGCTGAGTTTCATTA	1780			
QY	61	GCATCTAGAGCACTGAGCTGAGCTGAGGATTTGCCCCCATCTCGGGGAATGTC	120			
DB	1781	GCATCTAGAGCACTGAGCTGAGCTGAGGATTTGCCCCCATCTCGGGGAATGTC	1840			
QY	121	TGAAGCAATTTGTTTACTCTCATAGAGAGTGAAGATATCACTGTTACTTACCAAC	180			
DB	1781	TGAAGCAATTTGTTTACTCTCATAGAGAGTGAAGATATCACTGTTACTTACCAAC	1900			
QY	181	TATGATTAAGGCGAGGATGCTGCTCAACCTTCAATGATGAGGAGCTGCTCCCA	240			
DB	1901	TATGATTAAGGCGAGGATGCTGCTCAACCTTCAATGATGAGGAGCTGCTCCCA	1959			
QY	241	TTACCACTACCCATCCGAAAGTGTCACTGTGTGAGAGTAAAGAACTGTTTGAAT	300			
DB	1960	TTACCACTACCCATCCGAAAGTGTCACTGTGTGAGAGTAAAGAACTGTTTGAAT	2019			
QY	301	AGAAAAGGCGCTGAGAAAGGAGGAGCAAAATCTGTCTCTTCTTCAATTAGCAT	360			
DB	2020	AGAAAAGGCGCTGAGAAAGGAGGAGCAAAATCTGTCTCTTCTTCAATTAGCAT	2079			
QY	361	GGCAATTAAGCAATTCGTCTTGTGCTGCTGCTGAGACAGAGAGCAAGAACTATAC	420			

```
Db 2080 GGCATAATAGCATTCGTCTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
Qy 421 GGGCACCAGATTAACATCTCTCAGTGAACAAGTTGACAGAGCCCTATGGGAATGCTCTGA 480
Db 2140 GGGCACCAGATTAACATCTCTCAGTGAACAAGTTGACAGAGCCCTATGGGAATGCTCTGA 2199
Qy 481 TGGGATTAATCTCAGCTTGTGAGCTTCAAGTTTCTTCCCTCATCTTACCTGCAAG 540
Db 2200 TGGGATTAATCTCAGCTTGTGAGCTTCAAGTTTCTTCCCTCATCTTACCTGCAAG 2259
Qy 541 CCAAGTTCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 2260 CCAAGTTCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
Qy 601 TCTCCAGACCCCTTCTGCGCACAATTGAATTAAGGCAAAACATATACCTTCCATGAA 660
Db 2320 TCTCCAGACCCCTTCTGCGCACAATTGAATTAAGGCAAAACATATACCTTCCATGAA 2379
Qy 661 GCACACAGAGACTTTGAAAGCAGAGCAATGACTGCTGAATGAGGCTTGAAGATG 720
Db 2380 GCACACAGAGACTTTGAAAGCAGAGCAATGACTGCTGAATGAGGCTTGAAGATG 2439
Qy 721 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 780
Db 2440 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 2499
Qy 781 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCAGTATTAATGTTGTATATAGAAAC 840
Db 2500 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCAGTATTAATGTTGTATATAGAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTTCT 2609
```

RESULT 2

```
US-09-667-857-391
; Sequence 391, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-667-857-391
```

```
Query Match 98.7%; Score 878; DB 4; Length 2627;
Best Local Similarity 99.9%; Pred. No. 8.9e-267;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAAAGCTCTAGAGGCTTCTCTTCATCCGCGTGAAGTAGAGCTCAAGTTTCAATA 60
Db 1721 CAAAGCTCTAGAGGCTTCTCTTCATCCGCGTGAAGTAGAGCTCAAGTTTCAATA 1780
Qy 61 GCATCTAGAGCACTGGAGCTCAGCTGGGGTATTTGCCCCCATCTCCGGGGGAATGTC 120
```

```
Db 1781 GCATCTAGAGCACTGGAGCTCAGCTGGGGTATTTGCCCCCATCTCCGGGGGAATGTC 1840
Qy 121 TGAAGCAATTTTGGTTACTCTCAATGAGGAGTGAGAGGATACAGTGTACTACCAAC 180
Db 1841 TGAAGCAATTTTGGTTACTCTCAATGAGGAGTGAGAGGATACAGTGTACTACCAAC 1900
Qy 181 TAGTGATTAAGGCCAGGAGATGCTGCTCAACCTGCTCATGTACAGGAGCTTCCCA 240
Db 1901 TAGTGATTAAGGCCAGGAGATGCTGCTCAACCTGCTCATGTACAGGAGCTTCCCA 1959
Qy 241 TTACACTACCCCAATCCGCAATGTCTGTCTGTGAGAGCTTAAGAAACCTGGTTTGAAGT 300
Db 1960 TTACACTACCCCAATCCGCAATGTCTGTGAGAGCTTAAGAAACCTGGTTTGAAGT 2019
Qy 301 AGAAAGGGCCCTGAGAAAGGGGAGCCAAACAATGTCTGTCTGCTTCTCACTAGTCAATT 360
Db 2020 AGAAAGGGCCCTGAGAAAGGGGAGCCAAACAATGTCTGTCTGCTTCTCACTAGTCAATT 2079
Qy 361 GGCATAATAGCAATTCGTCTCTTGGCTGCTGCTCAGCAGACAGAGAGCCAGAACTCTATC 420
Db 2080 GGCATAATAGCAATTCGTCTCTTGGCTGCTGCTCAGCAGACAGAGAGCCAGAACTCTATC 2139
Qy 421 GGGCACCAGATTAACATCTCTCAGTGAACAAGTTGACAGAGCCCTATGGGAATGCTCTGA 480
Db 2140 GGGCACCAGATTAACATCTCTCAGTGAACAAGTTGACAGAGCCCTATGGGAATGCTCTGA 2199
Qy 481 TGGGATTAATCTCAGCTTGTGAGCTTCAAGTTTCTTCCCTCATCTACCTGCAAG 540
Db 2200 TGGGATTAATCTCAGCTTGTGAGCTTCAAGTTTCTTCCCTCATCTACCTGCAAG 2259
Qy 541 CCAAGTTCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 2260 CCAAGTTCTGTAGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
Qy 601 TCTCCAGACCCCTTCTGCGCACAATTGAATTAAGGCAAAACATATACCTTCCATGAA 660
Db 2320 TCTCCAGACCCCTTCTGCGCACAATTGAATTAAGGCAAAACATATACCTTCCATGAA 2379
Qy 661 GCACACAGAGACTTTGAAAGCAGAGCAATGACTGCTGAATGAGGCTTGAAGATG 720
Db 2380 GCACACAGAGACTTTGAAAGCAGAGCAATGACTGCTGAATGAGGCTTGAAGATG 2439
Qy 721 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 780
Db 2440 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 2499
Qy 781 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCAGTATTAATGTTGTATATAGAAAC 840
Db 2500 ACCACTGCTTCTCTGAGACCTTGAGCCAGGTCAGTATTAATGTTGTATATAGAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGATGATTAATATACATTTCT 2609
```

RESULT 3

```
US-09-404-879A-74
; Sequence 74, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
```

ORGANISM: Homo sapien
US-09-404-879A-74

US-09-404-879A-74

Query Match 97.3%; Score 866; DB 3; Length 1567;

Best Local Similarity	99.8%;	Pred. No. 4.3e-263;						
Matches 888;	Conservative	0;	Mismatches	0;	Indels	2;	Gaps	2;

1 CAGGCTGAGGCTTCTCTCCCTTCATCTGCGTGAAGAGCCGAGTTTCAATA 60

Qy	1	CAACCTCGAAGGCTCTCCCTTCCATCTGGGTGACAGCTAAGACCTCAGTTTCAATA	60
Db	679	CAACCTCGAAGGCTCTCTCTTCCATCTGGGTGACAGCTAAGACCTCAGTTTCAATA	738
Qy	61	GCATCTAGAGCAGTGGGACTCAGCTGGGGTAATTTGCCCCCATCTCCGGGGAAATGTC	120
Db	739	GCATCTAGAGCAGTGGGACTCAGCTGGGGTAATTTGCCCCCATCTCCGGGGAAATGTC	798
Qy	121	TGAAGACAATTTTGGTTACCTCAATAGAGAGTGGAGAGATACAGTGTACTATCCAAAC	180
Db	799	TGAAGACAATTTT-GTTACCTCAATAGAGAGTGGAGAGATACAGTGTACTATCCAAAC	857
Qy	181	TAGTGAATAAAGGCACAGGATGCTGCTCAACCTCTCACTAGTACAGGAGAGTCTCCCA	240
Db	858	TAGTGAATAAAGGCACAGGATGCTGCTCAACCTCTCACTAGTACAGGAGAGTCTCCCA	916
Qy	241	TTACACTAACCCCATTCGGAAGTGTCACTGTGTACAGACTAAGAAACCTTGATTTAGT	300
Db	917	TTACACTAACCCCATTCGGAAGTGTCACTGTGTACAGACTAAGAAACCTTGATTTAGT	976
Qy	301	AGAAAAGGGGCTGGAAAAGGGGGAGCCAAACAAATCTGTCTGTCTTCCATATTGTCAAT	360
Db	977	AGAAAAGGGGCTGGAAAAGGGGGAGCCAAACAAATCTGTCTGTCTTCCATATTGTCAAT	1036
Qy	361	GGCAATTAAGACTTCTGTCTTTGGCTGTGCTCCACAGACAGAGGCCAGAACTTATC	420
Db	1037	GGCAATTAAGACTTCTGTCTTTGGCTGTGCTCCACAGACAGAGGCCAGAACTTATC	1096
Qy	421	GGGACCAAGGATTAACATCTCTCAGTGAACAAGTGTGAACAAGGCTATGGGAAATGCTCGA	480
Db	1097	GGGACCAAGGATTAACATCTCTCAGTGAACAAGTGTGAACAAGGCTATGGGAAATGCTCGA	1156
Qy	481	TGGATTATCTTCAGCTGTGTGAGCTTCAAGTTCTTCCCTTCAATCTACCTCGCAAG	540
Db	1157	TGGATTATCTTCAGCTGTGTGAGCTTCAAGTTCTTCCCTTCAATCTACCTCGCAAG	1216
Qy	541	CCAAATTCTGTAGAAGAAATGCTGAGTTCTAAGCTCAGGTTTTCTTACTCGAATTTAGA	600
Db	1217	CCAAATTCTGTAGAAGAAATGCTGAGTTCTAAGCTCAGGTTTTCTTACTCGAATTTAGA	1276
Qy	601	TCTCCAGACCCCTTCTGGCCCAATTTCAATTTAAGGCAACAACATATACTTCCATGAA	660
Db	1277	TCTCCAGACCCCTTCTGGCCCAATTTCAATTTAAGGCAACAACATATACTTCCATGAA	1336
Qy	661	GCACACACAGACTTTTGAAGCAAGGACAAATGACTCTTGAATTGAGGCTTGAAGAAATG	720
Db	1337	GCACACACAGACTTTTGAAGCAAGGACAAATGACTCTTGAATTGAGGCTTGAAGAAATG	1396
Qy	721	AAGCTTTGAAGAAAAGAAATCTTTGTTTCCAGGCCCTTCCACACTCTTCAATGTGTA	780
Db	1397	AAGCTTTGAAGAAAAGAAATCTTTGTTTCCAGGCCCTTCCACACTCTTCAATGTGTA	1456
Qy	781	ACCACTGCTCTCTGAGCCTTGGAGCCACGGGTACTGATTATACATGTTGTTATGAAAAC	840
Db	1457	ACCACTGCTCTCTGAGCCTTGGAGCCACGGGTACTGATTATACATGTTGTTATGAAAAC	1516
Qy	841	TGATTTTAGAGTTCTGATGTTTCAAGAGATGATTAATATATCAATTTCT	890
Db	1517	TGATTTTAGAGTTCTGATGTTTCAAGAGATGATTAATATATCAATTTCT	1566

```

: APPLICANT: Mitcham, Jennifer Lynn
: APPLICANT: King, Gordon E.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
: TITLE OF INVENTION: OVARIAN CANCER
: FILE REFERENCE: 210121.462CI
: CURRENT APPLICATION NUMBER: US/09/338,933
: CURRENT FILING DATE: 1999-06-23
: NUMBER OF SEQ. ID NOS: 312
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 74
: LENGTH: 1567
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-338-933-74

```

Query Match	97.3%	Score 866;	DB 4;	Length 1567;
Best Local Similarity	99.8%	Pfed. No. 4.3e-263;		
Matches 888; Conservative	0;	Mismatches 0;	Indels 2;	Gaps 2;

1 CAAGCTTGAGGCTTTCCTTCCATCCGCGTGACAGCTAAGACCTCAGTTTTTCATA 60

679 CAGCGCTGAGGCGCTTCCATCGCGGTGGACAGCGTAGACCTTCAGGTTTCAATTA 738

QY	61	GCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGGCCCCCACTCCGGGGGAATGTC	120
Db	739	GCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGGCCCCCATCTCCGGGGGAATGTC	798
QY	121	TGAAACAATTTTGTTGTTACTCAATGAGGGAGTGGAGGAATACAGTGTCTACCAAC	180
Db	799	TGAAACAATTTT-GTTACTCAATGAGGAGTGGAGGAATACAGTGTCTACCAAC	857
QY	181	TAGTGGATTAAGGCGAGGATGCTGCTCAACTCTCTACATGTACAGGGAGCTCCCCA	240
Db	858	TAGTGGATTAAGGCGAGGATGCTGCTCAACTCTCTACATGTACAGAGTCTCCCA	916
QY	241	TTACACTTACCCAACTCCGAAGTGTCAACTGTGTACGACTAAGAAACCTTGTTTGGAGT	300
Db	917	TTACACTTACCCAACTCCGAAGTGTCAACTGTGTACGAGACTAAGAAACCTTGTTTGGAGT	976
QY	301	AGAAAGGGCTGGAAAGAGGGAGCCAAATTCGTGCTCTCCCTCAATTAAGTCAAT	360
Db	977	AGAAAGGGCTGGAAAGAGGGAGCCAAATTCGTGCTCTCTCAATTAAGTCAAT	1036
QY	361	GGCAAAATTAACATTTCTGCTTTTGGCTGTGCTCGCTCAGCAGAGAGCCGAATCTATC	420
Db	1037	GGCAAAATTAACATTTCTGCTTTTGGCTGTGCTCGCTCAGCAGAGAGCCGAATCTATC	1096
QY	421	GGGCACAGGATTAACATCTCTCAGTGAAACAGAGTTGACAAAGSCCTATGGAAATGCTTGA	480
Db	1097	GGGCACAGGATTAACATCTCTCAGTGAAACAGAGTTGACAAAGSCCTATGGAAATGCTTGA	1156
QY	481	TGGGATTAATCTTCAGCTGTTTGAGCTTCATAGTTTCTTCCCTCAATTCACCTCGAAG	540
Db	1157	TGGGATTAATCTTCAGCTGTTTGAGCTTCATAGTTTCTTCCCTCAATTCACCTCGAAG	1216
QY	541	CCAAGTCTCTAAGAGAAATGCTGAGTTTCTAGCTCAGTTTTCTTACTCTGAATTTAGA	600
Db	1217	CCAAGTCTCTAAGAGAAATGCTGAGTTTCTAGCTCAGTTTTCTTACTCTGAATTTAGA	1276
QY	601	TCTTCAGACCCCTTCTGGCCAACTTCAAAATTAAGCAACAACATATACCTTTCATGAA	660
Db	1277	TCTTCAGACCCCTTCTGGCCAACTTCAAAATTAAGCAACAACATATACCTTTCATGAA	1336
QY	661	GCACACACAACTTTTGAAGCAAGACAAATGACGTGTAATGATGAGGCGCTTGAAGAAAG	720
Db	1337	GCACACACAACTTTTGAAGCAAGACAAATGACGTGTAATGATGAGGCGCTTGAAGAAAG	1396
QY	721	AAGCTTGAAGGAAAAGAACTATTGTTTTCACACCCCTTCCACACTCTTCAATGTGTA	780
Db	1397	AAGCTTGAAGGAAAAGAACTATTGTTTTCACACCCCTTCCACACTCTTCAATGTGTA	1456
QY	781	ACCACTGCTTCTTGACCTTGAAGCCACGGTACGTGATTAATCATGTTGTTATGAAGAAC	840

Db 1457 ACCACTGCTTCTGAGACCTGGAGCAGGTGACTGATTTACATGTTGTATAGAAAAC 1516
QY 841 TGAATTTAGATTCGTGATCGTTCAAGAGAAATGATTAATATACATTTCT 890
Db 1517 TGAATTTAGATTCGTGATCGTTCAAGAGAAATGATTAATATACATTTCT 1566

RESULT 5
US-09-215-681-74
; Sequence 74, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-74

Query Match 97.3%; Score 866; DB 4; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4.3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCGCGGTGAGACACTAGACCTGAGTTTCAATA 60
Db 679 CAAGCTCTGAGGCTTCTCTTCCATCCGCGGTGAGACACTAGACCTGAGTTTCAATA 738
QY 61 GCATCTAGAGCAGTGGAGACTGAGCTGGGGTGAATTTGCCCATCTCCGGGGGAATGTC 120
Db 739 GCATCTAGAGCAGTGGAGACTGAGCTGGGGTGAATTTGCCCATCTCCGGGGGAATGTC 798
QY 121 TGAAGCAATTTTGGTTTACCTCAATGAGGAGTGGAGAGATACAGTCTACTACCAAC 180
Db 799 TGAAGCAATTTT - GTTACCTCAATGAGGAGTGGAGAGATACAGTCTACTACCAAC 857
QY 181 TAGTGATTAAGGCGGAGATGCTGCTCAACCTCCCAATGATGACAGGAGAGCTCCCA 240
Db 858 TAGTGATTAAGGCGGAGATGCTGCTCAACCTCCCAATGATGAC - GAGAGCTCCCA 916
QY 241 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 300
Db 917 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTGTCAAGACTAAGAAACCTGTGTTGAGT 976
QY 301 AGAAAAGGCGCTGGAAGAGGGAGCGCAACAAATCTGTCTCTCTCAATTAATGATTT 360
Db 977 AGAAAAGGCGCTGGAAGAGGGAGCGCAACAAATCTGTCTCTCTCAATTAATGATTT 1036
QY 361 GGAATAAAGCAATCTGTCTTTGGCTGTGCTGCTAGAGACAGAGGCGAGAACTCTATC 420
Db 1037 GGAATAAAGCAATCTGTCTTTGGCTGTGCTGCTAGAGACAGAGGCGAGAACTCTATC 1096
QY 421 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAATGCTGA 480
Db 1097 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCAAGTTGTGAGCTTCTAAGTTTCTTCTCTCAATTAATGATTT 540
Db 1157 TGGGATTAATCTTCAAGTTGTGAGCTTCTAAGTTTCTTCTCTCAATTAATGATTT 1216
QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTAGAGTTTCTTAATCTGAATTTAA 600
Db 1217 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTAGAGTTTCTTAATCTGAATTTAA 1276
QY 601 TCTCCAGACCCCTTCTGGGCAACAATTCAATTAAAGCAACAACATATACCTTCAATGA 660

Db 1277 TCTCCAGACCCCTTCTGGGCAACAATTCAATTAAAGCAACAACATATACCTTCAATGA 1336
QY 661 GCACACAGACTTTTGAAGCAAGAAATGACCTGCTGAATGAGGCTTGAAGATG 720
Db 1337 GCACACAGACTTTTGAAGCAAGAAATGACCTGCTGAATGAGGCTTGAAGATG 1396
QY 721 AAGCTTTGAAGAAAGAAATATCTTGTTCAGAGCCCTTCCCACTCTTCATGTGTA 780
Db 1397 AAGCTTTGAAGAAAGAAATATCTTGTTCAGAGCCCTTCCCACTCTTCATGTGTA 1456
QY 781 ACCACTGCTTCTGAGACCTTGGAGCCAGCGTGAATTAATATACATTTCT 840
Db 1457 ACCACTGCTTCTGAGACCTTGGAGCCAGCGTGAATTAATATACATTTCT 1516
QY 841 TGAATTTAGATTCGTGATCGTTCAAGAGAAATGATTAATATACATTTCT 890
Db 1517 TGAATTTAGATTCGTGATCGTTCAAGAGAAATGATTAATATACATTTCT 1566

RESULT 6
US-09-216-003A-74
; Sequence 74, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-216-003A-74

Query Match 97.3%; Score 866; DB 4; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4.3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCGCGGTGAGACACTAGACCTGAGTTTCAATA 60
Db 679 CAAGCTCTGAGGCTTCTCTTCCATCCGCGGTGAGACACTAGACCTGAGTTTCAATA 738
QY 61 GCATCTAGAGCAGTGGAGACTGAGCTGGGGTGAATTTGCCCATCTCCGGGGGAATGTC 120
Db 739 GCATCTAGAGCAGTGGAGACTGAGCTGGGGTGAATTTGCCCATCTCCGGGGGAATGTC 798
QY 121 TGAAGCAATTTTGGTTTACCTCAATGAGGAGTGGAGAGATACAGTCTACTACCAAC 180
Db 799 TGAAGCAATTTT - GTTACCTCAATGAGGAGTGGAGAGATACAGTCTACTACCAAC 857
QY 181 TAGTGATTAAGGCGGAGATGCTGCTCAACCTCCCAATGATGACAGGAGAGCTCCCA 240
Db 858 TAGTGATTAAGGCGGAGATGCTGCTCAACCTCCCAATGATGAC - GAGAGCTCCCA 916
QY 241 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTGTGTTGAGT 300
Db 917 TTACAACCTACCCCAATCCGAAGTGTCAACTGTGTGTCAAGAAACCTGTGTTGAGT 976
QY 301 AGAAAAGGCGCTGGAAGAGGGAGCGCAACAAATCTGTCTCTCTCAATTAATGATTT 360
Db 977 AGAAAAGGCGCTGGAAGAGGGAGCGCAACAAATCTGTCTCTCTCAATTAATGATTT 1036
QY 361 GGAATAAAGCAATCTGTCTTTGGCTGTGCTGCTCAGAGACAGAGGCGAGAACTCTATC 420
Db 1037 GGAATAAAGCAATCTGTCTTTGGCTGTGCTGCTCAGAGACAGAGGCGAGAACTCTATC 1096
QY 421 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGGAAATGCTGA 480

```
Db 1097 GGGGACCGAGTAATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTCGA 1156
Qy 481 TGGATTAATCTTGGCTTGTGAGCTTCTAGATTCTTCCCTTCACTTACCTCGAAG 540
Db 1157 TGGATTAATCTTGGCTTGTGAGCTTCTAGATTCTTCCCTTCACTTACCTCGAAG 1216
Qy 541 CCAAGTCTGTAAAGAAATGCTGAGTCTAGCTAGGTTTCTTACTGTAATTAGA 600
Db 1217 CCAAGTCTGTAAAGAAATGCTGAGTCTAGCTAGGTTTCTTACTGTAATTAGA 1276
Qy 601 TCTCCAGACCTTCTGCGCCCAATTCAAATTAAAGCAACAATATACCTTCATGAA 660
Db 1277 TCTCCAGACCTTCTGCGCCCAATTCAAATTAAAGCAACAATATACCTTCATGAA 1336
Qy 661 GCACACACAGACTTTTGAAGCAAGACATGCTGTAATTGAGGCTTGGAGAAAG 720
Db 1337 GCACACACAGACTTTTGAAGCAAGACATGCTGTAATTGAGGCTTGGAGAAAG 1396
Qy 721 AAGCTTTGAAGAAAGAAATCTTGTTCAGGCCCCCTCCACACTCTTCATGTGTA 780
Db 1397 AAGCTTTGAAGAAAGAAATCTTGTTCAGGCCCCCTCCACACTCTTCATGTGTA 1456
Qy 781 ACCACTGCTTCTGGAACCTTGAAGCAAGGTAAGTGTATTAATGAAAG 840
Db 1457 ACCACTGCTTCTGGAACCTTGAAGCAAGGTAAGTGTATTAATGAAAG 1516
Qy 841 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 890
Db 1517 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 1566
```

RESULT 7

```
US-09-667-857-74
; Sequence 74, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-667-857-74
```

```
Query Match 97.3%; Score 866; DB 4; Length 1567;
Best Local Similarity 99.8%; Pred. No. 4.3e-263;
Matches 888; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 1 CAAGCTCTGAGGCTTCTCTTTCATCTCTGCGTGAGACGTAAGACTTCAGTTTCAATA 60
Db 679 CAAGCTCTGAGGCTTCTCTTTCATCTCTGCGTGAGACGTAAGACTTCAGTTTCAATA 738
Qy 61 GCATCTAGACAGTGGAGCTCAGCTGGGGGATTTGGCCCGCATCTCGGGGGGAATGTC 120
Db 739 GCATCTAGACAGTGGAGCTCAGCTGGGGGATTTGGCCCGCATCTCGGGGGGAATGTC 798
Qy 121 TGAAGCAATTTTGTACTCTCATGAGGAGTGAGAGAGATACAGTGTACTATCAAC 180
Db 121 TGAAGCAATTTTGTACTCTCATGAGGAGTGAGAGAGATACAGTGTACTATCAAC 180
```

```
Db 799 TGAAGCAATTTT- GTTAACTCAATGAGGAGTGAGAGAGATACAGTGTACTATCAAC 857
Qy 181 TAGTGAATTAAGGCGCAGGATGCTGCTCAACCTTCTCAATGATAGAGGAGCTCTCCCA 240
Db 858 TAGTGAATTAAGGCGCAGGATGCTGCTCAACCTTCTCAATGATAGAGGAGCTCTCCCA 916
Qy 241 TTACAACTACCCCAATCCGAAGTGTCAACTGTGTGAGGACTTAAGAAACCCGTGTTGAGT 300
Db 917 TTACAACTACCCCAATCCGAAGTGTCAACTGTGTGAGGACTTAAGAAACCCGTGTTGAGT 976
Qy 301 AGAAAGGCGCTGAAAGAGGAGGAGCCAAACAAATCTGTCTTCTTCTCAATAGTCAAT 360
Db 977 AGAAAGGCGCTGAAAGAGGAGGAGCCAAACAAATCTGTCTTCTTCTCAATAGTCAAT 1036
Qy 361 GGCATAATAGCATTTCTGTCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 1037 GGCATAATAGCATTTCTGTCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096
Qy 421 GGGCACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 480
Db 1097 GGGCACAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTATGGGAAATGCTGA 1156
Qy 481 TGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCTTCTTCAATCTTACCTGCAAG 540
Db 1157 TGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCTTCTTCAATCTTACCTGCAAG 1216
Qy 541 CCAAGTCTGTAAAGAAATGCTGAGTCTTACTGAGTTTCTTACTGTAATTAGA 600
Db 1217 CCAAGTCTGTAAAGAAATGCTGAGTCTTACTGAGTTTCTTACTGTAATTAGA 1276
Qy 601 TCTCCAGACCTTCTGCGCCCAATTCAAATTAAAGCAACAATATACCTTCATGTGTA 660
Db 1277 TCTCCAGACCTTCTGCGCCCAATTCAAATTAAAGCAACAATATACCTTCATGTGTA 1336
Qy 661 GCACACACAGACTTTTGAAGCAAGACATGACTCTGAATTGAGGCTTGGAGAAAG 720
Db 1337 GCACACACAGACTTTTGAAGCAAGACATGACTCTGAATTGAGGCTTGGAGAAAG 1396
Qy 721 AAGCTTTGAAGAAAGAAATCTTGTTCAGGCCCCCTCCACACTCTTCATGTGTA 780
Db 1397 AAGCTTTGAAGAAAGAAATCTTGTTCAGGCCCCCTCCACACTCTTCATGTGTA 1456
Qy 781 ACCACTGCTTCTGGAACCTTGAAGCAAGGTAAGTGTATTAATGAAAG 840
Db 1457 ACCACTGCTTCTGGAACCTTGAAGCAAGGTAAGTGTATTAATGAAAG 1516
Qy 841 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 890
Db 1517 TGATTTAGAGTTCTGATCTTCAAGAGATGATTAATATACCTTCT 1566
```

RESULT 8

```
US-09-404-879A-27/c
; Sequence 27, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
```

OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-27

Query Match 50.4%; Score 448.2; DB 3; Length 461;
Best Local Similarity 99.1%; Pred. No. 2,6e-131;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATCCTGATGGAT 486
DB 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAGGCTTATGGAAATCCTGATGGAT 403
QY 487 TATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCACTTACCTTGAAGCCAACT 546
DB 402 TATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCACTTACCTTGAAGCCAACT 343
QY 547 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
DB 342 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
QY 607 GACCTTCTGCGCCACAATTCAATTAGGCAACAACATATACCTTCATGAGCACAC 666
DB 282 GACCTTCTGCGCCACAATTCAATTAGGCAACAACATATACCTTCATGAGCACAC 223
QY 667 ACAGACTTTTGAAGCAAGCAAGACATGCTGTAATTGAAGCTTGAAGCAATGAAGCTT 726
DB 222 ACAGACTTTTGAAGCAAGCAAGACATGCTGTAATTGAAGCTTGAAGCAATGAAGCTT 163
QY 727 TGAAGGAAAGAAATATCTTGTTCAGCCCCCTTCCACACTTTCATGTTAAACCACT 786
DB 162 TGAAGGAAAGAAATATCTTGTTCAGCCCCCTTCCACACTTTCATGTTAAACCACT 103
QY 787 GCTTCTGAGCACTTGGAGCCACGCTGACTGATTAATCATGTTTATAGAAAATGATTT 846
DB 102 GCTTCTGAGCACTTGGAGCCACGCTGACTGATTAATCATGTTTATAGAAAATGATTT 43
QY 847 TAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTC 888
DB 42 YAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTC 1

RESULT 9
US-09-338-933-27/C

Sequence 27, Application US/09338933
Patent No. 6488931
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(461)
OTHER INFORMATION: n = A,T,C or G
US-09-338-933-27

Query Match 50.4%; Score 448.2; DB 4; Length 461;
Best Local Similarity 99.1%; Pred. No. 2,6e-131;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATCCTGATGGAT 486
DB 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAGGCTTATGGAAATCCTGATGGAT 403
QY 487 TATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCACTTACCTTGAAGCCAACT 546

DB 402 TATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCACTTACCTTGAAGCCAACT 343

QY 547 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
DB 342 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283

QY 607 GACCTTCTGCGCCACAATTCAATTAGGCAACAACATATACCTTCATGAGCACAC 666
DB 282 GACCTTCTGCGCCACAATTCAATTAGGCAACAACATATACCTTCATGAGCACAC 223

QY 667 ACAGACTTTTGAAGCAAGCAAGACATGCTGTAATTGAAGCTTGAAGCAATGAAGCTT 726
DB 222 ACAGACTTTTGAAGCAAGCAAGACATGCTGTAATTGAAGCTTGAAGCAATGAAGCTT 163

QY 727 TGAAGGAAAGAAATATCTTGTTCAGCCCCCTTCCACACTTTCATGTTAAACCACT 786
DB 162 TGAAGGAAAGAAATATCTTGTTCAGCCCCCTTCCACACTTTCATGTTAAACCACT 103

QY 787 GCTTCTGAGCACTTGGAGCCACGCTGACTGATTAATCATGTTTATAGAAAATGATTT 846
DB 102 GCTTCTGAGCACTTGGAGCCACGCTGACTGATTAATCATGTTTATAGAAAATGATTT 43

QY 847 TAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTC 888
DB 42 YAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTC 1

RESULT 10
US-09-215-681-27/C

Sequence 27, Application US/09215681A
Patent No. 6528253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Brudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(461)
OTHER INFORMATION: n = A,T,C or G
US-09-215-681-27

Query Match 50.4%; Score 448.2; DB 4; Length 461;
Best Local Similarity 99.1%; Pred. No. 2,6e-131;
Matches 458; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATCCTGATGGAT 486
DB 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAGGCTTATGGAAATCCTGATGGAT 403
QY 487 TATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCACTTACCTTGAAGCCAACT 546
DB 402 TATCTTCAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCACTTACCTTGAAGCCAACT 343
QY 547 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
DB 342 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
QY 607 GACCTTCTGCGCCACAATTCAATTAGGCAACAACATATACCTTCATGAGCACAC 666
DB 282 GACCTTCTGCGCCACAATTCAATTAGGCAACAACATATACCTTCATGAGCACAC 223

RESULT 13
US-09-040-984-15
Sequence 15, Application US/09040984
Patent No. 6210883
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-282-6031
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-040-984-15
Query Match 48.7%; Score 433.8; DB 3; Length 695;
Best Local Similarity 80.2%; Pred. No. 1.2e-126;
Matches 551; Conservative 0; Mismatches 126; Indels 10; Gaps 7;
QY 179 ACTAGGATAAAGCCAGGATGCTGCTCAACCTCTCACTGTAAGAGGAGCTCTCC 238
DB 1 ACTAGGATAAAGCCAGGATGCTGCTCAACCTCTCACTGTAAGAGGAGCTCTCC 60
QY 239 CATTACAATACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGGTTTGA 298
DB 61 CATTACAATACCAATCCGAAGTGTCACTGTCTAGAGACTAAGAAACCTGGTTTGA 120
QY 299 GTAGAAAAGGCGCTGGAAGAGGGAGCCAACTGTGTCTCTCTCACTAAGTCA 358
DB 121 TTAATAAAGGCGCTGGAAGAGGGAGCC-ACAAATCTGTCTCTCTCACTAANTCN 179
QY 359 TTGGCAATAAAGCATCTCTCTCTGTGGTGTCTGCTGCTGCTGCTGCTGCTGCT 418
DB 180 TTGGCAATAAAGCATCTCTCTCTGTGGTGTCTGCTGCTGCTGCTGCTGCTGCT 239
QY 419 TCGGGACAGAGATAATCTCTCAAGTGAACAGAGTGAACAAGGCTTATGGAAATGCT 478
DB 240 TONGGC-CCAGGAATACATCTCNCAATNAACAAATTGACAGGNNTGGAAATGCCN 298
QY 479 GATGGATTATCTTCACTGCTGTGAGCTTCTAAGTTCTTCTCTCTCACTTCACTGCA 538
DB 299 GATGGATTATCTTCACTGCTGTGAGCTTCTAAGTTCTTCTCTCTCACTTCACTGCA 358
QY 539 AGCCAAGTCTGTAGAGAAATGCTGAGTCTAGTCAAGTCTTCTTCTTCTGTAATTTA 598
DB 359 AGCCNAGTCTGTAGAGAAATGCTGAGTCTTCAACNCGGTTTCTTCTGTAATTTA 418

QY 599 GATCTCAGACCTTCTGCGCACAAATTCAAATT-AGGCAACAACATATACCTTCCAT 657
DB 419 GATCTCAGAAACCTTCTGCGCACAAATTCAAATTNANGNACAGNACAAATNCTTCAT 478
QY 658 GAGACACACACAGACTTTTGAAGACAGACAAATGACTGCTTGAATTGAGCCTTGAGA 717
DB 479 NAANGNCAC-CCCACTTTGAGAGCAGACAAATGACTGCTTGAANTGAGCCTGAGA 537
QY 718 ATGAGCTTTGAGAGAAAGATACTTGTGTTCCAGCCCCCTTCCACACTCTTCATGTG 777
DB 538 AANAA-CTTTGAGAGAAAGAACTTGTGTTCCAGCCCCCTT-CCACNCTTCTGTG 592
QY 778 TTAACCACTGCTTCTCTGGA-ACCTTGAGCAAGGTAATGATTTATGATTTATAGA 836
DB 593 TTNACACTGCTTCTTGNAAACCTGGAAGCCCNAGACAGTGTACATGTTGTTCTANN 652
QY 837 AAACGATTTTGAAGTCTGATCTGCTC 863
DB 653 AAACGACNCTTNAATNCTTCTCC 679
RESULT 14
US-09-123-912-15
Sequence 15, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 695
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (105)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (172)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (176)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (179)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (189)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (203)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (212)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (219)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (221)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (229)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base


```

; NAME/KEY: modified_base
; LOCATION: (652)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (657)

```

```

Query Match      48.7%; Score 433.8; DB 3; Length 695;
Best Local Similarity 80.2%; Pred. No. 1.2e-126;
Matches 551; Conservative 0; Mismatches 126; Indels 10; Gaps 7;

```

```

QY 179 ACTAGTGATTAAGGCGCAGGAGATGCTGCTCAACCTCTTCCATGTACAGGAGCTCTCCC 238
   |||||
DB 1 ACTAGTGATTAAGGCGCAGGAGATGCTGCTCAACCTCTTCCATGTACAGGAGCTCTCCC 60

QY 239 CATTAACAATCCCAATCCGAAGTGCATGTCAGAGACTAAGAAACCTGGTTTGA 298
   |||||
DB 61 CATTAACAATCCCAATCCGAAGTGCATGTCAGAGACTAAGAAACCTGGTTTGA 120

QY 299 GTAGAAAAGGCGCTGGAAGAGGGAGCCAAACATCTGTCTCTTCTCTCAATTAGTCA 358
   |||||
DB 121 TTTAAAAAGGCGCTGAAAAAGGGAGGCC-ACAAATCTGTCTCTTCTCTCAANTTANTCN 179

QY 359 TTGGCAATTAAGATTTCTCTCTTTGGCTGCTGCTTCCACAGAGAGCCAGAACTCTA 418
   |||||
DB 180 TTGGCAATTAAGATTTCTCTCTTTGGCTGCTGCTTCCANCAAAAANCGAACTCTCA 239

QY 419 TCGGGACACAGGATACATCTCTCAGTGAACAGAGTTGAACAAGGCTATGGGAAATGCT 478
   |||||
DB 240 TCGGAC-CCAGGAATACATCTCNCATTAACAAATTTGANCAGGCGNTGGAAATGCCN 298

QY 479 GATGGATTATCTTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTTGA 538
   |||||
DB 299 GATGGATTATCTTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTTGA 358

QY 539 AGCGAAGTTCTGTAAAGAAATGCTGAGTTCTAGTCAAGTTTCTTCTCTGAATTGA 598
   |||||
DB 359 AGCGAAGTTCTGTAAAGAAATGCTGAGTTCTAAGTTTCTTCTCTGAATTGA 418

QY 599 GATCTCCAGACCTTCTGCGCCCAATTCAAATT- AAGCAACAACATATACCTTCAT 657
   |||||
DB 419 GATCTCCAGAAACTTCTGCGCCCAATTTTANANGNCAAGNACAAATNCTTCAT 478

QY 658 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTGAGGCGCTTGAGA 717
   |||||
DB 479 NAAACGAC-CCCACTTTGANAAGCCANGACATGACTGCTTGAAGGCTTGAAG 537

QY 718 ATGAAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCAATG 777
   |||||
DB 538 AANAA-CTTTGAAGAAAGAAAGAAATCTTTGTTCCAGCCCCCTT-CCAAACNCTTCTG 592

QY 778 TTAACCACTGCTTCTCTG-ACCTTGAGGCAAGGAGTATTAATGTTGTTATGA 836
   |||||
DB 593 TTAACCACTGCTTCTCTGNAACCTTGAGGCGCCNGAGAGTGTATGATGTTGTTTANN 652

QY 837 AAACGATTTTGAAGTTCTGATGTTTC 863
   |||||
DB 653 AAACGACNCTTAAATNTCNATCTTCC 679

```

```

RESULT 15
US-09-643-597-15
; Sequence 15, Application US/09643597
; Patent No. 6426072

```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.

```

```

; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(695)
; OTHER INFORMATION: n = A,T,C or G

```

```

Query Match      48.7%; Score 433.8; DB 3; Length 695;
Best Local Similarity 80.2%; Pred. No. 1.2e-126;
Matches 551; Conservative 0; Mismatches 126; Indels 10; Gaps 7;

```

```

QY 179 ACTAGTGATTAAGGCGCAGGAGATGCTGCTCAACCTCTTCCATGTACAGGAGCTCTCCC 238
   |||||
DB 1 ACTAGTGATTAAGGCGCAGGAGATGCTGCTCAACCTCTTCCATGTACAGGAGCTCTCCC 60

QY 239 CATTAACAATCCCAATCCGAAGTGCATGTCAGAGACTAAGAAACCTGGTTTGA 298
   |||||
DB 61 CATTAACAATCCCAATCCGAAGTGCATGTCAGAGACTAAGAAACCTGGTTTGA 120

QY 299 GTAGAAAAGGCGCTGGAAGAGGGAGCCAAACATCTGTCTCTTCTCTCAATTAGTCA 358
   |||||
DB 121 TTTAAAAAGGCGCTGAAAAAGGGAGGCC-ACAAATCTGTCTCTTCTCTCAANTTANTCN 179

QY 359 TTGGCAATTAAGATTTCTCTCTTTGGCTGCTGCTTCCACAGAGCCAGAACTCTA 418
   |||||
DB 180 TTGGCAATTAAGATTTCTCTCTTTGGCTGCTGCTTCCANCAAAAANCGAACTCTCA 239

QY 419 TCGGGACACAGGATACATCTCTCAGTGAACAGAGTTGAACAAGGCTATGGGAAATGCT 478
   |||||
DB 240 TCGGAC-CCAGGAATACATCTCNCATTAACAAATTTGANCAGGCGNTGGAAATGCCN 298

QY 479 GATGGATTATCTTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTTGA 538
   |||||
DB 299 GATGGATTATCTTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTCACTTGA 358

QY 539 AGCGAAGTTCTGTAAAGAAATGCTGAGTTCTAGTCAAGTTTCTTCTCTGAATTGA 598
   |||||
DB 359 AGCGAAGTTCTGTAAAGAAATGCTGAGTTCTAAGTTTCTTCTCTGAATTGA 418

QY 599 GATCTCCAGACCTTCTGCGCCCAATTCAAATT- AAGCAACAACATATACCTTCAT 657
   |||||
DB 419 GATCTCCAGAAACTTCTGCGCCCAATTTTANANGNCAAGNACAAATNCTTCAT 478

QY 658 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTGAGGCGCTTGAGA 717
   |||||
DB 479 NAAACGAC-CCCACTTTGANAAGCCANGACATGACTGCTTGAAGGCTTGAAG 537

QY 718 ATGAAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCAATG 777
   |||||
DB 538 AANAA-CTTTGAAGAAAGAAAGAAATCTTTGTTCCAGCCCCCTT-CCAAACNCTTCTG 592

QY 778 TTAACCACTGCTTCTCTG-ACCTTGAGGCAAGGAGTATTAATGTTGTTATGA 836
   |||||
DB 593 TTAACCACTGCTTCTCTGNAACCTTGAGGCGCCNGAGAGTGTATGATGTTGTTTANN 652

QY 837 AAACGATTTTGAAGTTCTGATGTTTC 863
   |||||
DB 653 AAACGACNCTTAAATNTCNATCTTCC 679

```

Search completed: May 31, 2005, 00:28:57

Job time : 169.951 secs

THIS PAGE LEFT BLANK

US-09-850-178-5	US-10-860-190-391	Sequence 391, Appl
12 878 98.7 2627 19	US-10-860-190-391	Sequence 2, Appl
13 878 98.7 3357 17	US-09-877-065-7	Sequence 1, Appl
14 877.6 98.6 2603 9	US-09-877-065-7	Sequence 7, Appl
15 876.4 98.5 2626 9	US-09-850-178-23	Sequence 23, Appl
16 867 97.3 2591 9	US-09-850-178-23	Sequence 74, Appl
17 866 97.3 1567 10	US-09-850-178-23	Sequence 74, Appl
18 866 97.3 1567 10	US-09-850-178-23	Sequence 74, Appl
19 866 97.3 1567 10	US-09-850-178-23	Sequence 74, Appl
20 866 97.3 1567 10	US-09-850-178-23	Sequence 74, Appl
21 866 97.3 1567 10	US-09-850-178-23	Sequence 74, Appl
22 856.6 96.2 2626 17	US-10-860-190-74	Sequence 74, Appl
23 807 90.7 846 10	US-09-850-178-30	Sequence 21446, A
24 711 79.9 725 9	US-09-850-178-30	Sequence 30, Appl
25 626.2 70.4 1811 14	US-10-097-340-106	Sequence 106, Appl
26 626.2 70.4 1811 14	US-10-097-340-331	Sequence 331, Appl
27 626.2 70.4 1811 15	US-10-177-293-163	Sequence 163, Appl
28 626.2 70.4 1811 17	US-10-173-999-71	Sequence 71, Appl
29 552 62.0 563 9	US-09-867-701-3948	Sequence 3948, Ap
30 544 61.1 555 9	US-09-833-790-388	Sequence 388, Ap
31 517 58.1 1596 14	US-10-198-846-13583	Sequence 13583, A
32 494.6 55.6 524 9	US-09-867-701-1498	Sequence 1498, Ap
33 494 55.5 524 9	US-09-867-701-2301	Sequence 2301, Ap
34 487.8 54.8 578 10	US-09-814-353-17682	Sequence 17682, A
35 480 53.9 491 9	US-09-850-178-3	Sequence 3, Appl
36 471.8 53.0 1891 14	US-10-097-340-347	Sequence 347, App
C 37 466.2 52.4 486 9	US-09-867-701-1482	Sequence 1482, Ap
C 38 448.2 50.4 461 9	US-09-884-441-27	Sequence 27, Appl
C 39 448.2 50.4 461 10	US-09-907-969-27	Sequence 27, Appl
C 40 448.2 50.4 461 10	US-09-827-771-27	Sequence 27, Appl
C 41 448.2 50.4 461 15	US-10-188-053-27	Sequence 27, Appl
C 42 448.2 50.4 461 19	US-10-860-190-27	Sequence 27, Appl
43 446.4 50.2 757 10	US-09-814-353-5006	Sequence 5006, Appl
44 446.4 50.2 757 10	US-09-814-353-11298	Sequence 11298, A
45 440 49.4 442 9	US-09-867-701-2832	Sequence 2832, Ap

ALIGNMENTS

RESULT 1

US-09-850-178-5

Sequence 5, Application US/09850178

Patent No. US20020034749A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Billing-Medel, Patricia A.

APPLICANT: Cohen, Maurice

APPLICANT: Colipites, Tracey L.

APPLICANT: Friedman, Paula N.

APPLICANT: Russell, John C.

APPLICANT: Granados, Edward N.

APPLICANT: Hodges, Steven C.

APPLICANT: Kloss, Michael R.

APPLICANT: Kratochvil, Jon D.

APPLICANT: Roberts-Rapp, Lisa

APPLICANT: Stroupe, Stephen D.

APPLICANT: Gordon, Julian

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR

TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST

FILE REFERENCE: 6251. US.P1

CURRENT APPLICATION NUMBER: US/09/850.178

CURRENT FILING DATE: 2001-05-07

PRIOR APPLICATION NUMBER: US 08/972,376

PRIOR FILING DATE: 1997-11-18

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 893

TYPE: DNA

ORGANISM: Homo sapiens

US-09-850-178-5

98.7%, Score 878, DB 9, Length 893;

Best Local Similarity 99.9%; Pred. No. 3.3e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTCGCGGAGCAGCTAAGACCTGATTTCAATA 60
Db 1 CAAGCTCTGAGGCTTCTCTTCCATCTCGCGGAGCAGCTAAGACCTGATTTCAATA 60
QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGAGTGTATTTGCCGCCATCTCCGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGAGTGTATTTGCCGCCATCTCCGGGGAATGTC 120
QY 121 TGAAGCAATTTTGGTTACTCTCATAGGAGTGGAGAGATACAGTCTACTACCAAC 180
Db 121 TGAAGCAATTTTGGTTACTCTCATAGGAGTGGAGAGATACAGTCTACTACCAAC 180
QY 181 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCCACATGATGAGGAGCGTCCCA 240
Db 181 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCCACATGATGAGGAGCGTCCCA 240
QY 241 TTACAACCTACCAATCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 300
Db 241 TTACAACCTACCAATCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 300
QY 301 AGAAAAGGCTCTGAGAAAGGAGGAGCCAACTCTGTCTCTCTCACTTATGTCATT 360
Db 301 AGAAAAGGCTCTGAGAAAGGAGGAGCCAACTCTGTCTCTCTCACTTATGTCATT 360
QY 361 GGGAAATTAAGCAATTCGTCTTGGCTGTGCTGCTGAGAGAGAGGAGGAGGAGTATC 420
Db 361 GGGAAATTAAGCAATTCGTCTTGGCTGTGCTGCTGAGAGAGAGGAGGAGGAGTATC 420
QY 421 GGGCAACGAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGGCTTAAGGAAATGCTGA 480
Db 421 GGGCAACGAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGGCTTAAGGAAATGCTGA 480
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCACTTACCTGCAAG 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCACTTACCTGCAAG 540
QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
QY 601 TCTCCAGACCTTCTCTGAGCAATTAATTAAGGCAACAAATATACCTTCCATGAA 660
Db 601 TCTCCAGACCTTCTCTGAGCAATTAATTAAGGCAACAAATATACCTTCCATGAA 660
QY 661 GCAACACAGACTTTTGAAGAGCAAGACATGACTGCTTGAATTGAGGCTTGAAGAAATG 720
Db 661 GCAACACAGACTTTTGAAGAGCAAGACATGACTGCTTGAATTGAGGCTTGAAGAAATG 720
QY 721 AAGCTTTGAAGAAAGAAATATCTTTTCCAGCCCCCTTCCACACTCTCATGTGTTA 780
Db 721 AAGCTTTGAAGAAAGAAATATCTTTTCCAGCCCCCTTCCACACTCTCATGTGTTA 780
QY 781 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTGTTATAGAAAC 840
Db 781 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGTGACTGTATTAATGTTGTTATAGAAAC 840
QY 841 TGAATTTAAGATTCTGATCTTCAAGAGATGATTAAATATACATTTCT 890
Db 841 TGAATTTAAGATTCTGATCTTCAAGAGATGATTAAATATACATTTCT 890
```

RESULT 2

US-09-850-178-6
; Sequence 6; Application US/09850178
; Patent No. US20020034749A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colipilts, Tracey L.

```
; APPLICANT: Friedman, Paula N.  
; APPLICANT: Russell, John C.  
; APPLICANT: Granados, Edward N.  
; APPLICANT: Hodges, Steven C.  
; APPLICANT: Klaes, Michael R.  
; APPLICANT: Kratochvil, Jon D.  
; APPLICANT: Roberts-Rapp, Lisa  
; APPLICANT: Stroupe, Stephen D.  
; APPLICANT: Gordon, Julian  
; TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST.  
; FILE REFERENCE: 6251, US, P1  
; CURRENT FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: US 08/972,376  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-850-178-6
```

Query Match 98.7%; Score 878; DB 9; Length 893;
Best Local Similarity 99.9%; Pred. No. 3.3e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 CAAGCTCTGAGGCTTCTCTTCCATCTCGCGGAGCAGCTAAGACCTGATTTCAATA 60
Db 1 CAAGCTCTGAGGCTTCTCTTCCATCTCGCGGAGCAGCTAAGACCTGATTTCAATA 60
QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGAGTGTATTTGCCGCCATCTCCGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGAGTGTATTTGCCGCCATCTCCGGGGAATGTC 120
QY 121 TGAAGCAATTTTGGTTACTCTCATAGGAGTGGAGAGATACAGTCTACTACCAAC 180
Db 121 TGAAGCAATTTTGGTTACTCTCATAGGAGTGGAGAGATACAGTCTACTACCAAC 180
QY 181 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCCACATGATGAGGAGGTCGCCCA 240
Db 181 TAGTGATTAAGGCGGAGGAGTGTCTCAACCTCCACATGATGAGGAGGTCGCCCA 240
QY 241 TTACAACCTACCAATCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 300
Db 241 TTACAACCTACCAATCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 300
QY 301 AGAAAAGGCTCTGAGAAAGGAGGAGCCAAATCTGTCTGCTTCTCACTTATGTCATT 360
Db 301 AGAAAAGGCTCTGAGAAAGGAGGAGCCAAATCTGTCTGCTTCTCACTTATGTCATT 360
QY 361 GGGAAATTAAGCAATTCGTCTTGGCTGTGCTGCTGAGAGAGGAGGAGGAGTATC 420
Db 361 GGGAAATTAAGCAATTCGTCTTGGCTGTGCTGCTGAGAGAGGAGGAGGAGTATC 420
QY 421 GGGCAACGAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGGCTTAAGGAAATGCTGA 480
Db 421 GGGCAACGAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGGCTTAAGGAAATGCTGA 480
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCACTTACCTGCAAG 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTCTTTCCCTTCACTTACCTGCAAG 540
QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
QY 601 TCTCCAGACCTTCTCTGAGCAATTAATTAAGGCAACAAATATACCTTCCATGAA 660
Db 601 TCTCCAGACCTTCTCTGAGCAATTAATTAAGGCAACAAATATACCTTCCATGAA 660
QY 661 GCAACACAGACTTTTGAAGAGCAAGACATGACTGCTTGAATTGAGGCTTGAAGAAATG 720
```

Db 660 GCACACAGACGCTTTGAAAGCAAGACATGATGCTTGAATTGAGCCCTGAGGAAATG 719
Qy 721 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 780
Db 720 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 779
Qy 781 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 840
Db 780 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 839
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 890
Db 840 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 889

RESULT 3
US-09-778-320-207
; Sequence 207, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778.320
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-320-207

Query Match 98.7%; Score 878; DB 9; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAAGCTCTGAGGCTTCTCTTCATCTCTGCGTGAGACGTAAGACCTCACTTTCAATA 60
Db 1721 CAAGCTCTGAGGCTTCTCTTCATCTCTGCGTGAGACGTAAGACCTCACTTTCAATA 1780
Qy 61 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGCGCCCATCTCCGGGGGAATGTC 120
Db 1781 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGCGCCCATCTCCGGGGGAATGTC 1840
Qy 121 TGAAGCAATTTTGTTTACTCATGAGGAGTGAGAGAGATACAGTGTACTACCAAC 180
Db 1841 TGAAGCAATTTTGTTTACTCATGAGGAGTGAGAGAGATACAGTGTACTACCAAC 1900
Qy 181 TAGTGATTAAGGCGCAGGAGTGTCTCAACTCTTCACTGATACAGGAGCTCTCCCA 240
Db 1901 TAGTGATTAAGGCGCAGGAGTGTCTCAACTCTTCACTGATACAGGAGCTCTCCCA 1959
Qy 241 TTAACAATCTCCCAATCCGAAGTGTCAACTGTGTCAGAGCTAAAGAAACCCGTTTGAAGT 300
Db 1960 TTAACAATCTCCCAATCCGAAGTGTCAACTGTGTCAGAGCTAAAGAAACCCGTTTGAAGT 2019
Qy 301 AGAAAGGAGGCTGAGAAAGAGGAGCCAAATCTGTCTGTCTTCTCAATTAATGATC 360
Db 2020 AGAAAGGAGGCTGAGAAAGAGGAGCCAAATCTGTCTGTCTTCTCAATTAATGATC 2079
Qy 361 GGAATTAAGCATTTCTGTCTTTGGCTGTGCTGCTCAGCAGAGAGCCAGAACTATC 420
Db 2080 GGAATTAAGCATTTCTGTCTTTGGCTGTGCTGCTCAGCAGAGAGCCAGAACTATC 2139

Qy 421 GGCACAGAGATTAACATCTCTCAGTAAAGAGGCTGACAAAGGCTTATGGAATGCTTGA 480
Db 2140 GGCACAGAGATTAACATCTCTCAGTAAAGAGGCTGACAAAGGCTTATGGAATGCTTGA 2199
Qy 481 TGGGATTAATCTCAGCTGTGTTGAGCTTCAAGTTTCTTCCCTTCAATTTACCTGCAAG 540
Db 2200 TGGGATTAATCTCAGCTGTGTTGAGCTTCAAGTTTCTTCCCTTCAATTTACCTGCAAG 2259
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTACTCAGGTTTCTTACTGTGAATTTAGA 600
Db 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTACTCAGGTTTCTTACTGTGAATTTAGA 2319
Qy 601 TCTCAGAGCCCTCTGCGCACAATCAATTAAGGCAACAAATATACCTTCCATGAA 660
Db 2320 TCTCAGAGCCCTCTGCGCACAATCAATTAAGGCAACAAATATACCTTCCATGAA 2379
Qy 661 GCACACAGACATTTTGAAGCAAGACATGATGCTGTAATGAGCCCTTGAAGGATG 720
Db 2380 GCACACAGACATTTTGAAGCAAGACATGATGCTGTAATGAGCCCTTGAAGGATG 2439
Qy 721 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 780
Db 2440 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 2499
Qy 781 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 840
Db 2500 AACCTTGAAGGAAAGAAATATCTTTGTTTCAAGCCCCCTTCCACACTCTTCATGTGTTA 2559
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 890
Db 2560 TGAATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 2609

RESULT 4
US-09-910-689-207
; Sequence 207, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910.689
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-689-207

Query Match 98.7%; Score 878; DB 9; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAAGCTCTGAGGCTTCTCTTCATCTCTGCGTGAGACGTAAGACCTCACTTTCAATA 60
Db 1721 CAAGCTCTGAGGCTTCTCTTCATCTCTGCGTGAGACGTAAGACCTCACTTTCAATA 1780
Qy 61 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGCGCCCATCTCCGGGGGAATGTC 120
Db 1781 GCATCTAGAGCAGTGGGACCTCAGCTGGGGGATTTGCGCCCATCTCCGGGGGAATGTC 1840
Qy 121 TGAAGCAATTTTGTTTACTCATGAGGAGTGAGAGAGATACAGTGTACTACCAAC 180

Query Match	98.7%;	Score 878;	DB 9;	Length 2627;
Best Local Similarity	99.9%;	Pred. NO. 6.2e-284;		

RESULT 6
US-09-907-969-391
Sequence 391, Application US/099079663
; Application No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Flinn, Steven P.
; APPLICANT: Retter, Marc W.


```

APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Hill, Paul
APPLICANT: Albone, Earl
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C8
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 391
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-969-391

```

Query Match	98.7%	Score 878;	DB 10;	Length 2627;
Best Local Similarity	99.9%	Pred. No. 6.2e-284;		
Matches 889;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;

Qy	Db	Qy
1	1721	61
CAAGCTCAGAGCCTTCTCTTCCATCCGCGGTGAGCAGCTAAACCGCACTTTCAATA	CAGCTCTGAGAGCCTTCTCTTCCATCTCGCGTGGACAGCTAAAGACTCAGATTTCAATA	GCATCTAGAGCAGTGGGACTCAGCTAGCTGGGGTATTTGGCCCCCATCTTCGGGGGAAATGTC
60	1780	120
GCATCTAGAGCAGTGGGACTCAGCTGGGGTATTTGGCCCCCATCTTCGGGGGAAATGTC		
1840		

QY	121	GAAGACAACTTTGGTATCCCTCANTGAGGGAGTGAAGAGATACAGGCTACATCAAC	180
Db	1841	TGAAGACAACTTTGGTATCCCTCAATGAGGGAGTGAAGAGATACAGGCTACATCAAC	1900
QY	181	TAGTGGATTAAGGCGAGGATGCTGCTCACTCTACATGTA CAGGGAAGTCTCCCA	240
Db	1901	TAGTGGATTAAGGCGAGGATGCTGCTCACTCTACATGTA CAGGGAAGTCTCCCA	1959

QY	241	TTACACCTACCCCAATCCGAAGTGTCAACTGTGTGTCAGAGCTTAAGAAACCCGTGTTTGAGT	300
QY	1960	TTACACCTACCCCAATCCGAAGTGTCAACTGTGTGTCAGAGCTTAAGAAACCCGTGTTTGAGT	2019
QY	301	AGAAAGGCGCTGGAAAGAGGGGAGCCAAACAATCTGTCTCTCTCCTCACAATTAGTCATT	360
DB	2020	AGAAAGGCGCTGGAAAGAGGGGAGCCAAACAATCTGTCTCTCTCCTCACAATTAGTCATT	2079

QY	361	GGCAATPAGCATTTCTGTCTCTTTGGCGTCTGCTCAGACAGAGAGCCAGAACTTATC	420
Db	2080	GGCAATPAGCATTTCTGTCTTTGGCGTCTGCTCAGACAGAGAGCCAGAACTTATC	2139
QY	421	GGGCAACCGATTAACATCTCTCAGTGAACAGATTGACAAAGCCTATGGGAAATGGCTGA	480
Db	2140	GGGCAACCGATTAACATCTCTCTGAGTGAACAGATTGACAAAGCCTATGGGAAATGGCTGA	2198

QY	481	TGGGATTATCTTCAGCTGTGAGCTCTTAAGTTCCTTCATTCTACCTGCAAG	540
Db	2200	TGGGATTATCTTCAGCTGTGAGCTCTTAAGTTCCTTCATTCTACCTGCAAG	2259
QY	541	CCAGTCTGTAAAGAAATGCCGAGTTCAGCTCAGCTTTCTTACTCGAATTTAGA	600
Db	2200	CCAGTCTGTAAAGAAATGCCGAGTTCAGCTCAGCTTTCTTACTCGAATTTAGA	2259

Qy	Db	Qy
601	2320	661
TCCTCAGACCTTCTCTGGCCACAATTCAATTAAGCAACAACATATACCTTCATGAA	TCCTCAGACCTTCTCTGGCCACAATTCAATTAAGCAACAACATATACCTTCATGAA	GCACACACAGACTTTGAAGCAAGACATGACTCTTGAATTGAGCCTTGAGGAATG
660	2379	720

721 AAGCTTGAAGAAAGATACTTGTTCAGCCCCCTCCACACTCTTCATGTTA 780

Db	2440	AAAGCTTTGAAGAAAAGAAATACCTTTGTTTCAGGCCCCCTTCCCAACACTCTTCAATGTTGA	2499
QY	781	ACCACTGCCCTTCTTGACACCTTTGAGCCACGGGTGACCTGATTAATCATGTTGTTATATGAAAC	840
Db	2500	ACCACTGCCCTTCTTGACACCTTTGAGCCACGGGTGACCTGATTAATCATGTTGTTATATGAAAC	2559
QY	841	TGATTTTATGAGTTCTGATCGTTCAGAGAAATGATTAATATATACATTTTCT	890
Db	2560	TGATTTTATGAGTTCTGATCGTTCAGAGAAATGATTAATATATACATTTTCT	2609

RESULT 7
US-09-827-271-391

```

; Sequence 391, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:

```

[illegible]

CONTAINS INFORMATION SUBJECT OF CONTROL
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEO ID NOS: 461

1 586 10 00 591
 2
 3 LENGTH: 2627
 4
 5 TYPE: DNA

```
US-03-821-211-391
Query Match
98 %: $Score 878: DB 10: length 2627:
```

	Seq. Local Similarity	99.3%	Fied. NO. 8.0e-268	Matches 889	Conservative 0	Mismatches 0	Indels 1	Gaps 1
Qy	1	CAAGCTCTGAGGCTTCTCTTCATCTGCGGAGCAGCTAAGACCTCAGTTTTCATA	60					
Db	1721	CAAGCTCTGAGGCTTCTCTTCATCTGCGGAGCAGCTAAGACCTCAGTTTTCATA	1780					
Qy	61	CGATTCAGAGCACTGGGATCTGACGCTGGGCGATTTTCCGCCCCCATCTCCGGGGGAAATGTC	120					

[illegible]

Db	1901	TAATGATTAAGGCGCAGGATGCTGCTCAACCTCTTACCATATACA-GGACGCTTCCCA	1959
Qy	241	TTTCAACTACCGAATCCGAAGTGTCAACTGTGTGACGACTTAAGAAACCCGATTTTGAGT	300
Db	1960	TTTCAACTACCGAATCCGAAGTGTCAACTGTGTGACGACTTAAGAAACCCGATTTTGAGT	2019

Db 2020 AGAAGGCGCTGAAAGAGGGAGCCAAATCTGTCTGCTTCCCTCAATTAGTCATT 2079

Qy 361 GGCAATTAAGCATTTCTGTCTCTTTGGCTGTGCTGACGACAGAGGCCAGAACTCTATC 420

Db 2080 GGCAATTAAGCATTTCTGTCTCTTTGGCTGTGCTGACGACAGAGGCCAGAACTCTATC 2139

Accession	Sequence	Position
Db	GGGCACCGAGTAAACATCTCTCAGTBAACAGAGTTBACAAGGCGTATGGGAATATGCTGA	2140 2199
Oy	TGGGATTATTTACGCTGTGAGCTTTCTAAGTTCTTTCCCTTCAATTGACCTGCAAG	481 540
Db	TGGATTATCTTACGCTGTGTGAGCTTCAAGTTCTTTCCCTCAATTCAACCTGCAG	2200 2259

Qy 541 CCAAGTTCTGTAGAGAAATGCGCTGAGTTCTTACGCTCAGTTTCTTACTCTGAATTAGA 600
|||||

```
Db      2260 CCAAGTCTGTGAAGAAAGCCGTGATCTAGCTCAGGTTTCTTACTCTGAATTGAGA 2319
Qy      601 TCTCCAGACCTTCTCTGCGCACAAATTAAGGCAACAAATATATACCTTCCATGAA 660
Db      2320 TCTCCAGACCTTCTCTGCGCACAAATTAAGGCAACAAATATATACCTTCCATGAA 2379
Qy      661 GCACACACAGACTTTTGAAGCAGACAAATGACTGCTTGAATTGAGGCTTGAGGAATG 720
Db      2380 GCACACACAGACTTTTGAAGCAGACAAATGACTGCTTGAATTGAGGCTTGAGGAATG 2439
Qy      721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCAATGTTGA 780
Db      2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCAATGTTGA 2499
Qy      781 ACCACTGCTCTCTGAGACCTTGAGCCAGGTGACTGATTAATGATTTGATTAAGAAAC 840
Db      2500 ACCACTGCTCTCTGAGACCTTGAGCCAGGTGACTGATTAATGATTTGATTAAGAAAC 2559
Qy      841 TGATTTTGAAGTTCTGATGCTTCAAGAGAAATTAATATACATTTCTCT 890
Db      2560 TGATTTTGAAGTTCTGATGCTTCAAGAGAAATTAATATACATTTCTCT 2609
```

RESULT 8

```
US-10-010-742-207
; Sequence 207, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-742-207
```

```
Query Match      98.7%; Score 878; DB 13; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      1 CAAGCTCTAGAGCTTCTCTTCCATCTCGCGTGAACAGCTAAGACCTCAGTTTCAATA 60
Db      1721 CAAGCTCTAGAGCTTCTCTTCCATCTCGCGTGAACAGCTAAGACCTCAGTTTCAATA 1780
Qy      61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGATTTTGGCCCCCATCTCGGGGGAATGTC 120
Db      1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGATTTTGGCCCCCATCTCGGGGGAATGTC 1840
Qy      121 TGAAGCAATTTTGTACTCTCAATGAGGAGTGAGAGAGATACAGTGTACTTACCAAC 180
Db      1841 TGAAGCAATTTTGTACTCTCAATGAGGAGTGAGAGAGATACAGTGTACTTACCAAC 1900
Qy      181 TGTGTGATTAAGGCGCAGGAGATGCTGTCAACCTCCATACATGACAGGAGCGTCTCCCA 240
Db      1901 TGTGTGATTAAGGCGCAGGAGATGCTGTCAACCTCCATACATGACAGGAGCGTCTCCCA 1959
```

```
Qy      241 TTCAACTATCCCAATCCGAAGTGTCACTGTGTGACGACTAAGAAACCTCGTTTTGAAT 300
Db      1960 TTCAACTATCCCAATCCGAAGTGTGTCACTGTGTGACGACTAAGAAACCTCGTTTTGAAT 2019
Qy      301 AGAAAGGCGCTGGAAGAGGGGAGCCCAACAAATGTGTGCTGCTCTCAATTAAGTAT 360
Db      2020 AGAAAGGCGCTGGAAGAGGGGAGCCCAACAAATGTGTGCTGCTCTCAATTAAGTAT 2079
Qy      361 GCGAATATAGCAATTTCTCTCTTTGGCTGTGCTCTCAGACACAGAGAGCCAGAACTATC 420
Db      2080 GCGAATATAGCAATTTCTCTCTTTGGCTGTGCTCTCAGACACAGAGAGCCAGAACTATC 2139
Qy      421 GGGCACCGAGATTAATCTCTCAAGTGAACAGAGTTGAACAAGGCTTAATGGAAATGCTCTGA 480
Db      2140 GGGCACCGAGATTAATCTCTCAAGTGAACAGAGTTGAACAAGGCTTAATGGAAATGCTCTGA 2199
Qy      481 TGGGATTAATCTTCACTGTTGAGGCTTGAAGTTTAAATTTCTTCCCTCATTTCACTGCAAG 540
Db      2200 TGGGATTAATCTTCACTGTTGAGGCTTGAAGTTTAAATTTCTTCCCTCATTTCACTGCAAG 2259
Qy      541 CCAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTGAA 600
Db      2260 CCAAGTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTGAA 2319
Qy      601 TCTCCAGACCTTCTCTGCGCACAAATTAAGGCAACAAATATATACCTTCCATGAA 660
Db      2320 TCTCCAGACCTTCTCTGCGCACAAATTAAGGCAACAAATATATACCTTCCATGAA 2379
Qy      661 GCACACACAGACTTTTGAAGCAGACAAATGACTGCTTGAATTGAGGCTTGAGGAATG 720
Db      2380 GCACACACAGACTTTTGAAGCAGACAAATGACTGCTTGAATTGAGGCTTGAGGAATG 2439
Qy      721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCAATGTTGA 780
Db      2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTCTTCAATGTTGA 2499
Qy      781 ACCACTGCTCTCTGAGACCTTGAGCCAGGTGACTGATTAATGATTTGATTAAGAAAC 840
Db      2500 ACCACTGCTCTCTGAGACCTTGAGCCAGGTGACTGATTAATGATTTGATTAAGAAAC 2559
Qy      841 TGATTTTGAAGTTCTGATGCTTCAAGAGAAATTAATATACATTTCTCT 890
Db      2560 TGATTTTGAAGTTCTGATGCTTCAAGAGAAATTAATATACATTTCTCT 2609
```

RESULT 9

```
US-10-198-053-391
; Sequence 391, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-391
```

```
Query Match      98.7%; Score 878; DB 15; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAACAGCTTAAGACCTCAGTTTCAATA 60
```

```

Db      1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGCAGTAAGACTCAGTTTTCATA 1780
Qy      61  GCATCTAGAGCAGTGGGACTCAGCTGGGGGATTTTGGCCCCCATCTCCGGGGGAATGTC 120
Db      1781 GCACTTAGAGCAGTGGGACTCAGCTGGGGGATTTTGGCCCCCATCTCCGGGGGAATGTC 1840
Qy      121 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGAAGAGATCAGTGTACTACCAAC 180
Db      1841 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGAAGAGATCAGTGTACTACCAAC 1900
Qy      181 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCTCAATGATACAGGAGCTGTCCCA 240
Db      1901 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCTCAATGATACAGGAGCTGTCCCA 1959
Qy      241 TTTCACATACCCCAATCCGAGTGTCACTGTCTCAAGACATTAAGAAACCCGTGTTTGAAT 300
Db      1960 TTTCACATACCCCAATCCGAGTGTCACTGTCTCAAGACATTAAGAAACCCGTGTTTGAAT 2019
Qy      301 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 360
Db      2020 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 2079
Qy      361 GGCATAATAGCATTCTGTCTTTTGGCTGTGCTCTGAGCAGAGAGCCAGAACTATC 420
Db      2080 GGCATAATAGCATTCTGTCTTTTGGCTGTGCTCTGAGCAGAGAGCCAGAACTATC 2139
Qy      421 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 480
Db      2140 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 2199
Qy      481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 540
Db      2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 2259
Qy      541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 600
Db      2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 2319
Qy      601 TCTCCAGACCCCTTCTGCGCAATTTGAATTAAGGCAACAAATATACCTTCCATGAA 660
Db      2320 TCTCCAGACCCCTTCTGCGCAATTTGAATTAAGGCAACAAATATACCTTCCATGAA 2379
Qy      661 GCACACACAGACTTTTGAAGCAAGACATGACTGTTGAATTTGAGGCGCTTGAAGAGATG 720
Db      2380 GCACACACAGACTTTTGAAGCAAGACATGACTGTTGAATTTGAGGCGCTTGAAGAGATG 2439
Qy      721 AAGCTTTGAAGAAAAAATACTTGTGTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 780
Db      2440 AAGCTTTGAAGAAAAAATACTTGTGTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 2499
Qy      781 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTATTAAGAAAC 840
Db      2500 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTATTAAGAAAC 2559
Qy      841 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
Db      2560 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 2609

```

```

RESULT 10
US-10-714-389-207
; Sequence 207, Application US/10714389
; Publication No. US20040101899A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

```

```

; FILE REFERENCE: 210121.491D1
; CURRENT APPLICATION NUMBER: US/10/714.389
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-389-207

Query Match      98.7%; Score 878; DB 18; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6,2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1  CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGCAGTAAGACTCAGTTTTCATA 60
Db      1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCTGAGCAGTAAGACTCAGTTTTCATA 1780
Qy      61  GCATCTAGAGCAGTGGGACTCAGCTGGGGGATTTTGGCCCCCATCTCCGGGGGAATGTC 120
Db      1781 GCACTTAGAGCAGTGGGACTCAGCTGGGGGATTTTGGCCCCCATCTCCGGGGGAATGTC 1840
Qy      121 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGAAGAGATCAGTGTACTACCAAC 180
Db      1841 TGAAGACAATTTTGGTTTACTCTCAATGAGGAGTGAAGAGATCAGTGTACTACCAAC 1900
Qy      181 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCTCAATGATACAGGAGCTGTCCCA 240
Db      1901 TAGTGATTAAGGCGCAGGAGTGTCTCAACCTTCTCAATGATACAGGAGCTGTCCCA 1959
Qy      241 TTTCACATACCCCAATCCGAGTGTCACTGTCTCAAGACATTAAGAAACCCGTGTTTGAAT 300
Db      1960 TTTCACATACCCCAATCCGAGTGTCACTGTCTCAAGACATTAAGAAACCCGTGTTTGAAT 2019
Qy      301 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 360
Db      2020 AGAAAAAGGCGCTGGAAAAAGAGGAGCCAAATCTGTCTGCTTCTCATTAGTCAAT 2079
Qy      361 GGCATAATAGCATTCTGTCTTTTGGCTGTGCTCTGAGCAGAGAGCCAGAACTATC 420
Db      2080 GGCATAATAGCATTCTGTCTTTTGGCTGTGCTCTGAGCAGAGAGCCAGAACTATC 2139
Qy      421 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 480
Db      2140 GGGCACCAAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTATGGGAAATGCTTGA 2199
Qy      481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 540
Db      2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 2259
Qy      541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 600
Db      2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGAATTTAGA 2319
Qy      601 TCTCCAGACCCCTTCTGCGCAATTTGAATTAAGGCAACAAATATACCTTCCATGAA 660
Db      2320 TCTCCAGACCCCTTCTGCGCAATTTGAATTAAGGCAACAAATATACCTTCCATGAA 2379
Qy      661 GCACACACAGACTTTTGAAGCAAGACATGACTCTGAAATTTGAGGCGCTTGAAGAGATG 720
Db      2380 GCACACACAGACTTTTGAAGCAAGACATGACTCTGAAATTTGAGGCGCTTGAAGAGATG 2439
Qy      721 AAGCTTTGAAGAAAAAATACTTGTGTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 780
Db      2440 AAGCTTTGAAGAAAAAATACTTGTGTTCCAGCCCCCTTCCACACTCTTCAATGTGTA 2499
Qy      781 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTATTAAGAAAC 840
Db      2500 ACCACTGCTTCTCTGAGACCTTGAAGCAGGTAAGTATTAATGTTTATTAAGAAAC 2559
Qy      841 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890

```

Db 2560 TGATTTAGAGTTCTGATGCTTCAGAGATGATTAAATATACATTTCCT 2609

RESULT 11

US-10-717-296-207

/ Sequence 207, Application US/10717296

/ Publication No. US20040142361A1

/ GENERAL INFORMATION:

/ APPLICANT: Dillon, Davin C.

/ APPLICANT: Jiang, Yudiu

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

/ FILE REFERENCE: 210121.491C8

/ CURRENT APPLICATION NUMBER: US/10/717,296

/ NUMBER OF SEQ ID NOS: 313

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 207

/ LENGTH: 2627

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-717-296-207

Query Match 98.7%; Score 878; DB 18; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6.2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTCCATCCGCGGAGCAGCTAAGACCTCAGTTTCAATA 60
DB 1721 CAAGCTGAGGCTTCTCTTCCATCCGCGGAGCAGCTAAGACCTCAGTTTCAATA 1780
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCATCTCCGGGGGAATGTC 120
DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCATCTCCGGGGGAATGTC 1840
QY 121 TGAAGCAATTTTGGTTACTCTCATAGAGGAGTGAAGATACAGTCTACTACCAAC 180
DB 1841 TGAAGCAATTTTGGTTACTCTCATAGAGGAGTGAAGATACAGTCTACTACCAAC 1900
QY 181 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGGAGTCTCCCA 240
DB 1901 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGGAGTCTCCCA 1959
QY 241 TTACAACCTACCCAAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 300
DB 1960 TTACAACCTACCCAAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 2019
QY 301 AGAAAAGGCGCTGGAAGAGGGGAGCCAACTGTCTGCTTCTTCACTTAATGTCATT 360
DB 2020 AGAAAAGGCGCTGGAAGAGGGGAGCCAACTGTCTGCTTCTTCACTTAATGTCATT 2079
QY 361 GCGAATAAGCAATTCGTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTTATC 420
DB 2080 GCGAATAAGCAATTCGTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTTATC 2139
QY 421 GGGCACCAGGATTAACATCTCTCAGTGACAGAGTTGACAAAGGCTATGGAAATGCTGA 480
DB 2140 GGGCACCAGGATTAACATCTCTCAGTGACAGAGTTGACAAAGGCTATGGAAATGCTGA 2199
QY 481 TGGGATTAATCTCAGCTTGTGAGCTTGAAGTTTCTTTCCTTCACTTACCTGCAAG 540
DB 2200 TGGGATTAATCTCAGCTTGTGAGCTTGAAGTTTCTTTCCTTCACTTACCTGCAAG 2259
QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTAGA 600
DB 2260 CCAAGTTCTGTAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTAGA 2319
QY 601 TCTCCAGACCTTCTGCGCACAAATTCATTTAAGGCAACAAACATATACCTTCCATGA 660
DB 2320 TCTCCAGACCTTCTGCGCACAAATTCATTTAAGGCAACAAACATATACCTTCCATGA 2379
QY 661 GCAACACAGACTTTTGAAGCAGAGCAATGACTGCTTGAATTGAGGCTTGAGGATG 720

Db 2380 GCACACACAGACTTTTGAAGCAGACATGACTGTTGAATTGAGGCTTGAGGAATG 2439

QY 721 AAGCTTGAAGAAAAGAAATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780

DB 2440 AAGCTTGAAGAAAAGAAATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 2499

QY 781 ACCACTGCTTCTGAGACCTTGGAGCCAGCGTACTGTAATTAATGTTATAGAAAAC 840

DB 2500 ACCACTGCTTCTGAGACCTTGGAGCCAGCGTACTGTAATTAATGTTATAGAAAAC 2559

QY 841 TGATTTAGAGTTCTGATGCTTCAGAGATGATTAAATATACATTTCCT 890

DB 2560 TGATTTAGAGTTCTGATGCTTCAGAGATGATTAAATATACATTTCCT 2609

RESULT 12

US-10-860-790-391

/ Sequence 391, Application US/10860790

/ Publication No. US20050031634A1

/ GENERAL INFORMATION:

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: Reiter, Marc W.

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Hill, Paul

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

/ FILE REFERENCE: 210121.462C11

/ CURRENT APPLICATION NUMBER: US/10/860,790

/ NUMBER OF SEQ ID NOS: 624

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 391

/ LENGTH: 2627

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-860-790-391

Query Match 98.7%; Score 878; DB 19; Length 2627;
Best Local Similarity 99.9%; Pred. No. 6.2e-284;
Matches 889; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTCCATCCTGCTGAGCAGCTAAGACCTCAGTTTCAATA 60
DB 1721 CAAGCTGAGGCTTCTCTTCCATCCTGCTGAGCAGCTAAGACCTCAGTTTCAATA 1780
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCATCTCCGGGGGAATGTC 120
DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTGAATTCGCCCATCTCCGGGGGAATGTC 1840
QY 121 TGAAGCAATTTTGGTTACTCTCATAGAGGAGTGAAGATACAGTCTACTACCAAC 180
DB 1841 TGAAGCAATTTTGGTTACTCTCATAGAGGAGTGAAGATACAGTCTACTACCAAC 1900
QY 181 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGTCTCCCA 240
DB 1901 TGTGATTAAGGCGGAGGATGCTCAACCTCCATCATGATGAGGAGTCTCCCA 1959
QY 241 TTACAACCTACCCAAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 300
DB 1960 TTACAACCTACCCAAATCCGAAGTGTCACTGTCTCAGAGCTAAGAAACCTGTGTTGAGT 2019
QY 301 AGAAAAGGCGCTGGAAGAGGGGAGCCAACTGTCTGCTTCTTCACTTAATGTCATT 360
DB 2020 AGAAAAGGCGCTGGAAGAGGGGAGCCAACTGTCTGCTTCTTCACTTAATGTCATT 2079
QY 361 GCGAATAAGCAATTCGTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTTATC 420
DB 2080 GCGAATAAGCAATTCGTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTTATC 2139
QY 421 GGGCACCAGGATTAACATCTCTCAGTGACAGAGTTGACAAAGGCTATGGAAATGCTGA 480
DB 2140 GGGCACCAGGATTAACATCTCTCAGTGACAGAGTTGACAAAGGCTATGGAAATGCTGA 2199

QY	1	AAAGCTCGAGGCTTCCTCTTCCATCCCGGTGGACAGCTAAAGCCACAGTTTCAATA	60
Db	1651	CAGGCTTGAAGGCTTCTCTCTTCCATCTCGGTGGACAGCTAAAGCTCAAGTTTCAATA	1755C
QY	61	GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC	120
Db	1751	GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC	1810
QY	121	TGAAGACAAATTTGGTTACCTCAATGAGGAGTGGAGGAGATACAGTGTACTTACCAAC	180
Db	1811	TGAAGACAAATTTGGTTACCTCAATGAGGAGTGGAGGAGATACAGTGTACTTACCAAC	1870
QY	181	TAGTGGATTAAGGCGCAGGAGATGCTCTCAACCTCTCACTATGACAGGAGAGTCTCCCA	240
Db	1871	TAGTGGATTAAGGCGCAGGAGATGCTCTCAACCTCTCACTATGATACAGGAGAGTCTCCCA	1929
QY	241	TTACAACCTAACCCATCCGAAAGTGTCAACTGTGTCAAGACTAAGAAACCTCGTGGTTGAGT	300
Db	1930	TTACAACCTAACCCATCCGAAAGTGTCAACTGTGTCAAGACTAAGAAACCTCGTGGTTGAGT	1989
QY	301	AGAAAAGGCGCTGGAAAAGAGGGAGCCAAATCTGTCTGCTCTCACTAATAGTCAAT	360
Db	1990	AGAAAAGGCGCTGGAAAAGAGGGAGCCAAATCTGTCTGCTCTCACTAATAGTCAAT	2049
QY	361	GGAATATTAAGCAATCTGTCTCTTTGGCTGTGCTCTCAAGACAGAGAGCCAGAACTATCT	420
Db	2050	GGAATATTAAGCAATCTGTCTCTTTGGCTGTGCTCTCAAGACAGAGAGCCAGAACTATCT	2109
QY	421	GGGCACCAAGATACATCTCTCAAGTGAACAGATTTGACAGGCGCTATGGGAAATGCTGA	480
Db	2110	GGGCACCAAGATACATCTCTCAAGTGAACAGATTTGACAGGCGCTATGGGAAATGCTGA	2165
QY	481	TGGGATTAATCTCACTGTTGAGGCTTCAAGTTCTTCCCTCATCTCAACCGCAG	540
Db	2170	TGGGATTAATCTCACTGTTGAGGCTTCAAGTTCTTCCCTCATCTCAACCGCAG	2229
QY	541	CCAAAGTCTGTAAGAGAAATGCGTAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA	600
Db	2230	CCAAAGTCTGTAAGAGAAATGCGTAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA	2289
QY	601	TCTCCAGACCTTCTCTGGCAGCAATTCAAATTAAAGGCAACAACTATACCTTCATGA	660
Db	2290	TCTCCAGACCTTCTCTGGCAGCAATTCAAATTAAAGGCAACAACTATACCTTCATGA	2349
QY	661	GCACACACAGACTTTTGAAGCAAGACATGACTGTGATTAAGGCGCTTGGAGAAATG	720
Db	2350	GCACACACAGACTTTTGAAGCAAGACATGACTGTGATTAAGGCGCTTGGAGAAATG	2409
QY	721	AAGCTTTGAAGAAAAGATACTTTGTTTCCAGCCCCCTTCCCACTCTTCATGTGTA	780
Db	2410	AAGCTTTGAAGAAAAGATACTTTGTTTCCAGCCCCCTTCCCACTCTTCATGTGTA	2469
QY	781	ACCACTGCTTCTCTGAGCTTGGAGCCACGGTGACTGTATTAACATGTTGTATAGAAAC	840
Db	2470	ACCACTGCTTCTCTGAGCTTGGAGCCACGGTGACTGTATTAACATGTTGTATAGAAAC	2529
QY	841	TGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT	890
Db	2530	TGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTAATATACATTTCT	2579

RESULT 15

US-09-877-065-7

; Sequence 7, Application US/09877065

; Patent No. US20020051990A1

; GENERAL INFORMATION:

; APPLICANT: OPLE, ERIC

; APPLICANT: MCLACHLAN, KAREN

; APPLICANT: HEARD, CHERYL J.

; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR

; FILE REFERENCE: 037003-0280631

```

1 CURRENT APPLICATION NUMBER: US/09/877,065
2
3 CURRENT FILING DATE: 2001-06-11
4
5 PRIOR APPLICATION NUMBER: 69/210,451
6
7 PRIOR FILING DATE: 2000-06-09
8
9 NUMBER OF SEQ ID NOS: 14
10
11 SOFTWARE: PatentIn Ver. 2.1
12
13 SEQ ID NO: 7
14
15 LENGTH: 2626
16
17 TYPE: DNA
18
19 ORGANISM: Homo sapiens
20
21 FEATURE:
22
23 NAME/KEY: modified_base
24
25 LOCATION: (1303)
26
27 OTHER INFORMATION: a, c, t, g, other or unknown
28
29 NAME/KEY: modified_base
30
31 LOCATION: (1394)
32
33 OTHER INFORMATION: a, c, t, g, other or unknown
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1
```

Query Match	98.5%;	Score 876.4;	DB 9;	Length 2626;
Best Local Similarity	99.8%;	Pred. No. 2.2e-283;		
Matches 888; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1

QY	1	CAGGCTCGAGGCTTCTCTTTCCATCTCGGGTGGACAGCTTAAGACCTCAAGTTTCAATA	60
Db	1699	CAAGCTCTGAGGCTTCTCTTTCCATCTCGGGTGGACAGCTTAAGACCTCAAGTTTCAATA	1756
QY	61	GCATCTAAGAGAGTGGGACTCAGAGCTGGGGGTGATTTGGCCCCCAATCTCGGGGGAAATGTC	120
Db	1759	GCATCTAAGAGAGTGGGACTCAGAGCTGGGGGTGATTTGGCCCCCAATCTCGGGGGAAATGTC	1811
QY	121	TGAAGACAATTTTGGTTACTCAATGAGGAGTGGAGAGGATACAGTCTACTACCAAC	180
Db	1819	TGAAGACAATTTTGGTTACTCAATGAGGAGTGGAGAGGATACAGTCTACTACCAAC	1876
QY	181	TAGTGATTAAGGCCAGGAGTGTCTCAACTCTCAATGATACGGAGGTCTTCCCA	240
Db	1879	TAGTGATTAAGGCCAGGAGTGTCTCAACTCTCAATGATACGGAGGTCTTCCCA	193
QY	241	TTACACATACCCCAATCCCAAGTGCACATGTGTACAGGACTAAGAAACCTGGTTTTGAGT	300
Db	1938	TTACACATACCCCAATCCCAAGTGCACATGTGTACAGGACTAAGAAACCTGGTTTTGAGT	1997
QY	301	AGAAAAGGGCTCGGAAAAGAGGGGAGCCAAACAATCTGTCTGTCTTCTCACAATTAGTCAAT	360
Db	1998	AGAAAAGGGCTCGGAAAAGAGGGGAGCCAAACAATCTGTCTGTCTTCTCACAATTAGTCAAT	205
QY	361	GGCAAAATTAAGCAATTCGTCTCTTTGGCTGTGCTCAGACACAGAGAGCCAGAACTTAATC	420
Db	2058	GGCAAAATTAAGCAATTCGTCTCTTTGGCTGTGCTCAGACACAGAGAGCCAGAACTTAATC	211
QY	421	GGGCAACCAAGATTAACATCTCTCAGTGAACAAGATTGACAGAGGCTATGGGAAATGCCCTGA	480
Db	2118	GGGCAACCAAGATTAACATCTCTCAGTGAACAAGATTGACAGAGGCTATGGGAAATGCCCTGA	2177
QY	481	TGGATTATCTTCAAGCTTTGAGGCTTCAAGTTCTTCCCTTCATCTCAACCCCTGCAAG	540
Db	2178	TGGATTATCTTCAAGCTTTGAGGCTTCAAGTTCTTCCCTTCATCTCAACCCCTGCAAG	2237
QY	541	CCAAGTTCTGTAAAGAAATGCTGAGTTCAGCTCAGGTTTTCTTACTCTGAATTTAGA	600
Db	2238	CCAAGTTCTGTAAAGAAATGCTGAGTTCAGCTCAGGTTTTCTTACTCTGAATTTAGA	2297
QY	601	TCTCCAGACCTTCTGTGGCCAATTCAAATTAAAGCAACAACATATACCTTCATGAA	660
Db	2298	TCTCCAGACCTTCTGTGGCCAATTCAAATTAAAGCAACAACATATACCTTCATGAA	2357
QY	661	GCAACACACAGACTTTGAAGCAAGAGCAATGACTGCTGAATTGAGGCTTGAAGAAATG	720
Db	2358	GCAACACACAGACTTTGAAGCAAGAGCAATGACTGCTGAATTGAGGCTTGAAGAAATG	2417
QY	721	AAGCTTGAAGAAAAGATATCTTTGTTCCAGCCCCCTTCCACACGCTTCATGTGTTA	780

Db	2418	AAGCTTGAAGAAAGAAATACCTTTGTTTCAGCCCTTCCACACTCTTCATGTGTA	2477
Qy	781	ACCACTGCCCTTCTGAGCTTGGAGCCACGGTGACTGATTTACATGTTGTTATAGAAAC	840
Db	2478	ACCACTGCCCTTCTGAGCTTGGAGCCACGGTGACTGATTTACATGTTGTTATAGAAAC	2537
Qy	841	TGATTTAGAGTTCTGATCGTTCAAGAGAAATGATTAAATATACATTTCCCT	890
Db	2538	TGATTTAGAGTTCTGATCGTTCAAGAGAAATGATTAAATATACATTTCCCT	2587

Search completed: May 31, 2005, 10:07:38
 Job time : 613.64 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:48:09 ; Search time 3461.52 Seconds

(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978B-11

Perfect score: 890
Sequence: 1 caagctctgagctctcct.....tgatataatatacttctcct 890

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846.2	95.1	2431	3	CR603772 full-length
2	741.8	83.3	1018	5	EX337228
3	695	78.1	737	6	CA313445 UI-CF-FNO
4	666	74.8	700	5	BU632767 UI-H-FEI
5	663	74.5	691	6	CB241729 UI-CF-FNO
6	662	74.4	691	6	CA314865 UI-CF-FNO
7	658.2	74.0	691	6	BU608696 UI-CF-FNO
8	637.8	71.7	660	6	CB852239 UI-CF-FNO
9	634.4	71.3	660	6	CA426580 UI-H-FEI
10	632.2	71.0	679	6	CA312678 UI-CF-FNO
11	568	63.8	594	6	CA503188 UI-CF-FNO
12	552	62.0	556	1	AI684143 tx79904.x
13	552	62.0	556	1	AA404225 tx43h04.x
14	551.2	61.9	568	6	CD632169 56084071H
15	544.2	61.1	560	6	CD632170 56084071U
16	529.2	59.5	557	5	BM982674 UI-CF-FNO
17	511	57.4	529	2	AM615203 tx78a06.x
18	494.6	55.6	598	1	AA075632 zmb8h04.s
19	494	55.5	524	1	AA171844 z098e08.s
20	478.4	53.8	482	1	AI683712 tw53a09.x
21	478	53.7	481	2	AA470108 tx29h08.x
22	466.2	52.4	486	1	AA075579 zmb8h04.s
23	462.2	51.9	485	1	AI859795 wmd0e07.x
24	440.4	49.5	474	2	BE819515 RC2-BN033

C 25	440	49.4	442	1	AA291512	AA291512 zc40f01.s
C 26	432	48.5	436	1	AI638559	AI638559 t650a07.x
C 27	431	48.4	530	4	BI963964	BI963964 t63c03.y
C 28	425.4	47.8	447	1	AI686571	AI686571 tx08d03.x
C 29	419.4	47.1	426	1	AA411046	AA411046 zv40c07.s
C 30	419	47.1	426	1	AI828762	AI828762 tw35f01.x
C 31	418	47.0	422	1	AA434329	AA434329 zw24g07.x
C 32	406	45.3	553	5	BU742690	BU742690 UI-E-EOL
C 33	403.2	45.3	416	1	AI539668	AI539668 cp71e07.x
C 34	400	44.9	737	7	CN259810	CN259810 17006001
C 35	386	43.4	391	1	AA404609	AA404609 zc43h04.s
C 36	373.8	42.0	398	1	AI858190	AI858190 w146b08.x
C 37	368.8	41.4	374	1	AA706376	AA706376 ag91h05.x
C 38	367.4	41.3	392	2	AM073686	AM073686 kb01d04.x
C 39	354.6	39.6	382	2	AM172459	AM172459 kj39d04.x
C 40	349	39.2	349	1	AA554431	AA554431 n14f07.s
C 41	333.4	37.5	352	1	AA953518	AA953518 om80b02.s
C 42	328.4	36.9	355	6	CA314209	CA314209 UI-CF-FNO
C 43	327	36.7	450	7	H51315	H51315 yp07f05.s1
C 44	323	36.3	345	1	AA172293	AA172293 z098e08.x
C 45	291	32.7	939	5	BX371687	BX371687 BX371687

ALIGNMENTS

RESULT 1
CR603772
LOCUS
DEFINITION
full-length cDNA clone CS0D1039YG21 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION
CR603772
VERSION
CR603772.1 GI:50484579
KEYWORDS
HTC; CDS; CDNA
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact: Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 2431)

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1. 2431
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 95.1% Score 846.2; DB 3; Length 2431;
Best Local Similarity 99.5%; Pred. No. 2.5e-241;
Matches 859; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CAAGCTCTGAGGCTTCCTTCATCTGCGTGAACAGCTAGACCTGAGTTTCAATA 60
DB 1570 CAAGCTCTGAGGCTTCCTTCATCTGCGTGAACAGCTAGACCTGAGTTTCAATA 1629

```
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAATGTC 120
| | | | |
DB 1630 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAATGTC 1689
QY 121 TGAAGCAATTTTGGTTACTCTAATGAGGAGTGGAGGATACAGTCTCTACCAAC 180
| | | | |
DB 1690 TGAAGCAATTTTGGTTACTCTAATGAGGAGTGGAGGATACAGTCTCTACCAAC 1749
QY 181 TAGTGATTAAGGCCGAGGATGCTGCAACCTCCACCATGTACAGGAGCTGCCCA 240
| | | | |
DB 1750 TAGTGATTAAGGCCGAGGATGCTGCAACCTCCACCATGTACAGGAGCTGCCCA 1808
QY 241 TTACAACCTACCCAAATCCGAAGTGTCACTGTGTGAGAGTAAAGAACCTGTGTTGAGT 300
| | | | |
DB 1809 TTACAACCTACCCAAATCCGAAGTGTCACTGTGTGAGAGTAAAGAACCTGTGTTGAGT 1868
QY 301 AGAAAAAGGCTTGGAAAAAGGGGAGCCAAATCTGTCTGCTCTCTACATTAGTCATT 360
| | | | |
DB 1869 AGAAAAAGGCTTGGAAAAAGGGGAGCCAAATCTGTCTGCTCTCTACATTAGTCATT 1928
QY 361 GGCATAATAGCAATTCCTCTTGGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGTATC 420
| | | | |
DB 1929 GGCATAATAGCAATTCCTCTTGGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGTATC 1988
QY 421 GGGCAACAGAGATACATCTCTCAGTGACAGAGTTGACAAAGGCTATGGAATGCTGA 480
| | | | |
DB 1989 GGGCAACAGAGATACATCTCTCAGTGACAGAGTTGACAAAGGCTATGGAATGCTGA 2048
QY 481 TGGGATTAATCTTCAAGTTGTTGAGTCTTAAGTCTTAACTTTCTTCTTCTTCTGCAAG 540
| | | | |
DB 2049 TGGGATTAATCTTCAAGTTGTTGAGTCTTAACTTTCTTCTTCTTCTTCTGCAAG 2108
QY 541 CCAAGTCTGTAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTCTTCTTCTTCTGCAAG 600
| | | | |
DB 2109 CCAAGTCTGTAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTCTTCTTCTTCTGCAAG 2168
QY 601 TCTCCAGACCTTCTCTGAGCACAATTCATTAAGGCAACAAATATACCTTCCATGAA 660
| | | | |
DB 2169 TCTCCAGACCTTCTCTGAGCACAATTCATTAAGGCAACAAATATACCTTCCATGAA 2228
QY 661 GCACACAGACCTTTGAAAGCAAGACAAATGCTGTAATGAGGCTTGAAGAAAG 720
| | | | |
DB 2229 GCACACAGACCTTTGAAAGCAAGACAAATGCTGTAATGAGGCTTGAAGAAAG 2288
QY 721 AAGCTTTGAAGAAAGAAATATCTTGTTCAGCCCCCTTCCACACTCTTCAATGTTA 780
| | | | |
DB 2289 AAGCTTTGAAGAAAGAAATATCTTGTTCAGCCCCCTTCCACACTCTTCAATGTTA 2348
QY 781 ACCACTGACCTTCTCTGAGCCTTGGAGCCAGGTAATGTAATGTTGTTAAGAAAC 840
| | | | |
DB 2349 ACCACTGACCTTCTCTGAGCCTTGGAGCCAGGTAATGTAATGTTGTTAAGAAAC 2408
QY 841 TGAATTTAAGTTTCAATGCTTC 863
| | | | |
DB 2409 TGAATTTAAGTTTCAATGCTTC 2431

RESULT 2
BX337228/c 1018 bp mRNA linear EST 08-APR-2004
LOCUS BX337228 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1039YG21.3-PRIME, mRNA sequence.
ACCESSION BX337228
VERSION BX337228.2 GI:46283446
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
```

```
JOURNAL
COMMENT
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30346952.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteux, CP 5705 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0D1039AD1JN1P1c=742.r.
Location/Qualifiers
1..1018
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/cisue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 83.3%; Score 741.8; DB 5; Length 1018;
Best Local Similarity 93.4%; Pred. No. 3,4e-210;
Matches 813; Conservative 29; Mismatches 19; Indels 9; Gaps 7;

QY 2 AAGCTGTAGAGGCTTCTCTTCCATCTGCTGAGACAGTAAAGCTCAGTTTCAATAG 61
| | | | |
DB 869 AAGCTGTAGAGGCTTCTCTTCCATCTGCTGAGACAGTAAAGCTCAGTTTCAATAG 810
QY 62 CATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGGCCCCC-ATCTCGGGGGAATGTC 120
| | | | |
DB 809 CATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGGCCCCC-ATCTCGGGGGAATGTC 750
QY 121 TGAAGCAATTTTGGTTA--CCTCAATGAGGAGTGGAGAGATACAGTGTACTTACCA 178
| | | | |
DB 749 TGAAGCAATTTTGGTTA--CCTCAATGAGGAGTGGAGAGATACAGTGTACTTACCA 690
QY 179 ACTAGTGATAAAGGCCAGGAGTGTCTCAACCTCTACATGACAGGAGCTCTCC 238
| | | | |
DB 689 ACTAGTGATAAAGGCCAGGAGTGTCTCAACCTCTACATGACAGGAGCTCTCC 631
QY 239 CATTCACAATACCCCAATCCGAAGTGTCAACTGTGTGACAGTAAAGAAACCTGTGTTGA 298
| | | | |
DB 630 CATTCACAATACCCCAATCCGAAGTGTCAACTGTGTGACAGTAAAGAAACCTGTGTTGA 571
QY 630 CATTCACAATACCCCAATCCGAAGTGTCAACTGTGTGACAGTAAAGAAACCTGTGTTGA 571
| | | | |
DB 239 CATTCACAATACCCCAATCCGAAGTGTCAACTGTGTGACAGTAAAGAAACCTGTGTTGA 358
QY 570 GTAGAAAAGGGCTTGAAGAGGGAGRCACAAATCTGTGCTTCTTCTTCAATAGTCA 511
| | | | |
DB 359 GTAGAAAAGGGCTTGAAGAGGGAGRCACAAATCTGTGCTTCTTCTTCAATAGTCA 418
QY 510 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 451
| | | | |
DB 419 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 475
QY 450 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 391
| | | | |
DB 476 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 390 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 331
| | | | |
DB 534 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 593
QY 330 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 271
| | | | |
DB 594 TTGGCAATTAAGCAATTCGTCTTCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 653
```

```

FEATURES
    source
        Location/Qualifiers
            1..737
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="UI-CF-FNO-aeY-b-10-0-ui"
                /issue_type="Human Lung Epithelial cells"
                /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                /clone_lib="UI-CF-FNO"
                /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
                modified polylinker; Site_1: Ecor I; Site_2: Not I;
                UI-CF-FNO is a subtracted cDNA library derived from two
                normalized Human lung epithelial cell libraries (EN1 and
                DU1) The library was subtracted according to according to
                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                1996. For additional information, contact:

```

QY	170	CTACTACCACTGATGGATTTAAAGGCCAGGGATGCTGTCAACCTCCACATGACATGACAGGG	223
Db	737	CTACTACCAACTGAT-GATTAAGGCCAGGGATGCTGTCAACCTCCTACCATGTACAC-GG	680
QY	230	ACGCTCTCCCATTTACAACTACCCCAATCCGAAGTGTCAACTGTGTCAAGACCTTAAGAAACC	289
Db	679	ACGCTCTCCCATTTACAACTACCCCAATCCGAAGTGTCAACTGTGTCAAGACCTTAAGAAACC	620
QY	290	TGTTTTGAGTAGAAAGAGCCCTGGAAAGAGGGAGCCAAACAATCTGTCTGTCTCTCA	349
Db	619	TGTTTTGAGTAGAAAGAGCCCTGGAAAGAGGGAGCCAAACAATCTGTCTGTCTCTCA	560
QY	350	CATTAGCTATTGGGAATTAAGCAATTCGTCTCTTTGGCTGTGCTGTGACACAGAGAGCC	409
Db	559	CATTAGCTATTGGGAATTAAGCAATTCGTCTCTTTGGCTGTGCTGTGACACAGAGAGCC	500
QY	410	AGAACTCTATCGGGACACAGGATTAACATCTCTCAGTAACAGAGTTGACAAGGCTTAAGG	469
Db	499	AGAACTCTATCGGGACACAGGATTAACATCTCTCAGTAACAGAGTTGACAAGGCTTAAGG	440
QY	470	GAATGCTGATGGGATTTATCTTCAGCTTGTGAGCTTCTTAAGTTCTTTCCCTTCATTC	529
Db	439	GAATGCTGATGGGATTTATCTTCAGCTTGTGAGCTTCTTAAGTTCTTTCCCTTCATTC	380
QY	530	TACCTTCGAAGCCCAAGTCTCTGTAAAGAAATGCCCTGAGTCTTAGCTCAAGTTTCTTAAT	589
Db	379	TACCTTCGAAGCCCAAGTCTCTGTAAAGAAATGCCCTGAGTCTTAGCTCAAGTTTCTTAAT	320
QY	590	CTGAATTTAGATCTCCGAGCCCTCTCCGGCCACAAATTCAAATTAAGGCAACAAACATATA	649
Db	319	CTGAATTTAGATCTCCGAGCCCTCTCCGGCCACAAATTCAAATTAAGGCAACAAACATATA	260
QY	650	CCTTCATGAAGACACACAGACTTTTGAAGAAGACACATGCTGTAATTTGAGGC	709
Db	259	CCTTCATGAAGACACACAGACTTTTGAAGAAGACACATGCTGTAATTTGAGGC	200
QY	710	CTTGAGGATGAAGCTTTGAAGAAAGAAATCTTTGTTTCAGCCCCCTTCCCACTC	769
Db	199	CTTGAGGATGAAGCTTTGAAGAAAGAAATCTTTGTTTCAGCCCCCTTCCCACTC	140
QY	770	TTGATGTGTAAACCACTGCTTCTGTGACCTTGGAGCAAGGTGACGTATTAACATGTG	829
Db	139	TTGATGTGTAAACCACTGCTTCTGTGACCTTGGAGCAAGGTGACGTATTAACATGTG	80
QY	830	TTATAGAAACGTATTTTAAAGTTCTGATCGTTCAAGAGATGATTTAAATATACATTTCC	889
Db	79	TTATAGAAACGTATTTTAAAGTTCTGATCGTTCAAGAGATGATTTAAATATATACATTTCC	20
QY	890	T 890	
Db	19	T 19	

RESULT 4	
LOCUS	BU632767/c
DEFINITION	BU632767
VERSION	UI-H-FEI1.bdy-k-03-0-UI.s1 NC1_CGAP FEI Homo sapiens cDNA clone UI-H-FEI1.bdy-k-03-0-UI 3' , mRNA sequence.
KEYWORDS	EST. BU632767.1 GI:23300022
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 700)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 623-700, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..700
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FBI-bdy-K-03-0-UI"
/cissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10b (Life Technologies)"
/clone_lib="NCI CCGAP FBI"
/note="Organ: Chondrosarcoma; Vector: pT773-Pac
(pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CCGAP FBI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCTACGGAC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG TISSUE=Human grade 2 chondrosarcoma cell line pool
TAG_LIB=UI-H-FBI
TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match 74.8%; Score 666; DB 5; Length 700;
Best Local Similarity 99.9%; Pred. No. 1.5e-187;
Matches 677; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
213 TCCTACCATGTACAGGAGCGTCTCCCATTAACCACTCCGAAGTGTCACTGTG 272
Db TCTTACCATGTACA-GGAGCGTCTCCCATTAACCACTCCGAAGTGTCACTGTG 642
273 TCAGGACTAAGAAACCTGTGTTGAGTACAAAAGGCGCTGGAAAAGGGGACCAACA 332
Db 641 TCAGGACTAAGAAACCTGTGTTGAGTACAAAAGGCGCTGGAAAAGGGGACCAACA 582
333 ATCTGCTGCTTCTTCACTTACTGATGGCAATAGAGCATCTGCTCTTGGGCTGCG 392
Db 581 ATCTGCTGCTTCTTCACTTACTGATGGCAATAGAGCATCTGCTCTTGGGCTGCG 522
393 CCTCAGACAGAGAGCCAGAACTCTATCGGGACACAGATAACATCTCTCAGTGAACAG 452
Db 521 CCTCAGACAGAGAGCCAGAACTCTATCGGGACACAGATAACATCTCTCAGTGAACAG 462
453 GTTGAACAAGCCCTATGGGAAATGCTGATGGGATTATCTTCAGCTTGTGAGCTTTAAG 512
Db 461 GTTGAACAAGCCCTATGGGAAATGCTGATGGGATTATCTTCAGCTTGTGAGCTTTAAG 402

513 TTTCTTCCCTCATTTCTACCGTCGACCAAGTTCTGTAAAGAAATGCTGAGTTCTA 572
Db 401 TTTCTTCCCTCATTTCTACCGTCGACCAAGTTCTGTAAAGAAATGCTGAGTTCTA 342
573 GCTCAGGTTTCTTACTGTAATTTGATCTTCAGACCCCTTCCTGGCCCAATTCAATT 632
Db 341 GCTCAGGTTTCTTACTGTAATTTGATCTTCAGACCCCTTCCTGGCCCAATTCAATT 282
633 AAGGACAAACATATTACTCTTCATGAAGACACACAGACTTTTGAAGCAAGCAATG 692
Db 281 AAGGACAAACATATTACTCTTCATGAAGACACACAGACTTTTGAAGCAAGCAATG 222
693 ACTGCTGAATTTAGAGCCCTTGAGAAATGAGCTTTGAAGAAAGAAATATTGTTTCCA 752
Db 221 ACTGCTGAATTTAGAGCCCTTGAGAAATGAGCTTTGAAGAAAGAAATATTGTTTCCA 162
753 GCCCCTTCCACACATCTTCACTGTTTAAACCACTGCTTCTTGACCTTGAGACCAAGT 812
Db 161 GCCCCTTCCACACATCTTCACTGTTTAAACCACTGCTTCTTGAGCCCTTGAGACCAAGT 102
813 GACTGATTTACATGTTGTTATGAAACCTGATTTTGAAGTTCTGATCGTTCAAGAAATG 872
Db 101 GACTGATTTACATGTTGTTATGAAACCTGATTTTGAAGTTCTGATCGTTCAAGAAATG 42
873 ATTAATATATACATTTCT 890
Db 41 ATTAATATATACATTTCT 24

RESULT 5
CB241729/c 691 bp mRNA linear EST 12-FEB-2003
LOCUS
DEFINITION
UI-CF-FN0-afz-p-01-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
VERSION
CB241729.1 GI:28363373
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 691)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL
MEDLINE
PUBMED
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.researchgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FN0-afz-p-01-0-UI"

/tissue type="Human Lung Epithelial cells"
 /lab host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: Sc0r 1; Site_2: Not 1;
 UI-CF-FNO is a subcloned cDNA library derived from two
 normalized Human lung epithelial cell libraries (EN1 and
 DU1). The library was subcloned according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_LIB=UI-CF-FNO
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 74.4%; Score 663; DB 6; Length 691;
 Best Local Similarity 100.0%; Pred. No. 1.1e-186;
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

228 GGAAGCTCTCCCATTTACACTACCAATCCGAAGTGTCACTGTGTAGAGACTTAAGAAC 287
 681 GGAAGCTCTCCCATTTACACTACCAATCCGAAGTGTCACTGTGTAGAGACTTAAGAAC 622
 288 CCGATTTTGAAGAAAAGGCTGTGAAGAGGAGGCAACAATCTGTCTGCTTCT 347
 621 CCGATTTTGAAGAAAAGGCTGTGAAGAGGAGGCAACAATCTGTCTGCTTCT 562
 348 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTCTGCTCTGACACAGAGAG 407
 561 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTCTGCTCTGACACAGAGAG 502
 408 CCGAACTCTATGGGACCAAGATTAACATCTCTGATGAACAGAGTTGCAAGGCTTAT 467
 501 CCGAACTCTATGGGACCAAGATTAACATCTCTGATGAACAGAGTTGCAAGGCTTAT 442
 468 GGAAGTGTCTGATGGATTAATCTGAGCTTGTGAGCTTCTAAGTTCTTCCCTTCAT 527
 441 GGAAGTGTCTGATGGATTAATCTGAGCTTGTGAGCTTCTAAGTTCTTCCCTTCAT 382
 528 TCTACCTGTGCAAGCAAGTTCTGTAAAGAAATGCTGATGTTCTGAGTCTGAGTTTCTTA 587
 381 TCTACCTGTGCAAGCAAGTTCTGTAAAGAAATGCTGATGTTCTGAGTCTGAGTTTCTTA 322
 588 CTGTGAATTTAGTCTTCCAGACCTTCTGTGCAATTAATTAAGGCAACAACATA 647
 321 CTGTGAATTTAGTCTTCCAGACCTTCTGTGCAATTAATTAAGGCAACAACATA 262
 648 TACCTTCATGAAGACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTTAG 707
 261 TACCTTCATGAAGACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATTTAG 202
 708 GCCTTGAAGAAAGCTTTGAAGAAAGAAATATCTTTTCCAGCCCCCTTCCACAC 767
 201 GCCTTGAAGAAAGCTTTGAAGAAAGAAATATCTTTTCCAGCCCCCTTCCACAC 142
 768 TCTTCAATGTGTAAACCACTGCTTCTGACCTTGAAGCAAGGATGATTAATTAAGT 827
 141 TCTTCAATGTGTAAACCACTGCTTCTGACCTTGAAGCAAGGATGATTAATTAAGT 82
 828 TGTATAGAAAGCTGATTTAGAGTTCTGATGCTTGAAGCAAGGATTAATTAATTAAGT 887
 81 TGTATAGAAAGCTGATTTAGAGTTCTGATGCTTGAAGCAAGGATTAATTAATTAAGT 22

QY 888 CCT 890
 DB 21 CCT 19

RESULT 6
 CA314865/c 691 bp mRNA linear EST 04-NOV-2002
 LOCUS CA314865/ 691 bp mRNA linear EST 04-NOV-2002
 DEFINITION UI-CF-FNO-afi-e-12-0-UI.81 UI-CF-FNO Homo sapiens cDNA clone

ACCESSION
 CA314865
 VERSION
 CA314865.1
 KEYWORDS
 EST
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 691)
 TITLE
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL
 MEDLINE
 PUBMED
 97044477
 8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 DNA Distribution: Researchers may obtain clones from Research
 Genetics (www.reagen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 618-691. >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 PolyA=yes.

FEATURES

source

Location/Qualifiers
 1. 691
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-afi-e-12-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: Sc0r 1; Site_2: Not 1;
 UI-CF-FNO is a subcloned cDNA library derived from two
 normalized Human lung epithelial cell libraries (EN1 and
 DU1). The library was subcloned according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_LIB=UI-CF-FNO
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 74.4%; Score 662; DB 6; Length 691;
 Best Local Similarity 99.8%; Pred. No. 2.3e-186;
 Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

228 GGAAGCTCTCCCATTTACACTACCAATCCGAAGTGTCACTGTGTAGAGACTTAAGAAC 287
 681 GGAAGCTCTCCCATTTACACTACCAATCCGAAGTGTCACTGTGTAGAGACTTAAGAAC 622
 288 CCGATTTTGAAGAAAAGGCTGTGAAGAGGAGGCAACAATCTGTCTGCTTCT 347
 621 CCGATTTTGAAGAAAAGGCTGTGAAGAGGAGGCAACAATCTGTCTGCTTCT 562
 348 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTCTGCTCTGACACAGAG 407
 561 CACATTAGTCATTGGCAATTAACATCTCTCTTGTGCTGCTCTGCTCTGACACAGAG 502
 408 CCGAACTCTATGGGACCAAGATTAACATCTCTGATGAACAGAGTTGCAAGGCTTAT 467

Db 501 CCAGAACTCTATCGGGCACCAGGATTAACCTCTCTCAGTGAAGAGATTGACAAAGCCTAT 442

Qy 468 GGGAAATGCTGATGGGATTTATCTTCTAGCTGTGTGAGCTTCTTAAGTTCTTCCCTTCAT 527

Db 441 GGGAAATGCTGATGGGATTTATCTTCTAGCTGTGTGAGCTTCTTCCCTTCAT 382

Qy 528 TCTACCTGTCAGAACCCAGATTCTGTAGAGAAATGCTGAGTTCTAGCTGAGTTTCTTA 587

Db 381 TCTACCTGTCAGAACCCAGATTCTGTAGAGAAATGCTGAGTTCTAGCTGAGTTTCTTA 322

Qy 588 CTCTGAATTTAGATCTCCAGACCCCTTCTGGCCCAATTCATTAATTAAGCAACAACATA 647

Db 321 CTCTGAATTTAGATCTCCAGACCCCTTCTGGCCCAATTCATTAATTAAGCAACAACATA 262

Qy 648 TACCTTCATGAGACACACAGACTTTTGAAGAAGCAAGATGACTCTTGAATTTAG 707

Db 261 TACCTTCATGAGACACACAGACTTTTGAAGAAGCAAGATGACTCTTGAATTTAG 202

Qy 708 GCCTTGAGAGATGAGACTTTGAGAGAAAGAAATACTTTGTTCCAGCCCTTCCACAC 767

Db 201 GCCTTGAGAGATGAGACTTTGAGAGAAAGAAATACTTTGTTCCAGCCCTTCCACAC 142

Qy 768 TCTTCATGTTTACCACTGCTCTCTGACCTTGGAGCCAGGTGACTGTATATACAT 827

Db 141 TCTTCATGTTTACCACTGCTCTCTGACCTTGGAGCCAGGTGACTGTATATACAT 82

Qy 828 TGTATAGAAAATGATTTTAAAGTCTGATCGTTCAAGAGATGATTAATATACAT 887

Db 81 TGTATAGAAAATGATTTTAAAGTCTGATCGTTCAAGAGATGATTAATATACAT 22

Qy 888 CCT 890

Db 21 CCT 19

RESULT 7
BU608696/c 691 bp mRNA linear EST 21-FEB-2003
LOCUS BU608696
DEFINITION UI-CF-FNO-aeg-c-07-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
VERSION UI-CF-FNO-aeg-c-07-0-UI 3', mRNA sequence.
KEYWORDS BU608696.1 GI:23274911
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 691)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 618-691. >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers

source 1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-aeg-c-07-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1ib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human Lung epithelial cell libraries (BN1 and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial cells Tissue nos 359-368
TAG_LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 74.0%; Score 658.2; DB 5; Length 691;

Best Local Similarity 99.5%; Pred. No. 3,1e-185; Indels 0; Gaps 0;

Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 228 GGACGCTCTCCCATTAACAATCAATCCAGATGTCATCTGTGTCAGACTTAAGAAAC 287

Db 681 GGAAGCTCTCCCATTAACAATCAATCCAGATGTCATCTGTGTCAGACTTAAGAAAC 622

Qy 288 CTTGCTTTGAGTGAAGAAAGGGCTGGAAGAGGGGAGCCAAACAATCTGTCTTCT 347

Db 621 CTTGCTTTGAGTGAAGAAAGGGCTGGAAGAGGGGAGCCAAACAATCTGTCTTCT 562

Qy 348 CACATTAGCATTTGGCAATAAAGCATTCCTCTTTGGCTGCTGCTCAGACAGAGAG 407

Db 561 CACATTAGCATTTGGCAATAAAGCATTCCTCTTTGGCTGCTGCTCAGACAGAGAG 502

Qy 408 CCAGAACTCTATCGGGCACCAGATTAACATCTCTGATGAACAGAGTTGACAGGCTAT 467

Db 501 CCAGAACTCTATCGGGCACCAGATTAACATCTCTGATGAACAGAGTTGACAGGCTAT 442

Qy 468 GGGAAATGCTGATGGGATTTATCTTCACTGTTTGAAGCTTCTTAAGTTTCTTCCCTTCAT 527

Db 441 GGGAAATGCTGATGGGATTTATCTTCACTGTTTGAAGCTTCTTAAGTTTCTTCCCTTCAT 382

Qy 528 TCTACCTGTCAGAACCCAGATTCTGTAGAGAAATGCTGAGTTCTAGCTGAGTTTCTTA 587

Db 381 TCTACCTGTCAGAACCCAGATTCTGTAGAGAAATGCTGAGTTCTAGCTGAGTTTCTTA 322

Qy 588 CTCTGAATTTAGATCTCCAGACCCCTTCTGGCCCAATTCATTAATTAAGCAACAACATA 647

Db 321 CTCTGAATTTAGATCTCCAGACCCCTTCTGGCCCAATTCATTAATTAAGCAACAACATA 262

Qy 648 TACCTTCATGAGACACACAGACTTTTGAAGAAGCAAGATGACTCTTGAATTTAG 707

Db 261 TACCTTCATGAGACACACAGACTTTTGAAGAAGCAAGATGACTCTTGAATTTAG 202

Qy 708 GCCTTGAGAGATGAGACTTTTGAAGAAGAAATACTTTGTTCCAGCCCTTCCACAC 767

Db 201 GCCTTGAGAGATGAGACTTTTGAAGAAGAAATACTTTGTTCCAGCCCTTCCACAC 142

Qy 768 TCTTCATGTTTACCACTGCTCTCTGACCTTGGAGCCAGGTGACTGTATATACAT 827

Db 141 TCTTCATGTTTACCACTGCTCTCTGACCTTGGAGCCAGGTGACTGTATATACAT 82

Qy 828 TGTATAGAAAATGATTTTAAAGTCTGATCGTTCAAGAGATGATTAATATACAT 887

Db 81 TGTATAGAAAATGATTTTAAAGTCTGATCGTTCAAGAGATGATTAATATACAT 22

Qy 888 CCT 890

Db 21 CCT 19

RESULT 8
CB852239/c

LOCUS CB852239 660 bp mRNA linear EST 22-APR-2003

DEFINITION UI-CF-FNO-aff-m-01-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone

ACCESSION CB852239

VERSION UI-CF-FNO-aff-m-01-0-UI 3', mRNA sequence.

KEYWORDS CB852239.1 GI:30047206

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 660)

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul.mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.researchgen.com) or from Open Biosystems (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

1..660

Location/Qualifiers

1..660

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-FNO-aff-m-01-0-UI"

/tissue_type="Human Lung Epithelial cells"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_1lb="UI-CF-FNO"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Score 1; Site 2: Not 1; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (BN1 and DN1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu

TAG_SEQ=None found"

ORIGIN

Query Match 71.7%; Score 637.8; DB 6; Length 660;

Best Local Similarity 99.5%; Pred. No. 3.9e-179;

Matches 639; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

249 ACCCAATCCGAAGTCACTGTCAGACTAGAAAGGCTGTTGAGTAGAAAGG 308

660 ACCCAATCCGAAGTCACTGTCAGACTAGAAAGGCTGTTGAGTAGAAAGG 601

309 GCCTGAAAGAGGGAGCCAAATCTGCTCTTCTTCACTTAGTCATTGGCAATA 368

600 GCCTGAAAGAGGGAGCCAAATCTGCTCTTCTTCACTTAGTCATTGGCAATA 541

369 AGATCTCTCTCTTTGGCTGCTGCTCAGACACAGAGAGCCAAATCTTAGTGGCAGCA 428

540 AGATCTCTCTCTTTGGCTGCTGCTCAGACACAGAGAGCCAAATCTTAGTGGCAGCA 481

429 GGATAATCTCTCACTGTAACAGAGTTGACAAAGGCTATGGAAATGCTGATGGATTA 488

Db

480 GGATAATCTCTCACTGTAACAGAGTTGACAAAGGCTATGGAAATGCTGATGGATTA 421

Qy

489 TCTTCAGCTGTTGAGCTTCAAGTTCTTCCCTTCATTCAACCTGCAGCGCAAGTTC 548

Db

420 TCTTCAGCTGTTGAGCTTCAAGTTCTTCCCTTCATTCAACCTGCAGCGCAAGTTC 361

Qy

549 TGTAAAGAAATCCGAGTTCAGCTCAGGTTTCTTCACTGTAATTAAGATTCACAGA 608

Db

360 TGTAAAGAAATCCGAGTTCAGCTCAGGTTTCTTCACTGTAATTAAGATTCACAGA 301

Qy

609 CCTTCCTGGCCCAATTCATTAAGCAACAATATACCTTCATGAGACACACAC 668

Db

300 CCTTCCTGGCCCAATTCATTAAGCAACAATATACCTTCATGAGACACACAC 241

Qy

669 AGACTTTTGAAGCAAGCAATGACTGTTGAATTAAGGCTTGAAGAAATGAAGCTTGG 728

Db

240 AGACTTTTGAAGCAAGCAATGACTGTTGAATTAAGGCTTGAAGAAATGAAGCTTGG 181

Qy

729 AAGGAAAGAAATCTTGTGTTCCAGGCCCTTCCACACTCTTCATGTTAACCAGCTGC 788

Db

180 AAGGAAAGAAATCTTGTGTTCCAGGCCCTTCCACACTCTTCATGTTAACCAGCTGC 121

Qy

789 CTTCCTGACCTTGAGCCACGCTGACTGATTAACATGTTGTTAAGAAATGATTTTA 848

Db

120 CTTCCTGACCTTGAGCCACGCTGACTGATTAACATGTTGTTAAGAAATGATTTTA 61

Qy

849 GAGTCTGATGTTCAAGAGATGATTAATATACATTTCTT 890

Db

60 GAGTCTGATGTTCAAGAGATGATTAATATACATTTCTT 19

RESULT 9
CA426580/c

LOCUS CA426580 660 bp mRNA linear EST 07-NOV-2002

DEFINITION UI-H-FEI-beh-p-14-0-UI.s1 NCI CGAP FEI Homo sapiens cDNA clone

ACCESSION CA426580

VERSION UI-H-FEI-beh-p-14-0-UI 3', mRNA sequence.

KEYWORDS CA426580.1 GI:24789306

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 660)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapdb-r@mail.nih.gov

Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

1..660

Location/Qualifiers

1..660

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FEI-beh-p-14-0-UI"

/tissue_type="Cell lines"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_1lb="NCI CGAP FEI"

/note="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Score 1; Site 2: Not 1; NCI CGAP FEI is a normalized cDNA library derived from a pool of mRNA obtained from 3 cell lines

from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTR73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGTACGAC. The cell lines were provided by Dr James Martin from the University of Iowa.

TAG TISSUE=Human Grade 2 chondrosarcoma cell line pool
TAG LIB=UI-H-FBI
TAG_SEQ=CGCTACGACG

ORIGIN

Query Match 71.3%; Score 634.4; DB 6; Length 660;
Best Local Similarity 99.7%; Pred. No. 4.1e-178;
Matches 635; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

254 ATCCGAAGTGAACACTGTCAGGACTAAGAAACCTGTTTGTAGTAAAGGCGCTG 313
|||||
660 ATCCGAAGTGAACACTGTCAGGACTAAGAAACCTGTTTGTAGTAAAGGCGCTG 601
|||||
314 GAAAGAGGAGGAGCAACAATCTGTCCTCTCACTTATGTCATTTGCAATATAGCAT 373
600 GAAAGAGGAGGAGCAACAATCTGTCCTCTCACTTATGTCATTTGCAATATAGCAT 541
|||||
374 TCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAACTTATCGGCGACAGGATA 433
540 TCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAACTTATCGGCGACAGGATA 481
|||||
434 ACATCTCTAGTGAACAGAGTTGACAAGGCTATGGGAATGCTGATGGATATATCTTC 493
480 ACATCTCTAGTGAACAGAGTTGACAAGGCTATGGGAATGCTGATGGATATATCTTC 421
|||||
494 AGCTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTACCTGCAAGCCAGTTCTGTA 553
420 AGCTTGTGAGCTTCTTAAGTTCTTCCCTTCACTTACCTGCAAGCCAGTTCTGTA 361
|||||
554 GAGAAATGCTGAGTCTTACGCTGAGTTTCTTACTCTGAATTTAGATCTCCAGACCTT 613
360 GAGAAATGCTGAGTCTTACGCTGAGTTTCTTACTCTGAATTTAGATCTCCAGACCTT 301
|||||
614 CCGGCGCACAATTAAGGCAACAATATATCTTCCATGAGGACACACAGACT 673
300 CCGGCGCACAATTAAGGCAACAATATATCTTCCATGAGGACACACAGACT 241
|||||
674 TTGGAAGCAAGCAATGACTGCTTGAATTGAGGCTTGAAGATGAGCTTTGAAGA 733
240 TTGGAAGCAAGCAATGACTGCTTGAATTGAGGCTTGAAGATGAGCTTTGAAGA 181
|||||
734 AAAAGATACTTGTGTCCAGCCCTTCCCACTCTTCAATGTTGTTAAACACGCTTCC 793
180 AAAAGATACTTGTGTTCAGCCCTTCCCACTCTTCAATGTTGTTAAACACGCTTCC 121
|||||
794 TGAGCTTGAGAGCAGGAGTGAATGATGATGTTTATAGAACTGATTTTAAAGTT 853
120 TGAGCTTGAGAGCAGGAGTGAATGATGATGTTTATAGAACTGATTTTAAAGTT 61
|||||
854 CTGATCGTTCAAGAGATGATTAATATATCACTTCT 890
60 CTGATCGTTCAAGAGATGATTAATATATCACTTCT 24
|||||

RESULT 10
CA312678/c 679 bp mRNA linear EST 04-NOV-2002
LOCUS CA312678 UI-CF-FNO-m-11-0-UI.s1 UI-FNO Homo sapiens cDNA clone
DEFINITION UI-CF-FNO-af1-m-11-0-UI 3', mRNA sequence.
ACCESSION CA312678
VERSION CA312678.1 GI:24530776

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 679)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@iowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source

Location/Qualifiers
1..679
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-af1-m-11-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="RDH108 (Life Technologies) (Ti phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pTR73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1
and DUI) The library was subtracted according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG TISSUE=Human Lung Epithelial Cell lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 71.0%; Score 632.2; DB 6; Length 679;
Best Local Similarity 97.3%; Pred. No. 1.9e-177;
Matches 643; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

230 ACGTCTCCCATTAACCTACCAATCCGAAGTCACTGTGACAGACTAAGAAACC 289
679 ACGTCTCCCATTAACCAATCCGAAGTCACTGTGACAGACTAAGAAACC 620
|||||
290 TGGTTTGAAGTGAAGAGGCTGGAAGAGGAGCAACAATCTGCTGCTCTCA 349
619 TGGTTTGAAGTGAAGAGGCTGGAAGAGGAGCAACAATCTGCTGCTCTCA 560
|||||
350 CATTAATGCTGGCAATTAAGATCTGCTTGTGGCTGCTGCTCAGACAGAGAGC 409
559 CATTAATGCTGGCAATTAAGATCTGCTTGTGGCTGCTGCTCAGACAGAGAGC 500
|||||
410 AGAAGCTATTCGGGAGCAGATTAACATCTCTAGTGAACAGAGTTGAACAGGCTATG 469
499 AGAAGCTATTCGGGAGCAGATTAACATATACATGTAACAGAGTTGAACAGGCTATG 440
|||||
470 GAAATGCTGATGAGATTAATCTTCAAGCTTGTGAGCTTCAAGTTCTTCCCTCATTC 529
|||||

Db 439 GAAATGCGTGAATGATTTATCTTCAGCTGTGTGAGCTTATAGTTCTTCCCTTCATTC 380
QY 530 TACCCGCAAGCAAGTTCGTAAAGAAATGCTGTTCTAGTCTAGGTTTTCTACT 589
Db 379 TACCCGCAAGCAAGTTCGTAAAGAAATGCTGTTCTAGTCTAGGTTTTCTACT 320
QY 590 CTGAATTTAGATCTCCAGACCCCTTCTGCGCACATTAATTAAGGCAACAAATATA 649
Db 319 CTGAATTTAGATCTCCAGACCCCTTCTGCGCACATTAATTAAGGCAACAAATATA 260
QY 650 CTTTCATGAAGCAACACAGACTTTTGAAGAGAGACATGACTGCTGAATGAGGC 709
Db 259 CTTTCATGAAGCAACACAGACTTTTGAAGAGAGACATGACTGCTGAATGAGGC 200
QY 710 CTGAGGAATGAAGCTTTGAAGAAATGATCTTTTCCAGCCCTTCCACACTC 769
Db 199 CTGAGGAATGAAGCTTTGAAGAAATGATCTTTTCCAGCCCTTCCACACTC 140
QY 770 TTGATGTGTTAACCACTGCTTCTGAGACCTTGAGCGAGTGAATTAATGATTTG 829
Db 139 TTGATGTGTTAACCACTGCTTCTGAGACCTTGAGCGAGTGAATTAATGATTTG 80
QY 830 TTATAGAAAATGATTTTGAAGTTTGATGCTTCAAGAGATGATTAATTAATTAATTTCC 889
Db 79 TTATAGAAAATGATTTTGAAGTTTGATGCTTCAAGAGATGATTAATTAATTAATTTCC 20
QY 890 T 890
Db 19 T 19

RESULT 11
CAS03188/c 594 bp mRNA linear EST 14-NOV-2002

DEFINITION UI-CE-FNO-aFP-D-10-0-UI .s1 UI-CE-FNO Homo sapiens cDNA clone
ACCESSION CAS03188
VERSION CAS03188.1 GI:24994142
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 594)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul.mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source 1..594
Location/Qualifiers
1..594
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CE-FNO-aFP-D-10-0-UI"
/issue_type="Human Lung Epithelial cells"

/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-CE-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
UI-CE-FNO is a subcloned cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1). The library was subcloned according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CE-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN
Query Match 63.8%; Score 568; DB 6; Length 594;
Best local Similarity 99.1%; Pred. No. 3e-158;
Matches 571; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 315 AAGAGGGGAGCCAAATCTGTCCTTCCATTAAGTATGCAAAATTAAGCATT 374
Db 594 AAGAGGGGAGCCAAATCTGTCCTTCCATTAAGTATGCAAAATTAAGCATT 535
QY 375 CTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAACTATGCGGACAGATTA 434
Db 534 CTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAACTATGCGGACAGATTA 475
QY 435 CATCTCTCAGTGAACAGAGTTGCAAGGCTTATGGAAATGCTGATGATTTCTCA 494
Db 474 CATCTCTCAGTGAACAGAGTTGCAAGGCTTATGGAAATGCTGATGATTTCTCA 415
QY 495 GCTTGTGAGCTTGAAGTTCTTCCCTTCAATTAAGTATGCAAAATTAAGCATT 554
Db 414 GCTTGTGAGCTTGAAGTTCTTCCCTTCAATTAAGTATGCAAAATTAAGCATT 355
QY 555 AGAATGCTGAGTTTACCTCAGTTTCTTACCTGATTAATTAAGTATGCAAAATTAAGCATT 614
Db 354 AGAATGCTGAGTTTACCTCAGTTTCTTACCTGATTAATTAAGTATGCAAAATTAAGCATT 295
QY 615 CTGGCCAACTTCAAAATTAAGGCAACAAATTAAGTATGCAAAATTAAGCATT 674
Db 294 CTGGCCAACTTCAAAATTAAGGCAACAAATTAAGTATGCAAAATTAAGCATT 235
QY 675 TTGAAGCAAGCAATGATGCTGTTGAATTAAGGCTTGAAGTATTAAGTATTAAGGAA 734
Db 234 TTGAAGCAAGCAATGATGCTGTTGAATTAAGGCTTGAAGTATTAAGTATTAAGGAA 175
QY 735 AAGATATCTTTGTTTCCAGCCCTTCCCACTCTTCAATGTTTAACACTGCTTCT 794
Db 174 AAGATATCTTTGTTTCCAGCCCTTCCCACTCTTCAATGTTTAACACTGCTTCT 115
QY 795 GGAAGCTTGAAGCCAGGTAATGATTAATTAAGTATTAAGTATTAAGTATTAAGGTT 854
Db 114 GGAAGCTTGAAGCCAGGTAATGATTAATTAAGTATTAAGTATTAAGTATTAAGGTT 55
QY 855 TGATGCTTGAAGGATTAATTAATTAAGTATTAAGTATTAAGTATTAAGGTT 890
Db 54 TGATGCTTGAAGGATTAATTAATTAAGTATTAAGTATTAAGTATTAAGGTT 19

RESULT 12
A1684143 556 bp mRNA linear EST 16-DEC-1999

DEFINITION Lx79g04.x1 NCI CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2275830 3',
mRNA sequence.
ACCESSION A1684143
VERSION A1684143.1 GI:4895437
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 556)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

ORIGIN

Query Match	62.0%;	Score 552;	DB 1;	Length 556;
Best Local Similarity	100.0%;	Pred. No. 1.8e-153;		
Matches 552;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	339	TTGCTTCTCCACATTAAGCATTTGGGAAATTAAGCATTTGTCCTTTGGCGTGGCTCGAG	398
Db	556	CTGCTTCTCCACATTAGTATTGGGCAAAATTAAGCATTTGTCCTTTGGCGTGGCTCGAG	497
Qy	399	CACAGAGAGCCGGAACCTCATCGGGGACCGAGATTAACATCTCTAGTGAACAGAGTTGAC	458
Db	496	CACAGAGAGCCGGAACCTCATCGGGGACCGAGATTAACATCTCTAGTGAACAGAGTTGAC	437
Qy	459	AAGGCTTAGGGAAAATGCCGTAGTGGATTAATCTCAGCTTGTGAGCTTTCTAAGTTTCTT	518
Db	436	AAGGCTTAGGGAAAATGCCGTAGTGGATTAATCTCAGCTTGTGAGCTTTCTAAGTTTCTT	377
Qy	519	TCCCTTCATTCTAACCTGCGAAGCCAAAGTTCTGTAAAGAGAAATGCCAGTTCCTAGCTCAG	578
Db	376	TCCCTTCATTCTAACCTGCGAAGCCAAAGTTCTGTAAAGAGAAATGCCAGTTCCTAGCTCAG	317
Qy	579	GTTTTCTTACTCGTAATTAGATTCCTCAGACCCCTCTGGGCCCAATTCGAATTAAGGCA	638
Db	316	GTTTTCTTACTCGTAATTAGATTCCTCAGACCCCTCTGGGCCCAATTCGAATTAAGGCA	257
Qy	639	ACAAACATATACCTTCCATGGAAGCACACAGACTTTGAAAGCAAGCAATGACTGCT	698
Db	256	ACAAACATATACCTTCCATGGAAGCACACAGACTTTGAAAGCAAGCAATGACTGCT	197
Qy	699	TGAATTGAGGCCCTTGAAGATGAAGAGCTTTGAAAGAAAAGATATCTTTGTTCCAGCCCC	758
Db	196	TGAATTGAGGCCCTTGAAGATGAAGAGCTTTGAAAGAAAAGATATCTTTGTTCCAGCCCC	137
Qy	759	TTCCCACTCTTCATGTGTAAACCACTGCTTCTGGAACCTTGGAGCCACGGTGAAGTGT	818
Db	136	TTCCCACTCTTCATGTGTAAACCACTGCTTCTGGAACCTTGGAGCCACGGTGAAGTGT	77
Qy	819	ATTACATGTGTATTAAGAAACGATATTTAAGTTCGTGATTCGTTCAAGAAATGATTTAA	878
Db	76	ATTACATGTGTATTAAGAAACGATATTTAAGTTCGTGATTCGTTCAAGAAATGATTTAA	17

QY	879	TATACATTTCCT	890
Db	16	TATACATTTCCT	5

RESULT 13	
AA040225	
LOCUS	563 bp
DEFINITION	mRNA
	linear
	EST 08-AUG-1997
IMAGE:725143 5'	Scars cvar tumor NbHOT Homo sapiens CDNA clone
	mRNA sequence.

ACCESSION	AA404425	GI:2058967
VERSION	AA404425.1	
KEYWORDS	EST	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE	AUTHORS
1 (bases 1 to 563)	Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, M., Hanks, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Madis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Roloff, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
PUBMED	8889549
COMMENT	Contact: Wilson RK

ORIGIN

Query Match	62.0%;	Score 552;	DB 1;	Length 563;
Best Local Similarity	-99.8%;	Pred. No. 1.8e-153;		
Matches 563;	Conservative	0;	Mismatches 0;	Indels 1;
				Gaps 1;

OY	206	CTAACTCCTACAGTACAGAGAAAGTCCCTCCATTGACATCAACCAATCCGAAGTGC	265
Db	1	CTAACTCCTACAGTACAC- GAAAGTCTCCCATTTGACATCAACCAATCCGAAGTGC	59
OY	266	AACTGTGTGACGACTAAGAAACCTCGTGTTTGAGTAGAAGAAAGGGCCCTGGAAGAGGGGAG	325
Db	60	AACGTGTGACGACTAAGAAACCTCGTGTTTGAGTAGAAGAAAGGGCCCTGGAAGAGGGGAG	119

QY 326 CCAACAATCTGTCTGCTTCTCATTAGTTCATTGGCAATAAGACATTCGTCTCTTGG 385
| | | | |
Db 120 CCAACAATCTGTCTGCTTCTCATTAGTTCATTGGCAATAAGACATTCGTCTCTTGG 179
| | | | |
QY 386 GCTGCTGCTCTCAGACAGAGAGCCAGAACTCTATCGGGCACAGAGATTAACATCTTCAGT 445
| | | | |
Db 180 GCTGCTGCTCTCAGACAGAGAGCCAGAACTCTATCGGGCACAGAGATTAACATCTTCAGT 239
| | | | |
QY 446 GAACAGAGTTGACAGAGCCCTATGGGAATGCCGTATGGGATTAATCTTCAGCTTGTAGC 505
| | | | |
Db 240 GAACAGAGTTGACAGAGCCCTATGGGAATGCCGTATGGGATTAATCTTCAGCTTGTAGC 299
| | | | |
QY 506 TTCTAAGTTCTTCTCCCTTCAATCTACCTGCAAGCCAAAGTTCGTAGAAGAAATGCTG 565
| | | | |
Db 300 TTCTAAGTTCTTCTCCCTTCAATCTACCTGCAAGCCAAAGTTCGTAGAAGAAATGCTG 359
| | | | |
QY 566 AGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCAGACCCCTCTGCGCAAT 625
| | | | |
Db 360 AGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCAGACCCCTCTGCGCAAT 419
| | | | |
QY 626 TCAATTTAAGGCAACAACATATACCTTCATGAGACACACAGACTTTTGAAGAAG 685
| | | | |
Db 420 TCAATTTAAGGCAACAACATATACCTTCATGAGACACACAGACTTTTGAAGAAG 479
| | | | |
QY 686 GACATAGACTGCTTGAATTTAGAGCCCTTGAAGAAATGAAGCTTTGAAGAAAGAAATACTT 745
| | | | |
Db 480 GACATAGACTGCTTGAATTTAGAGCCCTTGAAGAAATGAAGCTTTGAAGAAAGAAATACTT 539
| | | | |
QY 746 GTTTCAGCCCTCTCCACACTC 769
| | | | |
Db 540 GTTTCAGCCCTCTCCACACTC 563
| | | | |

RESULT 14
LOCUS CD632169 568 bp mRNA linear EST 12-JAN-2004
DEFINITION 5608407J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD632169
VERSION CD632169.1 GI:40280436

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 568) Yang, J., Au-Young, J., and Stuve, L.L.
AUTHORS Fu, G.-K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source 1..568
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 61.9%; Score 551.2; DB 6; Length 568;
Best Local Similarity 99.5%; Pred. No. 3,1e-153;
Matches 553; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 335 CTGTGCTCTTCTCAGACTTATGTCATTTGGCAATAAGACATTCGTCTCTTGGCTGCTGCC 394
| | | | |
Db 11 CAGTGTGCTCTTCTCAGACTTATGTCATTTGGCAATAAGACATTCGTCTCTTGGCTGCTGCC 70
| | | | |
QY 395 TCAGACAGAGAGCCAGAACTCTATCGGGCACAGAGATTAACATCTCTCAGTGAACAGAGT 454
| | | | |

Db 71 TCAGACAGAGAGCCAGAACTCTATCGGGCACAGAGATTAACATCTCTCAGTGAACAGAGT 120
| | | | |
QY 455 TCAGAGGCTTATGGGAATATGCTGATGGATTAATCTTACGCTTGTGACCTCTAAGT 514
| | | | |
Db 131 TCAGAGGCTTATGGGAATATGCTGATGGATTAATCTTACGCTTGTGACCTCTAAGT 190
| | | | |
QY 515 TCTTCCCTTCAATCTTACCTGCAAGCCAAAGTTCGTAGAAGAAATGCCGTAGCTTACG 574
| | | | |
Db 191 TCTTCCCTTCAATCTTACCTGCAAGCCAAAGTTCGTAGAAGAAATGCCGTAGCTTACG 250
| | | | |
QY 575 TCAGGTTTCTTACCTCTGAATTTAGATCTTCAGACCCCTCTGCGCAATTCAAATTA 634
| | | | |
Db 251 TCAGGTTTCTTACCTCTGAATTTAGATCTTCAGACCCCTCTGCGCAATTCAAATTA 310
| | | | |
QY 635 GGCACAAACATATACCTTCATGAGACACACAGACTTTTGAAGACAGACATGAC 694
| | | | |
Db 311 GGCACAAACATATACCTTCATGAGACACACAGACTTTTGAAGACAGACATGAC 370
| | | | |
QY 695 TGCTGAATTTAGAGCCCTGAGAAATGAAGCTTTGAAGAAAGAAATACCTTGTTCAGC 754
| | | | |
Db 371 TGCTGAATTTAGAGCCCTTGAAGAAATGAAGCTTTGAAGAAAGAAATACCTTGTTCAGC 430
| | | | |
QY 755 CCCCTTCCACACTCTTCATGTTTAAACAATGCTCTTCTGACCTTGAAGCCAGCTGA 814
| | | | |
Db 431 CCCCTTCCACACTCTTCATGTTTAAACAATGCTCTTCTGACCTTGAAGCCAGCTGA 490
| | | | |
QY 815 CTGTATTTACATGTTGTTATGAAAGAACTGATTTTGAAGTTTGATCTTCAAGAGATGAT 874
| | | | |
Db 491 CTGTATTTACATGTTGTTATGAAAGAACTGATTTTGAAGTTTGATCTTCAAGAGATGAT 550
| | | | |
QY 875 TAAATATACATTTGCT 890
| | | | |
Db 551 TAAATATACATTTGCT 566
| | | | |

RESULT 15
LOCUS CD632170 560 bp mRNA linear EST 12-JAN-2004
DEFINITION 5608407J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD632170
VERSION CD632170.1 GI:40280437

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 560) Yang, J., Au-Young, J., and Stuve, L.L.
AUTHORS Fu, G.-K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source 1..560
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 61.1%; Score 544.2; DB 6; Length 560;
Best Local Similarity 99.5%; Pred. No. 3,9e-151;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 335 CTGTGCTCTTCTCAGACTTATGTCATTTGGCAATAAGACATTCGTCTCTTGGCTGCTGCC 394
| | | | |
Db 549 CAGTGTGCTCTTCTCAGACTTATGTCATTTGGCAATAAGACATTCGTCTCTTGGCTGCTGCC 490
| | | | |

```
OY 395 TCAGACAGAGAGCCGAGACTCTATCGGCGCACCGAGATACATCTCTCAGTGAACAGAGT 454
DB 489 TCAGCACAGAGAGCCGAGACTCTATCGGCGCACCGAGATACATCTCTCAGTGAACAGAGT 430
OY 455 TCACAGAGGCTTATGGGAAATGCCCTGATGGGATTAATCTTCAGCTTGTAGCTTCTAAGTT 514
DB 429 TCACAGAGGCTTATGGGAAATGCCCTGATGGGATTAATCTTCAGCTTGTAGCTTCTAAGTT 370
OY 515 TCTTTCCCTTCATTCACCTCGAAGCCAAAGTTCTGTAGAGAAATGCCCTGAGTTCTAGC 574
DB 369 TCTTTCCCTTCATTCACCTCGAAGCCAAAGTTCTGTAGAGAAATGCCCTGAGTTCTAGC 310
OY 575 TCAGGTTTCTTACTCTGAATTTAGATCTCAGAGCCCTTCCTGGCCACAATTCAAATTAA 634
DB 309 TCAGGTTTCTTACTCTGAATTTAGATCTCAGAGCCCTTCCTGGCCACAATTCAAATTAA 250
OY 635 GGCACAAACATATACCTTCCATGAAGCACACACAGACTTTGAAAGCAAGACAATGAC 694
DB 249 GGCACAAACATATACCTTCCATGAAGCACACACAGACTTTGAAAGCAAGACAATGAC 190
OY 695 TCGTGAATTTGAGGCTTGAGAAATGAGACTTTGAGAAAGAAATACCTTGTTCAGC 754
DB 189 TCGTGAATTTGAGGCTTGAGAAATGAGACTTTGAGAAAGAAATACCTTGTTCAGC 130
OY 755 CCCCTCCACACTCTTCATGTGTTAACCACTGCCCTTCTGACCTTGAGCCACGCTGA 814
DB 129 CCCCTCCACACTCTTCATGTGTTAACCACTGCCCTTCTGACCTTGAGCCACGCTGA 70
OY 815 CTGATTTACATGTTGTTATAGAAACCTGATTTTGAAGTTCTGATGTTCAAGAGAAATGAT 874
DB 69 CTGATTTACATGTTGTTATAGAAACCTGATTTTGAAGTTCTGATGTTCAAGAGAAATGAT 10
OY 875 TAAATATAC 883
DB 9 TAAATATAC 1
```

Search completed: May 31, 2005, 00:10:52
Job time : 3464.52 secs

Query Match	99.3%; Score 403; DB 6; Length 406;
Best Local Similarity	100.0%; Pred. No. 2.2e-109;
Matches 406; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GTGAATGTGACTATTAATGACAGCTCAAGACCTTCGGGTGAGGCTCCCGATGTTTC 60
DB	1 GTGAATGTGACTATTAATGACAGCTCAAGACCTTCGGGTGAGGCTCCCGATGTTTC 60
QY	61 CCCGAGCCCAAGTGTCTGGGATGCCAAGTTGACGAGGAGGCAACTTCTCGGAAGTC 120
DB	61 CCCGAGCCCAAGTGTCTGGGATGCCAAGTTGACGAGGAGGCAACTTCTCGGAAGTC 120
QY	121 TCCAAATACAGACTTTGAGCTGAAGCTGGAATGATGACATGAAGTTGTGTGCTC 180
DB	121 TCCAAATACAGACTTTGAGCTGAAGCTGGAATGATGACATGAAGTTGTGTGCTC 180
QY	181 TACAATGTTTACGATCAACAACACATATCTCTGTATATGAAATGACATTGCCAAGCA 240
DB	181 TACAATGTTTACGATCAACAACACATATCTCTGTATATGAAATGACATTGCCAAGCA 240
QY	241 ACGAGGGATATCAAAATGACAGATGGAGATCAAAAAGGCGAGTCACTTACAGCTGCTA 300
DB	241 ACGAGGGATATCAAAATGACAGATGGAGATCAAAAAGGCGAGTCACTTACAGCTGCTA 300
QY	301 AACTCAAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGCACTTCTGCTT 360
DB	301 AACTCAAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGCACTTCTGCTT 360
QY	361 CTCAGCCCTTACTGATGCTAANAATATGTCCTTGGCCCAAAAA 406
DB	361 CTCAGCCCTTACTGATGCTAANAATATGTCCTTGGCCCAAAAA 406
RESULT 2	
LOCUS	BC074729 916 bp mRNA linear PRI 04-AUG-2004
DEFINITION	Homo sapiens immune costimulatory protein B7-H4, mRNA (cDNA clone
ACCESSION	MGC:103801 IMAGE:30915182), complete cds.
VERSION	BC074729
KEYWORDS	BC074729.2 GI:50959545
SOURCE	MGC.
ORGANISM	Homo sapiens (human)
REFERENCE	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 916)
	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., Mckernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hux, S.W., Villalón, D.K., Munz, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Rane, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
AUTHORS	2 (bases 1 to 916)
TITLE	Director MGC Project.
JOURNAL	Submitted (25-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT	NIH-MGC Project URL: http://mgc.ncl.nih.gov On Aug 4, 2004 this sequence version replaced gi:49901510. Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Genome Sequence Centre, British Columbia Cancer Center
FEATURES	CDNA Library Preparation: British Columbia Cancer Research Center CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Maason, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angeliq Scherch, Ursula Skalska, Duane Smalls, Jeff Stott, Miranda Teal, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.
source	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRBU Plate: 1 Row: B Column: 3. Location/Qualifiers 1..916 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:103801 IMAGE:30915182" /tissue_type="Brain, PCR rescued clones" /clone_lib="NIH MGC_272" /lab_host="DH10B" /note="Vector: PCR4 Topo TA with reversed insert" 1..916 /gene="B7-H4" /note="synonyms: B7X, B7S1, FLJ22418" /db_xref="LOCUSID:79679" 32..880 /gene="B7-H4" /codon_start=1 /product="Immune costimulatory protein B7-H4" /protein_id="AAH74729.1" /db_xref="GI:50959545" /db_xref="LOCUSID:79679" /db_xref="MIM:608162" /translation="MAISLGQILFWSIISIIITLACALALIGFGISGRHSITVTVAS AGNIGEDGILSCTFEPDILKLSIVIQMLKEGLGVHFKGKDELSEODEMFRGRTA VFADQIVGNASLRKLVOLDAGYKCYIITSKGGANALEYKGAISMEPVNDYV ASSFTLRCEAPRPPOPVWVASOVDOGANSSEVSTFELNSENVTKVSVLVNVT INNTYSCHIEDNDIAATGDIKTESBIRKSHLDLNSKASLCVSPFAIKSMALLPLS PFLMK"
gene	
CDS	
ORIGIN	
Query Match	99.3%; Score 403; DB 9; Length 916;
Best Local Similarity	100.0%; Pred. No. 2.2e-109;
Matches 403; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GTGAATGTGACTATTAATGACAGCTCAAGACCTTCGGGTGAGGCTCCCGATGTTTC 60
DB	494 GTGAATGTGACTATTAATGACAGCTCAAGACCTTCGGGTGAGGCTCCCGATGTTTC 553
QY	61 CCCGAGCCCAAGTGTCTGGGATGCCAAGTTGACGAGGAGGCAACTTCTCGGAAGTC 120
DB	554 CCCGAGCCCAAGTGTCTGGGATGCCAAGTTGACGAGGAGGCAACTTCTCGGAAGTC 613
QY	121 TCCAAATACAGACTTTGAGCTGAAGCTGGAATGATGACATGAAGTTGTGTGCTC 180
DB	614 TCCAAATACAGACTTTGAGCTGAAGCTGGAATGATGACATGAAGTTGTGTGCTC 673
QY	181 TACAATGTTTACGATCAACAACACATATCTCTGTATATGAAATGACATTGCCAAGCA 240

```
Db 674 TACATTTTGGATGATCAACAAACACTACTCCTGTATGATTTGAAATGACATTGCCAAAGCA 733
|
|
|
Qy 241 ACAGGGGATATCAAAAGTACAGAAATCGAATCAAAAGCGGAGTCACTTACAGCTGCTA 300
|
|
|
Db 734 ACAGGGGATATCAAAAGTACAGAAATCGAATCAAAAGCGGAGTCACTTACAGCTGCTA 793
|
|
|
Qy 301 AACCTAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCCGCT 360
|
|
|
Db 794 AACCTAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCT 853
|
|
|
Qy 361 CTCAGCCCTTACCTGATGCTAANATATGTCCTTGCCCAAAAA 406
|
|
|
Db 854 CTCAGCCCTTACCTGATGCTAANATATGTCCTTGCCCAAAAA 899
|
|
|
RESULT 3
AX375858 1065 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 5 from Patent WO0194641.
DEFINITION AX375858
ACCESSION AX375858.1 GI:19170330
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Ople,E., McLachlan,K. and Heard,C.
AUTHORS Gene targets and ligands that bind thereto for treatment and
TITLE diagnosis of ovarian carcinomas
JOURNAL Patent: WO 0194641-A 5 13-DEC-2001;
FEATURES Idex Pharmaceuticals Corporation (US)
source Location/Qualifiers
1..1065
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 99.3%; Score 403; DB 6; Length 1065;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTGAATGTGACTATTAATGCGCAGCTCAGANACCTTGGGTGTGAGGCTCCCGATGGTTC 60
|
|
|
Db 534 GTGAATGTGACTATTAATGCGCAGCTCAGAGACCTTGGGTGTGAGGCTCCCGATGGTTC 593
|
|
|
Qy 61 CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACAGAGAGCCAACTTCTGGGAAGTC 120
|
|
|
Db 594 CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACAGAGAGCCAACTTCTGGGAAGTC 653
|
|
|
Qy 121 TCCAAATACCAAGCTTGAAGTGAAGTCAATGAAAGTGTGTGTCTGCTC 180
|
|
|
Db 654 TCCAAATACCAAGCTTGAAGTGAAGTCAATGAAAGTGTGTGTCTGCTC 713
|
|
|
Qy 181 TACAATGTTCAGATCAACAACACTACTCTGTATGATTTGAAATGACATTGCCAAAGCA 240
|
|
|
Db 714 TACAATGTTCAGATCAACAACACTACTCTGTATGATTTGAAATGACATTGCCAAAGCA 773
|
|
|
Qy 241 ACAGGGGATATCAAAAGTACAGAAATCGAATCAAAAGCGGAGTCACTTACAGCTGCTA 300
|
|
|
Db 774 ACAGGGGATATCAAAAGTACAGAAATCGAATCAAAAGCGGAGTCACTTACAGCTGCTA 833
|
|
|
Qy 301 AACCTAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCT 360
|
|
|
Db 834 AACCTAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCT 893
|
|
|
Qy 361 CTCAGCCCTTACCTGATGCTAANATATGTCCTTGCCCAAAAA 406
|
|
|
Db 894 CTCAGCCCTTACCTGATGCTAANATATGTCCTTGCCCAAAAA 939
|
|
|
```

```
RESULT 4
AY346100 1070 bp mRNA linear PRI 09-SEP-2003
LOCUS Homo sapiens T cell costimulatory molecule B7x mRNA, complete cds.
DEFINITION AY346100
ACCESSION AY346100
VERSION AY346100.1 GI:33638210
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1070)
AUTHORS Zang,X., Locke,P., Kim,J., Murphy,K., Waite,R. and Allison,J.P.
TITLE B7x: A widely expressed B7 family member that inhibits T cell
activation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (18), 10388-10392 (2003)
MEDLINE 22833980
PUBMED 12920180
REFERENCE
2 (bases 1 to 1070)
AUTHORS Zang,X. and Allison,J.P.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2003) Howard Hughes Medical Institute, Department
of Molecular and Cell Biology, Cancer Research Laboratory,
University of California at Berkeley, LS4415, Berkeley, CA 94720,
USA
FEATURES
source Location/Qualifiers
1..1070
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="1p13.1-12"
61..909
/note="immunoglobulin superfamily; B7 family"
/codon_start=1
/product="T cell costimulatory molecule B7x"
/protein_id="AA024206.1"
/db_xref="GI:33638211"
/translacion="MASHQQLFWSIIISIIIIAGALAILGFGISGRSITVTTVAS
AGNIGDGLISCTFEPDILKSDIVIQMLEGVGLVHERFEGKDELSEDEMRGRTA
VFADQIVGNASIRLKNVOLDAGTYKYLIIISKGKNANLKYTGAFSPVAVDYN
ASEETLRCAEPRMFPQPTVMAASOVDOGANSFVSSTFELNSENATMKVSVLYNVT
INNTVSCMIENDIAKATGDIIVTESIRKSRSHQLNLSRSLVCSFPAISMLPLPS
PYLMK"
ORIGIN
Query Match 99.3%; Score 403; DB 9; Length 1070;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTGAATGTGACTATTAATGCGCAGCTCAGANACCTTGGGTGTGAGGCTCCCGATGGTTC 60
|
|
|
Db 523 GTGAATGTGACTATTAATGCGCAGCTCAGAGACCTTGGGTGTGAGGCTCCCGATGGTTC 582
|
|
|
Qy 61 CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACAGAGAGCCAACTTCTGGGAAGTC 120
|
|
|
Db 583 CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACAGAGAGCCAACTTCTGGGAAGTC 642
|
|
|
Qy 121 TCCAAATACCAAGCTTGAAGTGAAGTCAATGAAAGTGTGTGTCTGCTC 180
|
|
|
Db 643 TCCAAATACCAAGCTTGAAGTGAAGTCAATGAAAGTGTGTGTCTGCTC 702
|
|
|
Qy 181 TACAATGTTCAGATCAACAACACTACTCTGTATGATTTGAAATGACATTGCCAAAGCA 240
|
|
|
Db 703 TACAATGTTCAGATCAACAACACTACTCTGTATGATTTGAAATGACATTGCCAAAGCA 762
|
|
|
Qy 241 ACAGGGGATATCAAAAGTACAGAAATCGAATCAAAAGCGGAGTCACTTACAGCTGCTA 300
|
|
|
Db 763 ACAGGGGATATCAAAAGTACAGAAATCGAATCAAAAGCGGAGTCACTTACAGCTGCTA 822
|
|
|
Qy 301 AACCTAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCT 360
|
|
|
Db 823 AACCTAAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCAGCTGGGACCTTCTGCT 882
|
|
|
```

QY 361 CTCAGCCCTTACCTGATGCTAATATATGTCCTTGCCACCAAAAA 406
Db 883 CTCAGCCCTTACCTGATGCTAATATATGTCCTTGCCACCAAAAA 928

RESULT 5
BC065717
LOCUS
DEFINITION BC065717 1190 bp mRNA linear PRI 03-FEB-2004
Homo sapiens immune costimulatory protein B7-H4, mRNA (cDNA clone
MGC:71941 IMAGE:4295775), complete cds.
ACCESSION BC065717
VERSION BC065717.1 GI:41350861
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1190)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Utsdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Mortley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulys, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shcherchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL PUMED 12477932
REFERENCE 2 (bases 1 to 1190)
Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-1@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@gscc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao,
Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Telia Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabu,
Paraneel Sreed, JR Santos, Angeliqne Scherch, Ursula Skalska,
Dane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
Series: IRAL Plate: 51 Row: f Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13375849.
Location/Qualifiers
1. .1190

gene
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:71941 IMAGE:4295775"
/issue_type="Prostate"
/clone_lib="NIH_MGC_83"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
1. .1190
/gene="B7-H4"
/note="Synonyms: FLJ22418, B7S1, B7X"
/db_xref="locusid:79679"
/db_xref="MIM:608162"
452. .1015
/gene="B7-H4"
/codon_start=1
/product="B7-H4 protein"
/protein_id="AAH65717.1"
/db_xref="GI:41350862"
/db_xref="MIM:608162"
/translation="MFRKTRAVPADOVIVGNASLRKRVLTDACTYCYITTSKXG
NANLEKTKGASMPEDVNDVNASSETLKEAPKMPQPTVWASGVDDGAPSEVNT
SEFLSENVTWKVSVLVNVTINNTYSCMIENDIAKAGDIIKYESEIKRSHQLLN
SKASLCVSPFALISWALLPLSPYIMLK"
500. .871
/gene="B7-H4"
/note="CD2; Region: T-cell surface antigen CD2 protein.
This family consists of several mammalian T-cell surface
antigen CD2 proteins as well as homologous African swine
fever virus sequences. CD2 mediates T cell adhesion via
its ectodomain and signal transduction utilizing its
117-amino acid cytoplasmic tail. The structural and
functional similarities of the African swine fever virus
(ASFV) LMW-DR to CD2, a protein that is involved in
cell-cell adhesion and immune response modulation, suggest
a possible role in the pathogenesis of ASFV infection"
/db_xref="CDI:pfam05790"

misc_feature
Query Match 99.3%; Score 403; DB 9; Length 1190;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ORIGIN
1 GTGATGTGAGTATTAATATGCGAGCTCAGANACCTTGCGGTGAGGCTCCCGATGCTTC 60
|||||
629 GTGAATGTGACTAATAATGCGAGCTCAGAGACCTTGCGGTGAGGCTCCCGATGCTTC 688
|||||
61 CCCAGCCCAAGTGTGAGCTGAGGATCCCAAGTTGACAGGAGGCCACTTCGGAAGTTC 120
|||||
689 CCCAGCCCAAGTGTGAGCTGAGGATCCCAAGTTGACAGGAGGCCACTTCGGAAGTTC 748
|||||
121 TCCAAATACCAAGCTTTGAGCTGAACCTTGAGAAATGACCATGAGAGCTTGTCTGCTC 180
|||||
749 TCCAAATACCAAGCTTTGAGCTGAACCTTGAGAAATGACCATGAGAGCTTGTCTGCTC 808
|||||
181 TCAATGTATACATTAACAACAACATATCCGTATGATTTGAAATGACATTTGCCAAGCA 240
|||||
809 TCAATGTATACATTAACAACAACATATCCGTATGATTTGAAATGACATTTGCCAAGCA 868
|||||
241 ACAGGGATATGAAGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 300
|||||
869 AAGGGATATGAAGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 928
|||||
301 AACTCAAAAGCTTCTGTGTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
|||||
929 AACTCAAAAGCTTCTGTGTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 988
|||||
QY 361 CTCAGCCCTTACCTGATGCTAATATATGTCCTTGCCACCAAAAA 406
Db 989 CTCAGCCCTTACCTGATGCTAATATATGTCCTTGCCACCAAAAA 1034

[illegible]

Query Match	Best Local Similarity	Score	DB	Length
Matches 403; Conservative	99.3%; Pred. No. 2.2e-109; Mismatches 3; Indels 0; Gaps 0;	99.3%;	DB 6;	1658;
1	GTGAATGTGACCTTAAATGACAGCTCAGAGAACCTTTGGCGTGTGAGGCTCCCGATGGTTC	60		
523	GTGAATGTGACCTTAAATGACAGCTCAGAGAACCTTTGGCGTGTGAGGCTCCCGATGGTTC	582		
61	CCCCAGCCACAGTGTGTGGGCATCCCAAGTTGACGAGGAGCCAACTTCTCGGAATGC	120		
583	CCCCAGCCACAGTGTGTGGGCATCCCAAGTTGACGAGGAGCCAACTTCTCGGAATGC	642		
121	TCCAAATACCACTTTGAGCTGAACTCTGAGAAATGTGACATGAAAGTTGTGTCTGTGCTC	180		
643	TCCAAATACCACTTTGAGCTGAACTCTGAGAAATGTGACATGAAAGTTGTGTCTGTGCTC	702		
181	TACAATGTTCAGATCAACACACATCTCCGTATGATTTGAAATATGACATTTGCCAAAGCA	240		
703	TACATATGTTCAGATCAACACACATCTCCGTATGATTTGAAATATGACATTTGCCAAAGCA	762		
241	ACAGGGGATTCACAAAGTACAGAAATCGGAGATCAAAAGCGGAGTACCTTACAGTGTCTA	300		
763	ACAGGGGATTCACAAAGTACAGAAATCGGAGATCAAAAGCGGAGTACCTTACAGTGTCTA	822		
301	AACCTCAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTTGGCATCAGCTGGGCACTTCTGCTT	360		
823	AACCTCAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTTGGCATCAGCTGGGCACTTCTGCTT	882		
361	CTCAGCCCTTACCTGATCTAAATTAATGTGCTTGGCCACAAATAA	406		
883	CTCAGCCCTTACCTGATCTAAATTAATGTGCTTGGCCACAAATAA	928		

|||||
Db CCCACCCACAGTGTCTGGGCATCCCAAGTTGACACAGGAGCCAACTTCTCGAAGTC 642
121 TCCAAATACAGGCTTTAGAGTGAACCTGGAATGTGACATGAAAGGTGTGTGTC 180
643 TCCAAATACAGGCTTTAGAGTGAACCTGGAATGTGACATGAAAGGTGTGTGTC 702
Qy 181 TCAATGTTACGATCAACAACATATCTCTGTATGTTGAAATGACATTGGCAAGCA 240
703 TCAATGTTACGATCAACAACATATCTCTGTATGTTGAAATGACATTGGCAAGCA 762
Db 241 ACAGGGGNTATCAAAGTACAGATGAGATGAAAAGCGAGTCACTACAGCTGCTA 300
763 ACAGGGGNTATCAAAGTACAGATGAGATGAAAAGCGAGTCACTACAGCTGCTA 822
Qy 301 AACTCAAGGCTTCTGTGTGCTCTTCTTTCTTCCATCAGCTGGGCACTTGCGCT 360
823 AACTCAAGGCTTCTGTGTGCTCTTCTTTCTTCCATCAGCTGGGCACTTGCGCT 882
Db 361 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAA 406
883 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAA 928

RESULT 9
AX376150 1658 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 217 from Patent WO0168848.
DEFINITION AX376150
ACCESSION AX376150
VERSION AX376150.1 GI:19170467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, Y., Watanabe, C.K., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0168848-A 217 20-SEP-2001;
Genentech, Inc. (US)

FEATURES
source 1.1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.3%; Score 403; DB 6; Length 1658;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTGAATGTGACTATATATGCTGACCTGAGANACCTTGCCTGTGAGGCTCCCGATGTTTC 60
Db 523 GTGAATGTGACTATATATGCTGACCTGAGAGACCTTGCCTGTGAGGCTCCCGATGTTTC 582
Qy 61 CCCACGCCACAGTGTCTGGGATCCCAAGTTGACACAGGAGCCAACTTCTCGGAAGTC 120
Db 583 CCCACGCCACAGTGTCTGGGATCCCAAGTTGACACAGGAGCCAACTTCTCGGAAGTC 642
Qy 121 TCCAAATACAGGCTTTAGAGTGAACCTGGAATGTGACATGAAAGGTGTGTGTC 180
Db 643 TCCAAATACAGGCTTTAGAGTGAACCTGGAATGTGACATGAAAGGTGTGTGTC 702
Qy 181 TCAATGTTACGATCAACAACATATCTCTGTATGTTGAAATGACATTGGCAAGCA 240
Db 703 TCAATGTTACGATCAACAACATATCTCTGTATGTTGAAATGACATTGGCAAGCA 762
Qy 241 ACAGGGGNTATCAAAGTACAGATGAGATGAAAAGCGAGTCACTACAGCTGCTA 300
Db 763 ACAGGGGNTATCAAAGTACAGATGAGATGAAAAGCGAGTCACTACAGCTGCTA 822

Qy 301 AACTCAAGGCTTCTGTGTGCTCTTCTTTCTTTCATCAGCTGGGCACTTGCGCT 360
Db 823 AACTCAAGGCTTCTGTGTGCTCTTCTTTCTTTCATCAGCTGGGCACTTGCGCT 882
Qy 361 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAA 406
Db 883 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAA 928

RESULT 10
AX395215 1658 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 3 from Patent WO0216429.
DEFINITION AX395215
ACCESSION AX395215
VERSION AX395215.1 GI:21066246
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakis, P., Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216429-A 3 28-FEB-2002;
Genentech, Inc. (US)

FEATURES
source 1.1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.3%; Score 403; DB 6; Length 1658;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTGAATGTGACTATATATGCTGACCTGAGANACCTTGCCTGTGAGGCTCCCGATGTTTC 60
Db 523 GTGAATGTGACTATATATGCTGACCTGAGAGACCTTGCCTGTGAGGCTCCCGATGTTTC 582
Qy 61 CCCACGCCACAGTGTCTGGGATCCCAAGTTGACACAGGAGCCAACTTCTCGGAAGTC 120
Db 583 CCCACGCCACAGTGTCTGGGATCCCAAGTTGACACAGGAGCCAACTTCTCGGAAGTC 642
Qy 121 TCCAAATACAGGCTTTAGAGTGAACCTGGAATGTGACATGAAAGGTGTGTGTC 180
Db 643 TCCAAATACAGGCTTTAGAGTGAACCTGGAATGTGACATGAAAGGTGTGTGTC 702
Qy 181 TCAATGTTACGATCAACAACATATCTCTGTATGTTGAAATGACATTGGCAAGCA 240
Db 703 TCAATGTTACGATCAACAACATATCTCTGTATGTTGAAATGACATTGGCAAGCA 762
Qy 241 ACAGGGGNTATCAAAGTACAGATGAGATGAAAAGCGAGTCACTACAGCTGCTA 300
Db 763 ACAGGGGNTATCAAAGTACAGATGAGATGAAAAGCGAGTCACTACAGCTGCTA 822
Qy 301 AACTCAAGGCTTCTGTGTGCTCTTCTTTCTTCCATCAGCTGGGCACTTGCGCT 360
Db 823 AACTCAAGGCTTCTGTGTGCTCTTCTTTCTTCCATCAGCTGGGCACTTGCGCT 882
Qy 361 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAA 406
Db 883 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAA 928

RESULT 11
AX403403 1658 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 290 from Patent WO0073454.
DEFINITION AX403403
ACCESSION AX403403
VERSION AX403403.1 GI:21436923

ORIGIN	1. 1658	/organism="Homo sapiens"	/mol_type="unassigned DNA"	/db_xref="taxon:9606"
Query Match	99.3%	Score 403;	DB 6;	Length 1658;
Best Local Similarity	99.3%	Pred. No. 2.2e-109;		
Matches 403;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
OY	1	GTGAATGGGACTTAATGCGAGCTGAGAACCTGGCGGTGAGGCTCCCCAGTGTTC	60	
DB	523	GTGAATGGGACTTAATGCGAGCTGAGAACCTGGCGGTGAGGCTCCCCAGTGTTC	582	
OY	61	CCCCAGGCCACAGTGTCTGTGGGCAATCCCAAGTTGACCCAGGAGCCAACTTCTCGGAAGTC	120	
DB	583	CCCCAGGCCACAGTGTCTGTGGGCAATCCCAAGTTGACCCAGGAGCCAACTTCTCGGAAGTC	642	
OY	121	TCCAATACCAAGCTTTGAGCTGAACTCTGAGAAATGTGACCAATGAAGTTGTGTCTGTGCTC	180	
DB	643	TCCAATACCAAGCTTTGAGCTGAACTCTGAGAAATGTGACCAATGAAGTTGTGTCTGTGCTC	702	
OY	181	TACAAATGTGCGATCAACAACACATCTCTGTATGATTTGAAATGACATTTGCCAAAGCA	240	
DB	703	TACAAATGTGCGATCAACAACACATCTCTGTATGATTTGAAATGACATTTGCCAAAGCA	762	
OY	241	ACAGGGGNTATCAAAAGTGAAGAGATCGAGATCAAAAGGGGAGTCACTTACAGCTGTCTA	300	
DB	763	ACAGGGGNTATCAAAAGTGAAGAGATCGAGATCAAAAGGGGAGTCACTTACAGCTGTCTA	822	
OY	301	AACCTCAAGGCTTCTGTGTGTCTCTTTCTTTTTCATTCAGCTGGGCACTTTGTGCT	360	
DB	823	AACCTCAAGGCTTCTGTGTGTCTCTTTCTTTTTCATTCAGCTGGGCACTTTGTGCT	882	
OY	361	CTAGAGCCCTTACCTGATGCTAAATATATGCGCTTGGCCCAAAAA	406	
DB	883	CTAGAGCCCTTACCTGATGCTAAATATATGCGCTTGGCCCAAAAA	928	
RESULT 13				
AY358352				
LOCUS	AY358352	1658 bp	mRNA	linear PRI 03-OCT-2003
DEFINITION	Homo sapiens clone DNA59610 B7h.5 (UN0659)	mRNA	complete cds.	
ACCESSION	AY358352			
VERSION	AY358352.1	GI:37181828		
KEYWORDS	FLI CDNA			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 1658)			
	Clark, H.F., Gunney, A.L., Abaya, F., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Gimaldi, C., Gu, Q., Hass, P.E., Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seehagiri, S., Simmons, J., Singh, J., Smith, V., Stinson, J., Vagts, A., Vanden, R., Watanebe, C., Wiand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.			
TITLE	The Secretd Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secretd and Transmembrane Proteins: A Bioinformatics Assessment			
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)			
PUBMED	12973509			
REFERENCE	2 (bases 1 to 1658)			
AUTHORS	Clark, H.F.			
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA			
FEATURES	Location/Qualifiers			
source	1. 1658	/organism="Homo sapiens"		

```

gene
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="DNA59610"
  1..1658
  /locus_tag="UN0659"
  61..909
  /locus_tag="UN0659"
  /note="PRO1291"
  /codon_start=1
  /product="B7h 5"
  /protein_id="AA08718.1"
  /db_xref="GI:37181829"
  /translation="MASLQILFWISIIIIILAGIALIIFGRIISGRHSITVTVAS
  AGNIGEDGILSCFEPEDIKLSDIVIMLKEGVIGVHEKESKDEISEQDEMFRRTA
  VFADQYIVGNASIRLKNVOLDTAGTKYKIIISKGGANLLEKTKGAFEMPEVNDYN
  ASSETLRCAEPRMFPQPTVYMAVNDGANSFSEVNTSELSSENVTKVSVLVNVT
  INNTYSCTMIENDIAKATGDIKYTESIKRSHQLILNSKASLCVSSFPAISNALLPLS
  PYIMLK"

ORIGIN
Query Match      99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGACCTGAGANACCTTCGGGTGTGAGGCTCCCGATGTTTC 60
DB 523 GTGAATGTGACTATTAATGCGACCTGAGACCTTCGGGTGTGAGGCTCCCGATGTTTC 582
QY 61 CCCGAGCCCAAGTGTCTGGGATCCCAAGTTGACGAGGAGCCAACTTCTCGGAATGC 120
DB 583 CCCGAGCCCAAGTGTCTGGGATCCCAAGTTGACGAGGAGCCAACTTCTCGGAATGC 642
QY 121 TCCAAATACCAAGCTTTGAGCTGAACTCTGAGAAATGACCAATGAAGGTTGTGTGCTC 180
DB 643 TCCAAATACCAAGCTTTGAGCTGAACTCTGAGAAATGACCAATGAAGGTTGTGTGCTC 702
QY 181 TACAATGTTACGATCAACAACAACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 240
DB 703 TACAATGTTACGATCAACAACAACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 762
QY 241 ACAGGGGATATCAAAAGTACAGAAATGGAGATCAAAAAGCGAGTCACTACAGCTGCTA 300
DB 763 ACAGGGGATATCAAAAGTACAGAAATGGAGATCAAAAAGCGAGTCACTACAGCTGCTA 822
QY 301 AACTCAAAAGCTTCTCTGTGTGCTCTCTCTTTCTTTGCCATCAGCTGACATTTGACCT 360
DB 823 AACTCAAAAGCTTCTCTGTGTGCTCTCTCTTTCTTTGCCATCAGCTGACATTTGACCT 882
QY 361 CTCAGCCCTTACCTGATGCTAANAATATGTCCTTGCGCCACAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAANAATATGTCCTTGCGCCACAAAA 928

RESULT 14
CO412191      1965 bp      DNA      linear      PAT 23-JAN-2004
LOCUS      Sequence 19262 from Patent WO0170979.
DEFINITION      CO412191
ACCESSION      CO412191
VERSION      CO412191.1 GI:41319972
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Lee,J. and Lillie,J.
  Genes, compositions, kits, and method for identification,
  assessment, prevention, and therapy of ovarian cancer
  Patent: WO 0170979-A 19262 27-SEP-2001;
  Millennium Pharmaceuticals, Inc. (US)
FEATURES
source      Location/Qualifiers
            1..1965
            /organism="Homo sapiens"

```

```

ORIGIN
Query Match      99.3%; Score 403; DB 6; Length 1965;
Best Local Similarity 99.3%; Pred. No. 2.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGACCTGAGANACCTTCGGGTGTGAGGCTCCCGATGTTTC 60
DB 542 GTGAATGTGACTATTAATGCGACCTGAGACCTTCGGGTGTGAGGCTCCCGATGTTTC 601
QY 61 CCCGAGCCCAAGTGTCTGGGATCCCAAGTTGACGAGGAGCCAACTTCTCGGAATGC 120
DB 602 CCCGAGCCCAAGTGTCTGGGATCCCAAGTTGACGAGGAGCCAACTTCTCGGAATGC 661
QY 121 TCCAAATACCAAGCTTTGAGCTGAACTCTGAGAAATGACCAATGAAGGTTGTGTGCTC 180
DB 662 TCCAAATACCAAGCTTTGAGCTGAACTCTGAGAAATGACCAATGAAGGTTGTGTGCTC 721
QY 181 TACAATGTTACGATCAACAACAACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 240
DB 722 TACAATGTTACGATCAACAACAACATACCTCTGTATGATTGAANAATGACATTGCCAAGA 781
QY 241 ACAGGGGATATCAAAAGTACAGAAATGGAGATCAAAAAGCGAGTCACTACAGCTGCTA 300
DB 782 ACAGGGGATATCAAAAGTACAGAAATGGAGATCAAAAAGCGAGTCACTACAGCTGCTA 841
QY 301 AACTCAAAAGCTTCTCTGTGTGCTCTCTCTTTCTTTGCCATCAGCTGAGGCACTTGCTC 360
DB 842 AACTCAAAAGCTTCTCTGTGTGCTCTCTCTTTCTTTGCCATCAGCTGAGGCACTTGCTC 901
QY 361 CTCAGCCCTTACCTGATGCTAANAATATGTCCTTGCGCCACAAAA 406
DB 902 CTCAGCCCTTACCTGATGCTAANAATATGTCCTTGCGCCACAAAA 947

RESULT 15
BD235830      2587 bp      DNA      linear      PAT 17-JUL-2003
LOCUS      A novel method of diagnosing, monitoring, staging, imaging and
DEFINITION      treating various cancers.
ACCESSION      BD235830
VERSION      BD235830.1 GI:33045600
KEYWORDS      JP 2002523760-A/1.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 2587)
  Salceda,S., Sun,Y., Recipon,H. and Cafferty,R.
  A novel method of diagnosing, monitoring, staging, imaging and
  treating various cancers
  Patent: JP 2002523760-A 1 30-JUL-2002;
  DIADEXUS INC
COMMENT
OS      Homo sapiens (human)
PN      JP 2002523760-A/1
PD      30-JUL-2002
PR      02-SEP-1999 JP 2000567741
PI      SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFERKEY PC
GOINJ3/574,A6IK39/395,A6IK39/395,A6IK39/395,A6IK39/395 PC
,A6IK49/00,A6IK49/00,
PC      A6IK51/00,C07K16/32,C12N15/09,C12Q1/68,C12N15/00,A6IK49/02 CC
  A novel method of diagnosing, monitoring,
  staging, imaging and
  treating
CC      various cancers
FH      Key
FT      source      Location/Qualifiers
            1..2587
            /organism="Homo sapiens (human)".
FEATURES
source      Location/Qualifiers
            1..2587
            /organism="Homo sapiens"

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

```
Query Match      99.3%; Score 403; DB 6; Length 2587;
Best Local Similarity 99.3%; Pred. No. 2,1e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GTGAATGTGACTTAATGCGAGCTCAGANACCTTGGGCTGAGGCTCCCGATGCTTC 60
Db      524 GTGAATGTGACTTAATGCGAGCTCAGAGACTTGGGCTGAGGCTCCCGATGCTTC 583
QY      61  CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACCAAGGAGCCACTTCTGGAAAGTC 120
Db      584 CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACCAAGGAGCCACTTCTGGAAAGTC 643
QY      121 TCCAAATACAGCTTTGAGCTGAACCTGAGAAATGTGACCAATGAAGTTGTGTGCTC 180
Db      644 TCCAAATACAGCTTTGAGCTGAACCTGAGAAATGTGACCAATGAAGTTGTGTGCTC 703
QY      181 TACAATGTTCGATCAACCAACACTACTCTGTATGATTGAAATGACATTGCCAAGCA 240
Db      704 TACAATGTTCGATCAACCAACACTACTCTGTATGATTGAAATGACATTGCCAAGCA 763
QY      241 ACAGGGGNTATCAAGTGACAGAAATGGAGATCAAAAGGGGAGTCACTACAGTGTCTA 300
Db      764 ACAGGGGNTATCAAGTGACAGAAATGGAGATCAAAAGGGGAGTCACTACAGTGTCTA 823
QY      301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTTGGCAATCAAGCTGGGCACTTCTGCT 360
Db      824 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTTGGCAATCAAGCTGGGCACTTCTGCT 883
QY      361 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAAAA 406
Db      884 CTCAGCCCTTACCTGATGCTAANATATGTGCTTGGCCACAAAAA 929
```

Search completed: May 30, 2005, 17:54:07
Job time : 1875.08 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 05:15:03 ; Search time 249.008 Seconds
(without alignments)
9651.969 Million cell updates/sec

Title: US-09-763-978B-12

Perfect score: 406
Sequence: 1 gtagatgtgactataatgc.....atgtgcttgccacacaaa 406

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	403	99.3	406	3	AAZ90481 Cancer sp
2	403	99.3	1046	6	ABZ11450 Human pol
3	403	99.3	1046	12	ADMA43968 Human pol
4	403	99.3	1065	6	ABL55580 Nucleotid
5	403	99.3	1657	3	AAZ65059 Membrane
6	403	99.3	1657	10	ADB90935 Novel hum
7	403	99.3	1658	4	AA546033 Human DNA
8	403	99.3	1658	4	AA546033 Human DNA
9	403	99.3	1658	5	AA546033 Human DNA
10	403	99.3	1658	6	ABK11744 DNA encod
11	403	99.3	1658	6	ABK11744 DNA encod
12	403	99.3	1658	6	ABK11091 Human CDN
13	403	99.3	1658	6	ABK11091 Human CDN
14	403	99.3	1658	6	ABK11091 Human CDN
15	403	99.3	1658	6	ABK11091 Human CDN
16	403	99.3	1658	6	ABK11091 Human CDN
17	403	99.3	1658	6	ABK11091 Human CDN
18	403	99.3	1658	6	ABK11091 Human CDN
19	403	99.3	1658	6	ABK11091 Human CDN
20	403	99.3	1658	6	ABK11091 Human CDN

21	403	99.3	1658	8	ACF19603 Human sec
22	403	99.3	1658	8	ACD21891 Human sec
23	403	99.3	1658	8	ACF13056 Human sec
24	403	99.3	1658	8	ACD25159 Human sec
25	403	99.3	1658	8	ACF00208 Human sec
26	403	99.3	1658	8	ACA60392 Novel hum
27	403	99.3	1658	8	ACA72265 Novel hum
28	403	99.3	1658	8	ACD04789 Novel hum
29	403	99.3	1658	8	ACD18250 Human sec
30	403	99.3	1658	8	ACD08257 Human sec
31	403	99.3	1658	8	ACA88691 Novel hum
32	403	99.3	1658	8	ACA70133 Human sec
33	403	99.3	1658	8	ACD12355 Novel hum
34	403	99.3	1658	8	ACG74270 Human sec
35	403	99.3	1658	8	ACD15898 Human sec
36	403	99.3	1658	8	ACD25466 Novel hum
37	403	99.3	1658	8	ACD17943 Human sec
38	403	99.3	1658	8	ACD88230 Human sec
39	403	99.3	1658	8	ACD21584 Human sec
40	403	99.3	1658	8	ACD18651 Human sec
41	403	99.3	1658	8	ACA58839 CDNA enco
42	403	99.3	1658	8	ABX98261 Human CDN
43	403	99.3	1658	8	ACD14012 Human PRO
44	403	99.3	1658	8	ACD09792 Human sec
45	403	99.3	1658	8	ACC88537 Human sec

ALIGNMENTS

RESULT 1
AAZ90481
ID AAZ90481 standard; CDNA; 406 BP.
XX
AC AAZ90481;
XX
DT 06-JUN-2000 (first entry)
XX
DB Cancer specific gene (clone ID 16656542) fragment #12.
--XX
KW CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KW endometrial; uterine; lung; cytotoxic; ss.
XX
OS Homo sapiens.
XX
FN W0200012758-A1.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US019655.
XX
PR 02-SEP-1998; 98US-0098880P.
XX
PA (DIAD-) DIADEXUS LLC.
XX
PI Salceda S, Sun Y, Recipon H, Cafferty R;
XX
DR WPI; 2000-256657/22.
XX
PT Diagnosing, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer,
PT involves measuring cancer specific gene levels in cells and body fluids.
XX
PS Claim 9, Page 51-52, 58pp; English.
XX
CC The invention relates to detecting, diagnosing metastasis and staging
CC cancer by measuring levels of cancer specific genes (CSG) in cells,
CC tissues or body fluids. Their remission and progression, decreases and
CC increases in CSG levels, is also monitored, by periodic sample analysis.
CC The methods are useful for detecting cancers, especially gynecologic
CC cancers which include ovarian, breast, endometrial and uterine cancer and
CC lung cancer. Antibodies against the CSGs labeled with paramagnetic ions
CC or a radioisotope is useful for imaging cancer and when conjugated with a

CC cytotoxic agent are useful for treating cancer. The present sequence
CC represents a CSG (clone ID: 16565642 and gene ID: 234617) fragment
XX
SQ Sequence 406 BP, 106 A, 104 C, 92 G, 101 T, 0 U, 3 Other;

SQ Sequence 406 BP; 106 A; 104 C; 92 G; 101 T; 0 U; 3 Other;

Query Match	99.3%	Score 403;	DB 3;	Length 406;
Best Local Similarity	100.0%	Pred. No. 2.5e-121;		
Matches 406; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	GTAAATGTGGA	CTATATATATG	CAAGCTC	CAGANNAC	CTTGACG	GTGAGGCT	CCCCAT	TGGTTC	60
Db	1	GTAAATGTGGA	CTATATATATG	CCAGCTC	CAGANNAC	CTTGACG	GTGAGGCT	CCCCAT	TGGTTC 60
QY	61	CCCCAGGCCA	CAGTGGTCT	TGGGCAAT	CCCAAGTTG	ACGAGGAGCA	CTTCT	CGGAATGC	120
Db	61	CCCCAGGCCA	CAGTGGTCT	TGGGCAAT	CCCAAGTTG	ACGAGGAGCA	CTTCT	CGGAATGC	120
QY	121	TCCAAATAC	CAAGCTTTG	AGCTGAA	CTCTG	AGAAATGTG	ACCATGA	AGGTTGTCTG	180
Db	121	TCCAAATAC	CAAGCTTTG	AGCTGAA	CTCTG	AGAAATGTG	ACCATGA	AGGTTGTCTG	180
QY	181	TACAATGTTA	CCGATGCA	CAACAACAT	ATCTCTG	TATGATTTG	AAATGAC	ATTGGCA	240
Db	181	TACAATGTTA	CCGATGCA	CAACAACAT	ATCTCTG	TATGATTTG	AAATGAC	ATTGGCA	240
QY	241	ACAGAGGANT	ATCAAAATG	ACAAATCTG	GAGATCA	AAAGGCGAGAT	CACTTA	CAGCTGTA	300
Db	241	ACAGAGGANT	ATCAAAATG	ACAAATCTG	GAGATCA	AAAGGCGAGAT	CACTTA	CAGCTGTA	300
QY	301	AACTCAAAG	CTTCTCTG	TGTGTCTCTT	CTTTCTT	TGTCAT	CAGCTG	GGCACTT	360
Db	301	AACTCAAAG	CTTCTCTG	TGTGTCTCTT	CTTTCTT	TGTCAT	CAGCTG	GGCACTT	360
QY	361	CTAGAGCC	TTACTCTG	TATTAATAT	TATGTGCTT	TGGCCAA	CAAAAA	406	
Db	361	CTAGAGCC	TTACTCTG	TATTAATAT	TATGTGCTT	TGGCCAA	CAAAAA	406	

```

RESULT 2
ABZ11450
ID   ABZ11450 standard; cDNA; 1046 BP.
XX
AC   ABZ11450;
XX
DT   20-JAN-2003 (first entry)
XX
DE   Human polynucleotide SEQ ID NO 332.

```

KM Human, genome mapping; gene therapy; food supplement; virus; fungus;
KM cell-proliferative disorder; neurodegenerative disease; bacterial;
KM Parkinson's disease; Alzheimer's disease; autoimmune disease;
KM multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KM arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KM antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KM haemostatic; vulvareary; fungicide; antibacterial; virucide; protozoacide;
KM antihistaminic; gene; ss.

OS	Homo sapiens.
XX	
PN	W0200270539-A2.

PD 12-SEP-2002

PF 05-MAR-2002; 2002WO-US005095.

PR 05-MAR-2001; 2001US-00799451.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX

DR WPI; 2002-759812/82.
DR P-PSDB; ABP69233.

DR P-PSDB; ABP69233.

25 New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.

PS Claim 1; SEQ ID NO 332; 1012pp + Sequence Listing; English.

CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABZ68902-ABZ69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
 XX

Query Match	99.3%	Score 403;	DB 6;	Length 1046;
Best Local Similarity	99.3%;	Pred. No. 4e-121;		
Matches 403; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

Qy	1	GTGAATGTGACATTAATAAGCCAGCTCAGANNCTTTGGGGTGTGAGGCTCCCCAGATGGTTG	60
Db	505	GTGAATGTGACATTAATAAGCCAGCTCAGAGACCTTGGGGTGTGAGGCTCCCCAGATGGTTG	564
Qy	61	CCCCAGCCCAACAGTGGTCTGGGACATCCCAAGTTGACAGGAGGCAACTTCTCGGAAGTC	120
Db	565	CCCCAGCCCAACAGTGGTCTGGGACATCCCAAGTTGACAGGAGGCAACTTCTCGGAAGTC	624
Qy	121	TCCAAATACAGCTTTGAGCTGAACCTGTGAGAAATGTGACATGAAGTTGTGTCTGCTC	180
Db	625	TCCAAATACAGCTTTGAGCTGAACCTGTGAGAAATGTGACATGAAGTTGTGTCTGCTC	684
Qy	181	TACAAATGTTACGATCAACAACAACATCTCTGTATGATGAAATATGACATTTGCCAAMGA	240
Db	685	TACAAATGTTACGATCAACAACAACATCTCTGTATGATGAAATATGACATTTGCCAAMGA	744
Qy	241	ACAGGGGANTCAAAAGTGCAGAAATCGGAGATCAAAAGGCGGAGTCACTACAGCTGCTA	300
Db	745	ACAGGGGANTCAAAAGTGCAGAAATCGGAGATCAAAAGGCGGAGTCACTACAGCTGCTA	804
Qy	301	AACCTCAAGAGCTTCTCTGTGTCTCTTTCTTTTGGCATCAGCTGAGGCACTTTGCTCT	360
Db	805	AACCTCAAGAGCTTCTCTGTGTCTCTTTCTTTTGGCATCAGCTGAGGCACTTTGCTCT	864
Qy	361	CTAGGCTTACTGTATGCTAANATATATGTGCTTTGGGCACAAAAA	406
Db	865	CTAGGCTTACTGTATGCTAANATATATGTGCTTTGGGCACAAAAA	910

RESULT 3
ADM43968
ID ADM43968 standard; cDNA; 1046 BP

AC ADM43968;

DT 03-JUN-2004 (first entry)

DE Novel human arginine-rich protein cDNA #332.

ss; gene; human; arginine-rich protein; cancer; inflammation;

KX		genetic disorder.	
OS	Homo sapiens.		
XX	US2004053250-A1.		
XX	18-MAR-2004.		
XX	21-NOV-2002; 2002US-00302172.		
XX	05-MAR-2001; 2001US-00799451.		
PR	05-MAR-2002; 2002WO-US005095.		
PR	20-AUG-2002; 2002US-00225251.		
XX	(TANG/) TANG Y T.		
PA	(XUEB/) XUE A. T.		
PA	(DRMA/) DRMANAC R T.		
XX	Tang YT, Xue A, Drmanac RT;		
XX	WPI; 2004-236579/22.		
XX	The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel human arginine-rich protein cDNA.		
CC	Sequence 1046 BP; 306 A; 223 C; 250 G; 267 T; 0 U; 0 Other;		
SQ			
	Query Match	99.3%; Score 403; DB 12; Length 1046;	
	Best Local Similarity	99.3%; Pred. No. 4e-121;	
	Matches 403; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
OY	1 GTGAATGTGACTAATAATGCCAGCTCAGANNACCTTGCGGTGAGGGCTCCCCGATGTTTC	60	
Dd	505 GTGAATGTGACTAATAATGCCAGCTCAGAGACTTGCCTGTGAGGCTCCCCGATGTTTC	564	
OY	61 CCCCAAGCCCAAGTGTCTGTGGCATCCCAAGTTGACAGGAGGCCAACTTCTCGAAGTTC	120	
Dd	565 CCCCAGCCCAAGTGTCTGTGGCATCCCAAGTTGACAGGAGGCCAACTTCTCGAAGTTC	624	
OY	121 TCCAATACACAGCTTTGAGCTGAACCTGAGAATGAGCAATGAAGGTTGTGTCTGTGCTC	180	
Dd	625 TCCAATACACAGCTTTGAGCTGAACCTTAAGAATGAGCAATGAAGGTTGTGTCTGTGCTC	684	
OY	181 TACAATGTTAAGATCAACACACATCTCTGTATGATTGAAAATGACATTGCCAAGCA	240	
Dd	685 TACAATGTTAAGATCAACACACATCTCTGTATGATTGAAAATGACATTGCCAAGCA	744	
OY	241 ACAGGGGTTATCAAAGTAGACAGAACTCGAGATCAAAAAGCGGAGTCACTTACAGTGTCTA	300	
Dd	745 ACAGGGGTTATCAAAGTAGACAGAACTCGAGATCAAAAAGCGGAGTCACTTACAGTGTCTA	804	
OY	301 AACCTCAAAGGCTTCTGTGTGTCTCTTCTTTCTTTGGCATCAGCTGGGCACTTCTGCTT	360	
Dd	805 AACCTCAAAGGCTTCTGTGTGTGTCTCTTCTTTCTTTGGCATCAGCTGGGCACTTCTGCTT	864	
OY	361 CTCAGCCCTTAAGTGTATTAATATGATGTCCTTGGCCACAAAA 406		
Dd	865 CTCAGCCCTTAAGTGTATTAATATGATGTCCTTGGCCACAAAA 910		

ID	ABL55580	standard; cDNA; 1065 BP.
XX	ABL56580;	
XX	30-JUN-2002	(first entry)
XX	Nucleotide sequence of expressed sequence tag (EST) A1799522.	
XX	Human; gene A; ovarian tumour; gene B; ORO; ovarian cancer;	
XX	expressed sequence tag; EST; A1799522; ss.	
XX	Homo sapiens.	
XX	MO200194641-A2.	
XX	13-DEC-2001.	
XX	11-JUN-2001; 2001WO-US018700.	
XX	09-JUN-2000; 2000US-0210451P.	
XX	(IDEC-) IDEC PHARM CORP.	
XX	Opie E, McIlachlan K, Heard C;	
XX	WPI; 2002-404365/43.	
XX	New polynucleotide and corresponding antigens from human ovarian cancer	
XX	cells, useful for treatment and diagnosis of ovarian cancer.	
XX	Example 4; Fig 4c; 71pp: English.	
XX	The present sequence represents expressed sequence tag (EST) A1799522.	
XX	This EST was identified as a match to the novel gene B by database	
XX	analyses. Gene B was identified by representational difference analysis	
XX	(RDA) screening, and is selectively expressed by certain human ovarian	
XX	tumours. The specification also describes gene A, identified by the same	
XX	method. Gene A and B polynucleotides are useful for detecting ovarian	
XX	tumour. Gene A and B polynucleotides are useful for detecting ovarian	
XX	cancer. Their polypeptides are useful for treating ovarian cancer	
XX	Sequence 1065 BP; 293 A; 252 C; 257 G; 263 T; 0 U; 0 Other;	
XX	Query Match 99.3%; Score 403; DB 6; Length 1065;	
XX	Best Local Similarity 99.3%; Pred. No. 4.1e-121;	
XX	Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
XX	1 GTGAATGTGACCTTAATGACAGCTCAGAACCTTGCGGTGAGGCTCCCGATGGTTC	60
XX	534 GTGAATGTGACCTTAATGACAGCTCAGAACCTTGCGGTGAGGCTCCCGATGGTTC	593
XX	61 CCCAGGCCACAGTGTCTGGGACATCCCAAGTTGACGAGGACCACTTCGGAAGTC	120
XX	594 CCCAGGCCACAGTGTCTGGGACATCCCAAGTTGACGAGGACCACTTCGGAAGTC	653
XX	121 TCCAATACCAAGCTTTGAGCTGAAGCTTGAGATGTGACATGAAGGTTGTGTGCTC	180
XX	654 TCCAATACCAAGCTTTGAGCTGAAGCTTGAGATGTGACATGAAGGTTGTGTGCTC	713
XX	181 TACATGTGATGATCAACACACATCTCCGTGATGATGAAATGACATTTGCCAAAGCA	240
XX	714 TACATGTGATGATCAACACACATCTCCGTGATGATGAAATGACATTTGCCAAAGCA	773
XX	241 ACAGGGGATATCAAAAGTGACAGATTCGAGATTCAAAAGCGGAGTCACTTACAGTGTCTA	300
XX	774 ACAGGGGATATCAAAAGTGACAGATTCGAGATTCAAAAGCGGAGTCACTTACAGTGTCTA	833
XX	301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTCTTTGGCATCAGCTGGGCACTTCTGCT	360
XX	834 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTCTTTGGCATCAGCTGGGCACTTCTGCT	893

Qy 361 CTCAGCCCTTACTCTGATGCTAATATATGTCCTTGCCCAACAAAA 406
Db 894 CTCAGCCCTTACTCTGATGCTAATATATGTCCTTGCCCAACAAAA 939

RESULT 5

AAZ65059 standard; cDNA; 1657 BP.

AAZ65059;

05-APR-2000 (first entry)

Membrane-bound protein PRO1291 encoding cDNA.

Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.

Homo sapiens.

MO9963088-A2.

09-DEC-1999.

02-JUN-1999; 99WO-US012252.

02-JUN-1998; 98US-0087607P.

02-JUN-1998; 98US-0087609P.

03-JUN-1998; 98US-0087827P.

04-JUN-1998; 98US-0088021P.

04-JUN-1998; 98US-0088025P.

04-JUN-1998; 98US-0088028P.

04-JUN-1998; 98US-0088030P.

04-JUN-1998; 98US-0088033P.

04-JUN-1998; 98US-0088326P.

05-JUN-1998; 98US-0088167P.

05-JUN-1998; 98US-0088202P.

05-JUN-1998; 98US-0088212P.

05-JUN-1998; 98US-0088217P.

09-JUN-1998; 98US-0088655P.

10-JUN-1998; 98US-0088722P.

10-JUN-1998; 98US-0088730P.

10-JUN-1998; 98US-0088734P.

10-JUN-1998; 98US-0088740P.

10-JUN-1998; 98US-0088741P.

10-JUN-1998; 98US-0088742P.

10-JUN-1998; 98US-0088810P.

10-JUN-1998; 98US-0088811P.

10-JUN-1998; 98US-0088824P.

10-JUN-1998; 98US-0088825P.

10-JUN-1998; 98US-0088826P.

11-JUN-1998; 98US-0088858P.

11-JUN-1998; 98US-0088861P.

11-JUN-1998; 98US-0088863P.

11-JUN-1998; 98US-0088876P.

12-JUN-1998; 98US-0089090P.

12-JUN-1998; 98US-0089105P.

16-JUN-1998; 98US-0089400P.

16-JUN-1998; 98US-0089512P.

16-JUN-1998; 98US-0089514P.

17-JUN-1998; 98US-0089532P.

17-JUN-1998; 98US-0089538P.

17-JUN-1998; 98US-0089598P.

17-JUN-1998; 98US-0089599P.

17-JUN-1998; 98US-0089600P.

17-JUN-1998; 98US-0089653P.

18-JUN-1998; 98US-0089801P.

18-JUN-1998; 98US-0089907P.

18-JUN-1998; 98US-0089908P.

19-JUN-1998; 98US-0089947P.

PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090548P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092183P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.

PR 19-AUG-1998; 98US-0097141P.
 PR 20-AUG-1998; 98US-0097218P.
 PR 24-AUG-1998; 98US-0097661P.
 PR 26-AUG-1998; 98US-0097951P.
 PR 26-AUG-1998; 98US-0097952P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 26-AUG-1998; 98US-0097986P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098525P.
 PR 16-SEP-1998; 98US-0100634P.
 PR 12-JAN-1999; 99US-0115565P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX
 XX WPI, 2000-072883/06.
 DR P-PSDB; AAY66719.
 XX
 PT Membrane-bound proteins and related nucleotide sequences.
 XX
 PS Claim 2, Fig 207; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques
 XX
 XX Sequence 1657 BP; 521 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
 SO
 Query Match 99.3%; Score 403; DB 3; Length 1657;
 Best Local Similarity 99.3%; Pred. No. 5.1e-121;
 Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTGAATGTGACTATATATGCGAGCTCAGANACCTTGGGTGTGAGGCTCCCGATGTTTC 60
 DB 523 GTGAATGTGACTATATATGCGAGCTCAGACCTTGGGTGTGAGGCTCCCGATGTTTC 582
 QY 61 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGGCAACTTCTGGAAGTC 120
 DB 583 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGGCAACTTCTGGAAGTC 642
 QY 121 TCCAAATACAGAGCTTTGAGCTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 180
 DB 643 TCCAAATACAGAGCTTTGAGCTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 702
 QY 181 TACAATGTTCAGATCAACAACACATCTCTGTATGATTGAAATGACATTTGCCAAGCA 240
 DB 703 TACAATGTTCAGATCAACAACACATCTCTGTATGATTGAAATGACATTTGCCAAGCA 762
 QY 241 ACAGGGGATTCAGAGTGAAGAGATGAGAGATCAAAAGGCGAGTCACTTCAGAGTCTG 300
 DB 763 ACAGGGGATTCAGAGTGAAGAGATGAGAGATCAAAAGGCGAGTCACTTCAGAGTCTG 822
 QY 301 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCACTGAGTGGGCACTTTCGCT 360
 DB 823 AACTCAAGGCTTCTGTGTGTCTCTTTCTTTTCCATCACTGAGTGGGCACTTTCGCT 882

QY 361 CTCAGCCCTTACTGATGCTAATATATGTCCTTGGCCCAACAAAA 406
 DB 883 CTCAGCCCTTACTGATGCTAATATATGTCCTTGGCCCAACAAAA 928
 RESULT 6
 ADB90935
 ID ADB90935 standard; cDNA; 1657 BP.
 XX
 XX ADB90935;
 AC
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO1291 cDNA.
 XX
 XX ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
 KW affinity purification; secreted and transmembrane protein.
 XX
 OS Homo sapiens.
 OS
 XX
 PN US2003083473-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 03-MAY-2002; 2002US-00063595.
 PR
 PR 06-DEC-2001; 2001US-00006867.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 XX WPI; 2003-786922/74.
 DR P-PSDB; ADB90936.
 XX
 PT New antibody that binds a secreted and transmembrane polypeptide (PRO)
 PT for treating cancer and for diagnostic assays and affinity purification
 PT of PRO.
 PS
 PS Disclosure; Fig 59; 408pp; English.
 XX
 CC The invention describes an antibody that specifically binds to a PRO
 CC polypeptide having a fully defined amino acid sequence given in the
 CC specification. The antibody is useful in identifying PRO polypeptides,
 CC useful for various industrial applications, including pharmaceuticals,
 CC diagnostics, biosensors and bioreactors. The antibody is also used for
 CC affinity purification of PRO polypeptides from recombinant cell culture
 CC or natural sources. The antibody, PRO polypeptide, or its agonists or
 CC antagonists, may be used for preparing a medicament for diagnosing or
 CC treating a condition responsive to the antibody, PRO polypeptide, or its
 CC agonists or antagonists. This sequence encodes a novel human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX Sequence 1657 BP; 522 A; 357 C; 366 G; 412 T; 0 U; 0 Other;
 SO
 Query Match 99.3%; Score 403; DB 10; Length 1657;
 Best Local Similarity 99.3%; Pred. No. 5.1e-121;
 Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTGAATGTGACTATATATGCGAGCTCAGANACCTTGGGTGTGAGGCTCCCGATGTTTC 60
 DB 522 GTGAATGTGACTATATATGCGAGCTCAGACCTTGGGTGTGAGGCTCCCGATGTTTC 581
 QY 61 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGGCAACTTCTGGAAGTC 120
 DB 582 CCCAGGCCCAAGTGTGCTGGGATCCCAAGTTGACCAAGGAGGCAACTTCTGGAAGTC 641
 QY 121 TCCAAATACAGAGCTTTGAGCTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 180
 DB 642 TCCAAATACAGAGCTTTGAGCTGAACCTTGAGAAATGTGACATGAAGTTGTGTGCTC 701

```
QY 181 TACAAATGTTACGATCAACAACATATCTCTGTATGATGAAATGACATTGCCAAAGCA 240
DB 702 TTTTATGTTACGATCAACAACATATCTCTGTATGATGAAATGACATTGCCAAAGCA 761
QY 241 ACAGGGGATATCAAAAGTGCAGAAATGAGATCAAAAAGGCGAGTACTTACAGCTGCTA 300
DB 762 ACAGGGGATATCAAAAGTGCAGAAATGAGATCAAAAAGGCGAGTACTTACAGCTGCTA 821
QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTCTTCCATGACGTGGGCACTTGTGCT 360
DB 822 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTCTTCCATGACGTGGGCACTTGTGCT 881
QY 361 CTCAGCCCTTACCTGATGCTAANATATATGTGCTTGCCCAAAA 406
DB 882 CTCAGCCCTTACCTGATGCTAANATATATGTGCTTGCCCAAAA 927

RESULT 7
AAS46033
ID AAS46033 standard; cDNA; 1658 BP.
AC AAS46033;
XX
XX 18-DEC-2001 (first entry)
DT
XX
DE Human DNA encoding PRO polypeptide sequence #109.
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
XX PCR primer.
OS
XX Homo sapiens.
XX
XX MO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
XX 01-MAR-2000; 2000WO-US006501.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189320P.
XX 15-MAR-2000; 2000US-0189328P.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192555P.
XX 29-MAR-2000; 2000US-0193032P.
XX 29-MAR-2000; 2000US-0193053P.
XX 30-MAR-2000; 2000WO-US008439.
XX 04-APR-2000; 2000US-0194449P.
XX 04-APR-2000; 2000US-0194647P.
XX 11-APR-2000; 2000US-0195975P.
XX 11-APR-2000; 2000US-0196000P.
XX 11-APR-2000; 2000US-0196187P.
XX 11-APR-2000; 2000US-0196690P.
XX 11-APR-2000; 2000US-0196820P.
XX 18-APR-2000; 2000US-0198121P.
XX 18-APR-2000; 2000US-0198585P.
XX 25-APR-2000; 2000US-0199377P.
XX 25-APR-2000; 2000US-0199550P.
XX 25-APR-2000; 2000US-0199554P.
XX 03-MAY-2000; 2000US-0201516P.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
```

```
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH ) GENENTECH INC.
XX
XX PA
XX PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
XX
XX P-PSDB; AAU29132.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX PT presence of tumors, such as prostate and breast tumors, in mammals and to
XX PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 217; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
XX primers for PRO polypeptides of the invention. The sequences of the
XX CC invention can be used to detect the presence of a tumour in a mammal by
XX CC comparing the level of expression of a PRO polypeptide in a test sample
XX CC of cells from the animal and a control sample of normal cells, whereby a
XX CC higher level of expression in the test sample indicates the presence of a
XX CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
XX CC pigs, goats and rabbits but are preferably human. The polypeptides can be
XX CC used to stimulate tumour necrosis factor (TNF) alpha release from human
XX CC blood, when contacted with it. A specific polypeptide can be used to
XX CC stimulate the proliferation or differentiation of chondrocyte cells. The
XX CC PRO proteins can be used to determine the presence of tumours and also
XX CC susceptibility to tumour development, particularly adrenal, lung, colon,
XX CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
XX CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
XX CC can be used for genetic analysis of individuals with genetic disorders
XX
XX SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
XX
XX Query Match 99.3%; Score 403; DB 4; Length 1658;
XX Best Local Similarity 99.3%; Pred. No. 5,1e-121;
XX Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 GTGAATGTGACATTAATATCCAGCTCAGANACCTTGCGGTGAGGCTCCCGATGCTTC 60
DB 523 GTGAATGTGACATTAATATCCAGCTCAGAGACCTTGCGGTGAGGCTCCCGATGCTTC 582
QY 61 CCCAGCCCAAGTGTGTGGGATCCCAAGTTGACAGGAGGCCAATCTTCGGAGTTC 120
DB 583 CCCAGCCCAAGTGTGTGGGATCCCAAGTTGACAGGAGGCCAATCTTCGGAGTTC 642
QY 121 TCCATATACAGCTTGAAGCTGAACCTGAGAAATGACATGAGAGTGTGTGCTC 180
DB 643 TCCATATACAGCTTGAAGCTGAACCTGAGAAATGACATGAGAGTGTGTGCTC 702
QY 181 TACAAATGTTACGATCAACAACATATCTCTGTATGATGAAATGACATTGCCAAAGCA 240
DB 703 TTTTATGTTACGATCAACAACATATCTCTGTATGATGAAATGACATTGCCAAAGCA 762
QY 241 ACAGGGGATATCAAAAGTGCAGAAATGAGATCAAAAAGGCGAGTACTTACAGCTGCTA 300
DB 763 ACAGGGGATATCAAAAGTGCAGAAATGAGATCAAAAAGGCGAGTACTTACAGCTGCTA 822
QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTCTTCCATGACGTGGGCACTTGTGCT 360
DB 823 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTCTTCCATGACGTGGGCACTTGTGCT 882
QY 361 CTCAGCCCTTACCTGATGCTAANATATATGTGCTTGCCCAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAANATATATGTGCTTGCCCAAAA 928
```

RESULT 8

AAFP92087 standard; cDNA; 1658 BP.

AAFP92087;

15-MAY-2001 (first entry)

Human PRO1291 cDNA.

Human; PRO protein; mapping; ss.

Homo sapiens.

WO200116318-A2.

08-MAR-2001.

24-AUG-2000; 2000WO-US023328.

01-SEP-1999; 99WO-US020111.

15-SEP-1999; 99WO-US021090.

07-DEC-1999; 99US-0169495P.

09-DEC-1999; 99US-0170262P.

11-JAN-2000; 2000US-0175481P.

18-FEB-2000; 2000WO-US004341.

22-FEB-2000; 2000WO-US004414.

01-MAR-2000; 2000WO-US005601.

03-MAR-2000; 2000US-0187202P.

21-MAR-2000; 2000US-0191007P.

30-MAR-2000; 2000WO-US006439.

25-APR-2000; 2000US-0199397P.

22-MAY-2000; 2000WO-US014042.

05-JUN-2000; 2000US-0209832P.

(GETH) GENENTECH INC.

Batton DL, Filvaroff E, Gerritson ME, Goddard A, Godowski PJ;

Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

WPI; 2001-183260/18.

P-PSDB; AAB87555.

Eighty four nucleic acids encoding PRO polypeptides, useful in molecular

biology, including use as hybridization probes, and in chromosome and

gene mapping.

Claim 2; Fig 59; 278bp; English.

The present sequence is the coding sequence for a human PRO polypeptide

(secreted and transmembrane). The PRO protein, and PRO agonists, PRO

antagonists or anti-PRO antibodies are useful for preparation of a

medicament useful in the treatment of a condition which is responsive to

the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

protein may also be employed as molecular weight markers for protein

electrophoresis. The PRO coding sequence has applications in molecular

biology, including use as hybridisation probes, and in chromosome and

gene mapping

Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 99.3%; Score 403; DB 4; Length 1658;

Best Local Similarity 99.3%; Pred. NO. 5.1e-121;

Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GTGAATGTGACATATATGACAGCTGAGACCTTGGGTAGAGCTCCCGATGGTTC 60

523 GTGAATGTGACATATATGACAGCTGAGACCTTGGGTAGAGCTCCCGATGGTTC 582

61 CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACAGGAGCCAACTTCTCGAAGTC 120

Db 583 CCCAGGCCACAGTGTCTGGGATCCCAAGTTGACAGGAGCCAACTTCTCGAAGTC 642

Qy 121 TCCATATACAGCTTTAGAGTGAATCTGGAATGACATGAGGTGTCGTGCTC 180

Db 643 TCCATATACAGCTTTAGAGTGAATCTGGAATGACATGAGGTGTCGTGCTC 702

Qy 181 TACATGTTACGATCAACACATATCTCTGTATGTAATGACATTTGCCAAGCA 240

Db 703 TACATGTTACGATCAACACATATCTCTGTATGTAATGACATTTGCCAAGCA 762

Qy 241 ACAGGGGATATCAAGTGAAGATGAGATCAAAAAGCGAGTCACTACAGCTGCTA 300

Db 763 ACAGGGGATATCAAGTGAAGATGAGATCAAAAAGCGAGTCACTACAGCTGCTA 822

Qy 301 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATGAGTGGGCACTTGCCCT 360

Db 823 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATGAGTGGGCACTTGCCCT 882

Qy 361 CTCAGCCCTTACCTGATGCTAATATATGCTTGGCCACAAAA 406

Db 883 CTCAGCCCTTACCTGATGCTAATATATGCTTGGCCACAAAA 928

RESULT 9

AAFP4205 standard; cDNA; 1658 BP.

AAFP4205;

02-APR-2001 (first entry)

Human PRO1291 (UNQ659) nucleotide sequence SEQ ID NO:290.

Human; secreted and transmembrane protein; PRO; cytosolic; cell death;

cancer; Chromosomal mapping; gene mapping; tissue typing;

diagnostic assay; ss.

Homo sapiens.

WO200073454-A1.

07-DEC-2000.

30-MAR-2000; 2000WO-US008439.

02-JUN-1999; 99WO-US012252.

23-JUN-1999; 99US-0141037P.

07-JUL-1999; 99US-0143048P.

20-JUL-1999; 99US-0144758P.

26-JUL-1999; 99US-0145698P.

28-JUL-1999; 99US-0146222P.

17-AUG-1999; 99US-0149396P.

15-SEP-1999; 99WO-US021090.

15-SEP-1999; 99WO-US021547.

08-OCT-1999; 99US-0158633P.

30-NOV-1999; 99WO-US028313.

01-DEC-1999; 99WO-US028301.

16-DEC-1999; 99WO-US030095.

20-DEC-1999; 99WO-US030911.

06-JAN-2000; 2000WO-US000219.

PR 11-FEB-2000; 2000WO-US003565.

PR 16-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 02-MAR-2000; 2000WO-US005004.

PR 15-MAR-2000; 2000WO-US005841.

PR 20-MAR-2000; 2000WO-US006884.

(GETH) GENENTECH INC.

Aahkenazi AJ, Baker KP, Botstein D, Desnoyers L, Batton DL;

PI Ferrara N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Matanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR P-PSDB; AAB65242.

PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.

PS Claim 2; Fig 207; 935pp; English.

CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention

XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

XX Query Match 99.3%; Score 403; DB 5; Length 1658;

XX Best Local Similarity 99.3%; Pred. No. 5.1e-121;

XX Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGAGTATTAATGCGAGCTGAGAACCTTGGGTGAGGCTCCCGAGTCTTC 60

DB 523 GTGAATGTGAGTATTAATGCGAGCTGAGAACCTTGGGTGAGGCTCCCGAGTCTTC 582

QY 61 CCCGAGCCCAAGTGTGTCGGGATCCCAAGTTGACAGAGGCCCACTTCCGGAAGTC 120

DB 583 CCCGAGCCCAAGTGTGTCGGGATCCCAAGTTGACAGAGGCCCACTTCCGGAAGTC 642

QY 121 TCCATATCAGAGCTTGTAGGCTGAACTCTGAGAAATGTGAGTGAAGGTTGTCTGTCTC 180

DB 643 TCCATATCAGAGCTTGTAGGCTGAACTCTGAGAAATGTGAGTGAAGGTTGTCTGTCTC 702

QY 181 TACAATGTTACGATCAACAACACATACCTCTGTATGATTGAATAATGACATTGCCAAGA 240

DB 703 TACAATGTTACGATCAACAACACATACCTCTGTATGATTGAATAATGACATTGCCAAGA 762

QY 241 ACAAGGGGATTCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300

DB 763 ACAAGGGGATTCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 822

QY 301 AACTCAAGAGCTCTCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

DB 823 AACTCAAGAGCTCTCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 882

QY 361 CTCAGCCCTTACCTGATGCTAANATATGTCCTTGCCCAAAAA 406

DB 883 CTCAGCCCTTACCTGATGCTAANATATGTCCTTGCCCAAAAA 928

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Tumour associated antigenic target polypeptide; TAT; cancer;
XX breast cancer; colorectal cancer; lung cancer; ovarian cancer;
XX central nervous system cancer; liver cancer; bladder cancer;
XX pancreatic cancer; cervical cancer; melanoma; leukaemia; TAT136; gene;
XX ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 61..909

XX FT /tag= b

XX FT /product= "TAT136"

XX FT /note= "Tumour associated antigenic target polypeptide"

XX FT sig_peptide 61..144

XX FT /tag= a

XX FT mat_peptide 145..906

XX FT /tag= c

XX FT /label= Mature_TAT136

XX PN WO200216581-A2.

XX PD 28-FEB-2002.

XX PF 14-AUG-2001; 2001WO-US025464.

XX PF 24-AUG-2000; 2000WO-US023328.

XX PR 28-FEB-2001; 2001WO-US006520.

XX PR 22-JUN-2001; 2001US-00888257.

XX PR 22-JUN-2001; 2001WO-US020118.

XX PA (GENENTECH INC.

XX PI Gao W, Polakis P, Shou J, Smith V, Soriano R, Williams PM;

XX PI Wu TD, Zhang Z;

XX PI WPI; 2002-280928/32.

XX DR P-PSDB; AAU77766.

XX DR

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

XX Query Match 99.3%; Score 403; DB 6; Length 1658;

XX Best Local Similarity 99.3%; Pred. No. 5.1e-121;

XX Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGAGTATTAATGCGAGCTGAGAACCTTGGGTGAGGCTCCCGAGTCTTC 60

DB 523 GTGAATGTGAGTATTAATGCGAGCTGAGAACCTTGGGTGAGGCTCCCGAGTCTTC 582

QY 61 CCCGAGCCCAAGTGTGTCGGGATCCCAAGTTGACAGAGGCCCACTTCCGGAAGTC 120

DB 583 CCCGAGCCCAAGTGTGTCGGGATCCCAAGTTGACAGAGGCCCACTTCCGGAAGTC 642

XX

XX

XX

XX

XX

XX

XX

```

QY      121  TCCAAATACGACCTTTGAGTGAAGTCTGAGATGTGACATGAGAAAGTTGTGTCCTC 180
        |||||
Db      643  TCCAAATACGACCTTTGAGTGAAGTCTGAGATGTGACATGAGAAAGTTGTGTCCTC 702
QY      181  TACAAATGTACGATCAACAACACATCTCTGTATGATTTAAAAATGACATTTGCCAAGCA 240
        |||||
Db      703  TACAAATGTACGATCAACAACACATCTCTGTATGATTTAAAAATGACATTTGCCAAGCA 762
QY      241  ACGAGGGATTCAAAGTGAAGATTCGAGATCAAAAAGGGGAGTCACTTACAGTCTCTA 300
        |||||
Db      763  ACGAGGGATTCAAAGTGAAGATTCGAGATCAAAAAGGGGAGTCACTTACAGTCTCTA 822
QY      301  AACTCAAAAGGCTCTCTGTGTGCTCTTCTTTCTTTGGCATACGCTGGGACCTTCTGCT 360
        |||||
Db      823  AACTCAAAAGGCTCTCTGTGTGCTCTTCTTTCTTTGGCATACGCTGGGACCTTCTGCT 882
QY      361  CTCAGCCCTTACCTGATGTANATATATGTCCTTGCCCAAAAA 406
        |||||
Db      883  CTCAGCCCTTACCTGATGTANATATATGTCCTTGCCCAAAAA 928

RESULT 11
ID      ABS74407 standard; cDNA; 1658 BP.
XX      ABS74407;
AC      ABS74407;
XX      10-DEC-2002 (first entry)
DT      Human cDNA encoding secreted/transmembrane protein PRO1291.
XX      Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
XX      antirheumatic; osteopathic; sports-related joint problem;
XX      articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX      Homo sapiens.
XX      US2002119130-A1.
XX      29-AUG-2002.
XX      06-DEC-2001; 2001US-0006867.
XX      29-OCT-1997; 97US-0063435P.
XX      29-OCT-1997; 97US-0064215P.
XX      22-APR-1998; 98US-0082797P.
XX      29-APR-1998; 98US-0083495P.
XX      15-MAY-1998; 98US-0085579P.
XX      02-JUN-1998; 98US-0087759P.
XX      04-JUN-1998; 98US-0088021P.
XX      04-JUN-1998; 98US-0088029P.
XX      04-JUN-1998; 98US-0088030P.
XX      10-JUN-1998; 98US-0088734P.
XX      10-JUN-1998; 98US-0088740P.
XX      10-JUN-1998; 98US-0088811P.
XX      10-JUN-1998; 98US-0088824P.
XX      10-JUN-1998; 98US-0088825P.
XX      11-JUN-1998; 98US-0088863P.
XX      12-JUN-1998; 98US-0089105P.
XX      16-JUN-1998; 98US-0089514P.
XX      17-JUN-1998; 98US-0089653P.
XX      19-JUN-1998; 98US-0089952P.
XX      22-JUN-1998; 98US-0090246P.
XX      24-JUN-1998; 98US-0090444P.
XX      25-JUN-1998; 98US-0090688P.
XX      25-JUN-1998; 98US-0090696P.
XX      26-JUN-1998; 98US-0090862P.
XX      02-JUL-1998; 98US-0091628P.
XX      10-AUG-1998; 98US-0096012P.
XX      17-AUG-1998; 98US-0096757P.
XX      18-AUG-1998; 98US-0096949P.
XX      18-AUG-1998; 98US-0096959P.
XX      26-AUG-1998; 98US-0097954P.

```

```

PR      26-AUG-1998; 98US-0097971P.
PR      26-AUG-1998; 98US-0097979P.
PR      01-SEP-1998; 98US-0098749P.
PR      10-SEP-1998; 98US-0099741P.
PR      10-SEP-1998; 98US-0099763P.
PR      10-SEP-1998; 98US-0099792P.
PR      10-SEP-1998; 98US-0099812P.
PR      10-SEP-1998; 98US-0099815P.
PR      16-SEP-1998; 98US-0100627P.
PR      16-SEP-1998; 98US-0100662P.
PR      16-SEP-1998; 98US-01019330.
PR      17-SEP-1998; 98US-0100683P.
PR      17-SEP-1998; 98US-0100684P.
PR      17-SEP-1998; 98US-0100930P.
PR      22-SEP-1998; 98US-0101279P.
PR      23-SEP-1998; 98US-0101475P.
PR      24-SEP-1998; 98US-0101738P.
PR      24-SEP-1998; 98US-0101743P.
PR      24-SEP-1998; 98US-0101916P.
PR      30-SEP-1998; 98US-0102570P.
PR      06-OCT-1998; 98US-0103449P.
PR      08-MAR-1999; 99US-05005028.
PR      14-MAY-1999; 99US-05010733.
PR      02-JUN-1999; 99US-05012252.
PR      01-SEP-1999; 99US-05020111.
PR      15-SEP-1999; 99US-05021090.
PR      15-SEP-1999; 99US-05021194.
PR      22-DEC-1999; 99US-05030720.
PR      18-FEB-2000; 2000US-05004341.
PR      18-FEB-2000; 2000US-05004342.
PR      22-FEB-2000; 2000US-05004414.
PR      01-MAR-2000; 2000US-05005601.
PR      30-MAR-2000; 2000US-05008439.
PR      22-MAY-2000; 2000US-05014042.
PR      02-JUN-2000; 2000US-05015264.
PR      23-AUG-2000; 2000US-05023522.
PR      24-AUG-2000; 2000US-05023328.
PR      10-NOV-2000; 2000US-05030873.
PR      01-DEC-2000; 2000US-05032378.
PR      20-DEC-2000; 2000US-05034956.
PR      28-FEB-2001; 2001US-05006520.
PR      01-MAR-2001; 2001US-05006666.
PR      30-MAY-2001; 2001US-05017443.
PR      01-JUN-2001; 2001US-05017800.
PR      20-JUN-2001; 2001US-05019692.
PR      29-JUN-2001; 2001US-05021066.
PR      09-JUL-2001; 2001US-05021735.
XX      (GENTH ) GENENTECH INC.
XX      Batton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX      Pi Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX      WPI; 2002-731348/79.
XX      P-RSDB; ABG95880.
XX      New isolated secreted and transmembrane PRO polypeptide useful for
XX      PT modulating biological activity of a cell, or for treating sports-related
XX      PT joint problems, osteoarthritis or rheumatoid arthritis.
XX      Claim 2; Fig 59; 39pp; English.
XX      The invention relates to an isolated secreted and transmembrane PRO
XX      CC polypeptide having 80 % sequence identity to a sequence appearing as
XX      CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
XX      CC extracellular domain of the proteins with their associated signal peptide
XX      CC or lacking its associated signal peptide. Also included are the nucleic
XX      CC acids encoding the proteins, vectors, host cells, fusion proteins and
XX      CC antibodies which specifically bind to the proteins. The proteins are
XX      CC useful for detecting a polypeptide designated as A, B, C or D in a sample
XX      CC suspected of containing an A, B, C or D polypeptide, by contacting the
XX      CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
XX      CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide

```

CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the
 CC invention

XX SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

XX Query Match 99.3%; Score 403; DB 6; Length 1658;
 XX Best Local Similarity 99.3%; Pred. No. 5.1e-121;
 XX Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGAGCTATATATGCGAGCTGAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 60
 DB 523 GTGAATGTGAGCTATATATGCGAGCTGAGAGACCTTGCGGTGTGAGGCTCCCGATGTTTC 582
 QY 61 CCCGACCCCAAGTGTCTGGGATCCCAAGTTGACAGAGAGCCCACTTTCGGAAGTC 120
 DB 583 CCCGACCCCAAGTGTCTGGGATCCCAAGTTGACAGAGAGCCCACTTTCGGAAGTC 642
 QY 121 TCCAAATACAGCTTGTAGCTGAACTCTGGAATGTGACCATGAAAGTTGTCTGTGCTC 180
 DB 643 TCCAAATACAGCTTGTAGCTGAACTCTGGAATGTGACCATGAAAGTTGTCTGTGCTC 702
 QY 181 TCAATGTGTAGATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 240
 DB 703 TCAATGTGTAGATCAACAACATCTCTGTATGATTTGAAATGACATTTGCCAAGCA 762
 QY 241 ACAAGGGGATATCAAAAGTGCAGATGCAAAAGGCGAGTCACTACAGCTGCTA 300
 DB 763 ACAAGGGGATATCAAAAGTGCAGATGCAAAAGGCGAGTCACTACAGCTGCTA 822
 QY 301 AACTCAAAAGGCTTCTGTGTGCTCTTCTTTCTTTGCGATCAGCTGGGACATTCGCT 360
 DB 823 AACTCAAAAGGCTTCTGTGTGCTCTTCTTTCTTTGCGATCAGCTGGGACATTCGCT 882
 QY 361 CTTCAGCCCTTACCTGATGCTAANATATGATGCTTGGCCACAAAAA 406
 DB 883 CTTCAGCCCTTACCTGATGCTAANATATGATGCTTGGCCACAAAAA 928

RESULT 12
 ABK11091
 ID ABK11091 standard; cDNA; 1658 BP.
 AC ABK11091;
 XX
 DT 05-JUN-2002 (first entry)

XX DE cDNA encoding tumour-associated antigenic target protein, TAT136.
 XX TAT136: Tumour-associated Antigenic Target; tumour; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer;
 KW central nervous system cancer; liver cancer; bladder cancer; melanoma;
 KW pancreatic cancer; leukemia; gene therapy; gene; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 61..909
 FT /*tag= a
 FT /product= "TAT136"
 FT /note= "Tumour-associated antigenic target"
 XX PN WO200216428-A2.
 XX PD 28-FEB-2002.
 XX PF 22-JUN-2001; 2001WO-US020118.
 XX PR 24-AUG-2000; 2000WO-US023328.
 XX PR 26-SEP-2000; 2000US-0235451P.
 XX PR 01-DEC-2000; 2000WO-US032678.
 XX PR 28-FEB-2001; 2001WO-US006520.
 XX PR 01-MAR-2001; 2001WO-US006666.
 XX PA (GENTECH) GENENTECH INC.
 XX PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,
 XX PI Wood WI, Wu TD, Zhang Z;
 XX DR MPI: 2002-280917/32.
 XX DR P-PsDB; AAU76536.
 XX PT Novel isolated tumor-associated antigenic target polypeptides which are
 XX PT useful as targets for cancer therapy and diagnosis in mammals.
 XX PS Claim 1; Fig 3; 121pp; English.

XX The invention relates to an isolated tumour-associated antigenic target
 CC polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the
 CC polynucleotides (II) encoding them. (II) is useful for diagnosing the
 CC presence of a tumour in a mammal, where the level of expression of (II)
 CC is indicative on the presence of tumour in the mammal from which the test
 CC sample was obtained. Antibody to (I) is useful for killing a cancer cell,
 CC (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
 CC an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
 CC liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
 CC melanoma cell or a leukemia cell) that expresses (I). Oligonucleotides
 CC hybridising to (II) are useful as diagnostic probes, antisense
 CC oligonucleotide probes or for encoding fragments of full length TAT
 CC polypeptide. (II) is also useful in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA probes, for constructing
 CC hybridisation probes for mapping the gene encoding TAT and for genetic
 CC analysis of individuals with genetic disorders. (II) is also useful for
 CC generating either transgenic animals or knockout animals, and in gene
 CC therapy. The TAT polypeptides and nucleic acids may also be used for
 CC tissue typing and the TAT polypeptides are useful for screening compounds
 CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
 CC polypeptide (antagonist). The antibody is useful for staging TAT
 CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT
 CC polypeptide from cells, for detection and quantitation of TAT polypeptide
 CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
 CC Western blot. The antibodies are also useful for treating a TAT-
 CC expressing cancer or alleviating one or more symptoms of cancer in a
 CC mammal. The present sequence represents the coding sequence of TAT136
 XX
 XX SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

XX Query Match 99.3%; Score 403; DB 6; Length 1658;
 XX Best Local Similarity 99.3%; Pred. No. 5.1e-121;

PR	24-NOV-1997;	97US-0066772P
PR	11-DEC-1997;	97US-0069335P
PR	12-DEC-1997;	97US-0069425P
PR	17-DEC-1997;	97US-0069870P
PR	18-DEC-1997;	97US-0068017P
PR	10-MAR-1998;	98US-0077450P
PR	11-MAR-1998;	98US-0077632P
PR	11-MAR-1998;	98US-0077649P
PR	20-MAR-1998;	98US-0078886P
PR	20-MAR-1998;	98US-0078939P
PR	27-MAR-1998;	98US-0079664P
PR	27-MAR-1998;	98US-0079786P
PR	31-MAR-1998;	98US-0080107P
PR	31-MAR-1998;	98US-0080194P
PR	01-APR-1998;	98US-0080377P
PR	01-APR-1998;	98US-0080333P
PR	08-APR-1998;	98US-0081049P
PR	08-APR-1998;	98US-0081070P
PR	09-APR-1998;	98US-0081195P
PR	15-APR-1998;	98US-0081838P
PR	21-APR-1998;	98US-0082568P
PR	21-APR-1998;	98US-0082592P
PR	22-APR-1998;	98US-0082704P
PR	22-APR-1998;	98US-0082797P
PR	28-APR-1998;	98US-0083322P
PR	29-APR-1998;	98US-0083452P
PR	29-APR-1998;	98US-0083466P
PR	29-APR-1998;	98US-0083499P
PR	29-APR-1998;	98US-0083559P

PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.

PR	07-MAY-1998;	9805-0084643P;
PR	15-MAY-1998;	9805-0085579P;
PR	15-MAY-1998;	9805-0085580P;
PR	15-MAY-1998;	9805-0085582P;
PR	15-MAY-1998;	9805-0085700P;
PR	18-MAY-1998;	9805-0086023P;
PR	22-MAY-1998;	9805-0086392P;

PR 28-MAY-1998; 98US-0087098P;
PR 28-MAY-1998; 98US-0087208P;
PR 02-JUN-1998; 98US-0087609P;
PR 02-JUN-1998; 98US-0087759P;
PR 03-JUN-1998; 98US-0087827P;
PR 04-JUN-1998; 98US-0088025P;
PR 04-JUN-1998; 98US-0088028P;
PR 04-JUN-1998; 98US-0088028P;

PR	04-JUN-1998:	98US-0088033P.
PR	04-JUN-1998:	98US-0088029P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088212P.

PR 09-JUN-1998; 98US-0088655P.

PR	10-JUN-1998	98US-0088738P
PR	10-JUN-1998	98US-0088740P
PR	10-JUN-1998	98US-0088811P
PR	10-JUN-1998	98US-0088824P
PR	10-JUN-1998	98US-0088825P
PR	10-JUN-1998	98US-0088826P
PR	10-JUN-1998	98US-0088831P
PR	11-JUN-1998	98US-0088863P
PR	11-JUN-1998	98US-0088866P
PR	11-JUN-1998	98US-0088876P
PR	12-JUN-1998	98US-0089090P
PR	12-JUN-1998	98US-0089105P
PR	16-JUN-1998	98US-0089512P
PR	16-JUN-1998	98US-0089514P
PR	17-JUN-1998	98US-0089538P
PR	17-JUN-1998	98US-0089598P
PR	17-JUN-1998	98US-0089653P

PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090680P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095988P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096899P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0098602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 23-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.

PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 99.3%; Score 403; DB 8; Length 1658;
Best Local Similarity 99.3%; Pred No. 5; Ie-121;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATATATGCGAGTCCAGAACTTGGGGTGTGAGGCTCCCGATGTTTC 60
DB 523 GTGAATGTGACTATATATGCGAGTCCAGAACTTGGGGTGTGAGGCTCCCGATGTTTC 582
QY 61 CCCGAGCCCAAGTGTGTGGGCATCCCAAGTTGACCAAGGAGCCCACTTCCGAAATC 120
DB 583 CCCGAGCCCAAGTGTGTGGGCATCCCAAGTTGACCAAGGAGCCCACTTCCGAAATC 642
QY 121 TCCAAATACCACTTTGAGGCTGAACTCTGAGAAATGAGCAATGAGTTGTGTGCTC 180
DB 643 TCCAAATACCACTTTGAGGCTGAACTCTGAGAAATGAGCAATGAGTTGTGTGCTC 702
QY 181 TCAATGTTAGCATCAACAACATATCTCTGTATGATTGAATAATGACATTGCCAAAGCA 240
DB 703 TCAATGTTAGCATCAACAACATATCTCTGTATGATTGAATAATGACATTGCCAAAGCA 762
QY 241 AAGAGGATATCAAAAGTGCACAAATCGAGATCAAAAGGCGAGTCACTAGCTGCTA 300
DB 763 AAGAGGATATCAAAAGTGCACAAATCGAGATCAAAAGGCGAGTCACTAGCTGCTA 822
QY 301 AACTCAAAAGCTTCTGTGTGTCTCTCTTTCTTTGCAATGAGTGGGCACTTGTGCT 360
DB 823 AACTCAAAAGCTTCTGTGTGTCTCTCTTTCTTTGCAATGAGTGGGCACTTGTGCT 882
QY 361 CTCAGCCCTTACCTGATGCTAATATATGTCCTTGGCCCAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAATATATGTCCTTGGCCCAAAA 928
RESULT 14
ACA73493
ID ACA73493 standard; cDNA; 1658 BP.
XX
AC ACA73493;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #109.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
OS Homo sapiens.
XX
PN US2003036146-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187603.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98US-00193330.
PR 07-OCT-1998; 98US-00168978.

PR 07-OCT-1998; 98MO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98MO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99MO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012352.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99MO-US028301.
PR 02-DEC-1999; 99MO-US028551.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 15-MAR-2000; 2000MO-US006884.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014841.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000MO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001MO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001MO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2003-332034/31.
DR P-PSDB; ABUS6301.
XX
XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
PT gene therapy, chromosome identification, tissue typing, and for detecting

PT the presence of tumor in a mammal.

XX
XX Claim 2; Fig 217; 707bp; English.

XX
XX The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
CC them, or encoding a PRO polypeptide lacking its associated signal peptide
CC or an extracellular domain of the PRO polypeptide, with or lacking its
CC associated signal peptide. Also included are the encoded PRO proteins,
CC PRO expression vectors, host cells transformed with the vector (used to
CC produce PRO proteins), a chimeric molecule comprising the PRO
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, a method for stimulating the release of tumor necrosis factor
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
CC PRO827, PRO791, PRO1131, PRO3316, PRO1183, PRO1343, PRO1760, PRO1567 or
CC PRO4333), a method for stimulating the proliferation or differentiation
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
CC a method for detecting the presence of tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating the
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a cDNA encoding a PRO
XX protein

XX
SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 99.3%; Score 403; DB 8; Length 1658;

Best Local Similarity 99.3%; Pred. No. 5,1e-121;

Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATATATGCGAGCTCAGAAACCTTGCGGTGAGGCTCCCGATGCTTC 60
DB 523 GTGAATGTGACTATATATGCGAGCTCAGAAACCTTGCGGTGAGGCTCCCGATGCTTC 582
QY 61 CCCAGCCCAAGTGTGCGGATCCCAAGTTGACCAAGGAGCCAACTTTGCGAAGTC 120
DB 583 CCCAGCCCAAGTGTGCGGATCCCAAGTTGACCAAGGAGCCAACTTTGCGAAGTC 642
QY 121 TCCATATCAGAGCTTTGAGCTGGAAGTGTGAGATGTCACATGAAGTTGTGTGCTC 180
DB 643 TCCATATCAGAGCTTTGAGCTGGAAGTGTGAGATGTCACATGAAGTTGTGTGCTC 702
QY 181 TACATGTTACGATCAACAACACATATCTCTGTATGATTGAANAATGACATTGCCAAGCA 240
DB 703 TACATGTTACGATCAACAACACATATCTCTGTATGATTGAANAATGACATTGCCAAGCA 762
QY 241 ACAGGGGATATCAAAATGACAGAAATGGAGATCAAAAGGCGAGTACCTACAGCTGCTTA 300
DB 763 ACAGGGGATATCAAAATGACAGAAATGGAGATCAAAAGGCGAGTACCTACAGCTGCTTA 822
QY 301 AACTCAAGGCTTCTGTGTGTGTCTCTTTCTTTGCGATCAGCTGAGGACCTTTCGCT 360
DB 823 AACTCAAGGCTTCTGTGTGTGTCTCTTTCTTTGCGATCAGCTGAGGACCTTTCGCT 882
QY 361 CTCAGCCCTTACCTGATGCTAANAATATGAGTGGCTTGCCCACAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAANAATATGAGTGGCTTGCCCACAAAA 928

Db	763	ACAGGGATATCAAAAGTGAAGAAATCGAGATCAAAAGGCGAGTCACTACAGCTGTIA	822
Qy	301	AACTCAAAGGCTTCTCTGTGTCTCTCTTTCTTTTGGCAATCAAGTGGGCACTTCTGCT	360
Db	823	AACTCAAAGGCTTCTCTGTGTCTCTCTTTCTTTTGGCAATCAAGTGGGCACTTCTGCT	882
Qy	361	CTGAGCCCTTACCTGATGCTAATATATGTCCTTGGCCACAAAA	406
Db	883	CTGAGCCCTTACCTGATGCTAATATATGTCCTTGGCCACAAAA	928

Search completed: May 30, 2005, 10:27:13
Job time : 251.008 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 ; Search time 75.2473 Seconds

(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-12

Perfect score: 406
1 ggcagatgctgacataatgc.....atgtgccttgcccaaaaa 406

Sequence: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403	99.3	1046	US-09-799-451-332	Sequence 332, App
2	403	99.3	2627	US-09-404-879A-391	Sequence 391, App
3	403	99.3	2627	US-09-667-857-391	Sequence 391, App
4	38	9.4	69813	US-09-949-016-12455	Sequence 12455, A
5	38	9.4	69813	US-09-949-016-13905	Sequence 13905, A
6	38	9.4	69813	US-09-949-016-13905	Sequence 13905, A
7	38	9.4	69813	US-09-949-016-13905	Sequence 13905, A
8	34.8	8.6	1141	US-09-806-708B-22	Sequence 22, Appl
9	34.6	8.5	13204	US-09-054-272-49	Sequence 49, Appl
10	32.4	8.0	364	US-09-621-976-17202	Sequence 17202, A
11	32.2	7.9	38564	US-09-734-673-3	Sequence 3, Appl1
12	32	7.9	6749	US-08-961-527-84	Sequence 84, Appl
13	32	7.9	9062	US-08-956-171B-85	Sequence 85, Appl
14	32	7.9	9062	US-08-781-986A-85	Sequence 85, Appl
15	32	7.9	36611	US-09-949-016-11900	Sequence 11287, A
16	32	7.9	144362	US-09-949-016-16066	Sequence 16066, A
17	31.8	7.8	94156	US-09-949-016-12388	Sequence 12388, A
18	31.8	7.8	102406	US-09-949-016-14673	Sequence 14673, A
19	31.4	7.7	61777	US-09-949-016-17278	Sequence 17278, A
20	31.4	7.7	89716	US-09-949-016-11900	Sequence 11900, A
21	30.8	7.6	809	US-09-248-796A-6226	Sequence 6226, Ap
22	30.8	7.6	809	US-08-441-629-1	Sequence 1, Appl1
23	30.8	7.6	809	US-08-776-207-1	Sequence 1, Appl1
24	30.8	7.6	809	US-09-507-773-1	Sequence 1, Appl1
25	30.8	7.5	809	PCT-US95-09172-1	Sequence 1, Appl1
26	30.6	7.5	601	US-09-949-016-25615	Sequence 25615, A
27	30.6	7.5	601	US-09-949-016-25616	Sequence 25616, A

C 28	30.6	7.5	601	4	US-09-949-016-52403	Sequence 52403, A
C 29	30.6	7.5	601	4	US-09-949-016-52404	Sequence 52404, A
C 30	30.6	7.5	654	4	US-09-252-991A-3291	Sequence 3291, Ap
C 31	30.6	7.5	1623	4	US-09-252-991A-3226	Sequence 3226, Ap
C 32	30.6	7.5	2024	4	US-09-799-451-813	Sequence 813, App
C 33	30.6	7.5	2322	4	US-09-252-991A-3345	Sequence 3345, Ap
C 34	30.6	7.5	2364	4	US-09-252-991A-3420	Sequence 3420, Ap
C 35	30.6	7.5	4159	4	US-09-614-912-139	Sequence 139, App
C 36	30.6	7.5	36156	4	US-09-949-016-12128	Sequence 12128, A
C 37	30.6	7.5	36156	4	US-09-949-016-13261	Sequence 13261, A
C 38	30.6	7.5	91831	4	US-09-949-016-13694	Sequence 13694, A
C 39	30.4	7.5	252	4	US-09-328-352-2876	Sequence 2876, Ap
C 40	30.4	7.5	601	4	US-09-949-016-79104	Sequence 79104, A
C 41	30.4	7.5	2166	4	US-09-134-000C-2061	Sequence 2061, Ap
C 42	30.4	7.5	98567	4	US-09-949-016-11750	Sequence 11750, A
C 43	30.4	7.5	107140	4	US-09-949-016-14834	Sequence 14834, A
C 44	30.4	7.5	784019	4	US-09-949-016-14033	Sequence 14033, A
C 45	30.4	7.5	828152	4	US-09-949-016-12777	Sequence 12777, A

ALIGNMENTS

RESULT 1
US-09-799-451-332
; Sequence 332, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryje
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aildong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Keena
; APPLICANT: Dymnac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 332
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(888)
US-09-799-451-332
Query Match 99.3%; Score 403; DB 4; Length 1046;
Best Local Similarity 99.3%; Pred. No. 3; 4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 505 GTGATGTGACATATATGACAGCTCAGANACCTTGAGGTGAGGCTCCCATGATTC 60
DB 505 GTGATGTGACATATATGACAGCTCAGANACCTTGAGGTGAGGCTCCCATGATTC 564
DB 61 CCCAGGCCACAGTGTGCTGGGATCCCAAGTTGACCGAGGACCACTTCTCGGAAGTC 120
DB 565 CCCAGGCCACAGTGTGCTGGGATCCCAAGTTGACCGAGGACCACTTCTCGGAAGTC 624


```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12455
; LENGTH: 69813
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12455
```

```

Query Match
Best Local Similarity 51.5%; Score 38; DB 4; Length 69813;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
```

```

QY 127 ACCAGCTTTGAGCTGAACCTGTGAGATGTGACCATGAGGTTGTGCTGTCTACAAAT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27710 AACAAATTGATGATGGAGAGATGATGATCTTTGAAAGATGATGTTCTTAATAAA 27651

QY 187 GTTACGATCAACACACATCTCCTGTATGATTTGAAATGACATTGCCAAAGCAACAGG 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27650 GGGACATTTCAAGAAATAGAGCCCTTGAAATTTAAATGTGTAGCATAGCTAGAAG 27591

QY 247 GATATCAAAAGTGCAGAGATGGAGATCAAAAGCGGAGTCACTTACA 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27590 CCATTCAAAAGCATGAGAAATTAAGTTAAATCTCCAGAAAGTAAACA 27544
```

```

RESULT 5
US-09-949-016-13905/c
; Sequence 13905, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13905
; LENGTH: 69813
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13905
```

```

Query Match
Best Local Similarity 51.5%; Score 38; DB 4; Length 69813;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
```

```

QY 127 ACCAGCTTTGAGCTGAACCTGTGAGATGTGACCATGAGGTTGTGCTGTCTACAAAT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27710 AACAAATTGATGATGGAGAGATGATGATCTTTGAAAGATGATGTTCTTAATAAA 27651

QY 187 GTTACGATCAACACACATCTCCTGTATGATTTGAAATGACATTGCCAAAGCAACAGG 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27650 GGGACATTTCAAGAAATAGAGCCCTTGAAATTTAAATGTGTAGCATAGCTAGAAG 27591

QY 247 GATATCAAAAGTGCAGAGATGGAGATCAAAAGCGGAGTCACTTACA 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27590 CCATTCAAAAGCATGAGAAATTAAGTTAAATCTCCAGAAAGTAAACA 27544
```

```

RESULT 6
US-09-949-016-13906/c
; Sequence 13906, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13906
; LENGTH: 69813
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13906
```

```

Query Match
Best Local Similarity 51.5%; Score 38; DB 4; Length 69813;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
```

```

QY 127 ACCAGCTTTGAGCTGAACCTGTGAGATGTGACCATGAGGTTGTGCTGTCTACAAAT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27710 AACAAATTGATGATGGAGAGATGATGATCTTTGAAAGATGATGTTCTTAATAAA 27651

QY 187 GTTACGATCAACACACATCTCCTGTATGATTTGAAATGACATTGCCAAAGCAACAGG 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27650 GGGACATTTCAAGAAATAGAGCCCTTGAAATTTAAATGTGTAGCATAGCTAGAAG 27591

QY 247 GATATCAAAAGTGCAGAGATGGAGATCAAAAGCGGAGTCACTTACA 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27590 CCATTCAAAAGCATGAGAAATTAAGTTAAATCTCCAGAAAGTAAACA 27544
```

```

RESULT 7
US-09-949-016-12861/c
; Sequence 12861, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12861
; LENGTH: 69813
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12861
```

```

Query Match
Best Local Similarity 51.5%; Score 38; DB 4; Length 69813;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
```

```

QY 127 ACCAGCTTTGAGCTGAACCTGTGAGATGTGACCATGAGGTTGTGCTGTCTACAAAT 186
```

Db 27730 AACAAATTTAGATGGAGAGATATGATCTTCTGAAAGAAATGATGCTCTTAAAC 27671
Qy 187 GTTAGCATCAACACACATCTCTGTATGATTTGAAAAATGACATTCGCAACACACAGG 246
Db 27670 GGACATTCATAAGAAATTAAGACGCTTGAAAAATTAAGATGATGATGATGATGAAAG 27611
Qy 247 GATATCAAGTACAGATTCGAGATCAAAAGCGGAGTCACTACA 293
Db 27610 CCATTCAAAGGATGAAATAAGTTAATCTCCAGAAAGTAAACA 27564

RESULT 8

US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match

8.6%; Score 34.8; DB 4; Length 1141;
Best Local Similarity 10.4%; Pred. No. 0.38;
Matches 34; Conservative 150; Mismatches 141; Indels 2; Gaps 1;

Qy 4 AATGGAGCTATTAATCCAGCTCAGAACCTTGGGCTGAGGCTCCCGATGCTCCCC 63
Db 415 WWTWTKYMKAAACNNNNBRAMYRVAMMYSRDTTDMWMTSDMBWMTYVDYTMKA 356
Qy 64 CAGCCACAGTGGTCTGGGATCCCAAGTTGACACGAGCCACTTCGGAAGCTCC 123
Db 355 WNNNNNNNRBCKTTSWMMMDHMTHTCTYGNNTWSAYBMAAMSMMAAGASBVTYMC 296
Qy 124 AATACCAAGCTTGAAGCTGAGAAATGAGCAATGAGGTTGCTGCTCTAC 183
Db 295 WHTWTGKTMNNNNNNKAMYYRTKTVAMCNRYYDTAVMTBKRYKCYAVBMYMY 236
Qy 184 AATGTTACATCAACACATCTCTGTATGATTTGAAAAATGACATTCGCAACACACA 243
Db 235 M--GKHMMWMBRABHRSNNMMWVKCRNXYMSWHTAMRYBMTABAVGNNWMDRMAH 178
Qy 244 GGGGATATCAAGTACAGATTCGAGATCAAAAGCGGAGTCACTACA 303
Db 177 HHWCATNNNNMMWVAIYMHMHKGAAMNNKTABRDBAHVKTYYWRIDYMCAMCW 118
Qy 304 TCAAGGCTTCTGTGTGCTCTCTCT 330
Db 117 NNAKAKVRTAMKHMWYTTDRYVSANNT 91

RESULT 9

US-09-054-272-49
; Sequence 49, Application US/09054272
; Patent No. 6692909
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George Q.
; APPLICANT: Caregill, Michele

APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI98-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 13204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-054-272-49

Query Match

8.5%; Score 34.6; DB 4; Length 13204;
Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 117; Conservative 0; Mismatches 120; Indels 1; Gaps 1;

Qy 129 CAGCTTGAAGCTGAGATCTGAGAAATGACATGAGGTTGCTGCTTACAAATGT 188
Db 8817 CATCTGTATATCAGAAAGAGATGAGACCGAGGTGCTGTGTGAGCTGGGCAACC 8876
Qy 189 TAGATCAACAACATCTCTGTATGATGAAATGACATTCGCAACACAGGAGN 248
Db 8877 CATGAAGAAAGACGCCAGGTGAGGCTGCTGGTACCGGGTCTCCACAGGGGC 8936
Qy 249 TATCAAGTACAGATGCG--GAGATCAAAAGCGGAGTCACTACAGCTGCTAACTCA 307
Db 8937 TCATGAATTAACAGATTTTAAAGGAGTGAAGTTTAAAGCCACATAGTTCTGGCCGAATC 8996
Qy 308 AGGCTTCTGTGTGCTCTCTCTTCTTTCATGATGAGCTGGGCACTTCGCTCTAG 365
Db 8997 TTGCTCTCAGACCTCCCTTTGCAACATGCTGCTGGTGAATGACTTCCCTCTCTG 9054

RESULT 10

US-09-621-976-17202/c
; Sequence 17202, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976

;;
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17202
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17202

Query Match 8.0%; Score 32.4; DB 4; Length 364;
Best Local Similarity 13.2%; Pred. No. 1.3;
Matches 21; Conservative 79; Mismatches 60; Indels 0; Gaps 0;

QY 15 TAAAGCAGCTCGANACCTTGGCGGTGAGCTCCCGATGTTCCCGACGACAGT 74
DB 248 KMTGTSTCTSKKKRKGSTSTSTGSKSKTKSKSKKRYSATYISCMKW 189
QY 75 GGTCTGGGCACTCCCAAGTTCAGGAGGCACTTCTCGAAGTCTCAATACAGCTT 134
DB 188 KKYCMSATYSGGMMWYCYSCMSRYSCYSGKSCGTCMKGKGCYRYMYRGMWK 129
QY 135 TGAGCTGAAGCTGAGCAATGTGACCATGAAGTTGTCTC 173
DB 128 YRMSRGARRYTKSRGWCSTKRYRTKCAWGAATGTC 90

RESULT 11

US-09-734-673-3/C
; Sequence 3, Application US/09734673
; Patent No. 6410294
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001020
; CURRENT APPLICATION NUMBER: US/09/734,673
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 38564
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(38564)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-673-3

Query Match 7.9%; Score 32.2; DB 3; Length 38564;
Best Local Similarity 53.2%; Pred. No. 22;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 233 CCAAGCAAGAGGGGATCAAGTGCAGATCGGATCAAGGCGGAGTACCTAC 292
DB 33759 CCACAGCCCAAGCACTTAATGATGATGTCATATACAGGCTTAAACATTCAC 33700
QY 293 AGCTGCTAAACTCAAGGCTTCTGTGTCTCTTCTTCTTCTTGGCCATCAGCTGGGAC 352
DB 33699 CACCATCAGTCAAGCTTCTTCCCTGCTCACTTCTTCTTCTTCTTCTTCTTCC 33640
QY 353 TTCTGC 358
DB 33639 TACTGC 33634

RESULT 12

US-08-961-527-84/C
; Sequence 84, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

;;
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS: 391
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 6749 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-84

Query Match 7.9%; Score 32; DB 3; Length 6749;
Best Local Similarity 53.1%; Pred. No. 9.3;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 102 AGCCAATTCTCGAAGTCTCCATACCAAGCTTTGAGTGAAGTGAAGTGAAT 161
DB 4344 AACCAATTGAGGGAAGCTTACTAGAGTTTGGGTAATATGTAAGATTTCCAC 4285
QY 162 GAAGTTGTGTCTGCTCTCAATGTACATGATCAACAAACATTAATCTGATGATGA 221
DB 4284 GCTGCTCGTGTCTTCTCTGTTATGAACCTGACCAACAAATCAAGCTTGGCAAGATTG 4225
QY 222 AATGACA 229
DB 4224 AAGAGCA 4217

RESULT 13

US-08-956-171E-85/C
; Sequence 85, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GIL H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
ZIP: 20850

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 9062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-08-956-171E-85

Query Match
Best Local Similarity 49.1%; Score 32; DB 4; Length 9062;
Matches 83; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 106 AACTTCTCGGAAGTCTCCATATACAGCTTTGAGCTGAATCTGAGAAATGACCAAG 165
DB 7443 AACTGTGTATAGTCCGACGATTTCTTTAACCGCATATATCAAGCTTCTTTAA 7384
QY 166 GTTGTCTGTGCTCTACATGTTAGATCAACACATCACTCCGTATGATTGAAT 225
DB 7383 TTTCGATTTTATCTGCGGTATGTCACACATGATATATCTGCTCTTTGACAC 7324
QY 226 GACATTGCCAAGCAACAGGGGNTATCAAGTGACAGAAATCGAGATCA 274
DB 7323 ATCTTTGTTACTAACAACAGGCTTACCAACTGCATGACATGACATCA 7275

RESULT 14
US-08-781-986A-85/c
Sequence 85, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kneuch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
```

```
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 9062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-85

Query Match
Best Local Similarity 49.1%; Score 32; DB 4; Length 9062;
Matches 83; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 106 AACTTCTCGGAAGTCTCCATATACAGCTTTGAGCTGAATCTGAGAAATGACCAAG 165
DB 7443 AACTGTGTATAGTCCGACGATTTCTTTAACCGCATATATCAAGCTTCTTTAA 7384
QY 166 GTTGTCTGTGCTCTACATGTTAGATCAACACATCACTCCGTATGATTGAAT 225
DB 7383 TTTCGATTTTATCTGCGGTATGTCACACATGATATATCTGCTCTTTGACAC 7324
QY 226 GACATTGCCAAGCAACAGGGGNTATCAAGTGACAGAAATCGAGATCA 274
DB 7323 ATCTTTGTTACTAACAACAGGCTTACCAACTGCATGACATGACATCA 7275

RESULT 15
US-09-949-016-17287
Sequence 17287, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYOMPHISMS IN KNOWN GENES ASSOCIATED
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17287
LENGTH: 36611
TYPE: DNA
ORGANISM: Human
US-09-949-016-17287

Query Match
Best Local Similarity 50.3%; Score 32; DB 4; Length 36611;
Matches 77; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 201 CACATACCTCTGTATGATGTAATGATGCAATGCAACAGGGGNTATCAAGTGAC 260
DB 32049 CACATACATATGACAGGTGGGAAACAACCTGTCTTACGGGGAAGTTTATTCATTCAT 32108
QY 261 AGAATGGAGATCAAAAGCGGAGTCACTTACAGCTGCTAAACTAAAGGCTTCTGTG 320
DB 32109 TCCATCAGAGCAAACTGGCCAGAGAACTCAAGGATGATATGACAAGACTCACTGTC 32168
QY 321 TGTCTCTTCTTCTTGGCATAGCTGGGACT 353
DB 32169 CATGCTTCTCTCTAGCCAGCTTGAGACT 32201
```

Search completed: May 31, 2005, 00:29:00
Job time : 78.2473 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 17:54:16 ; Search time 278.562 Seconds
(without alignments)
8948.327 Million cell updates/sec

Title: US-09-763-978B-12

Perfect score: 406
Sequence: 1 gtaaatgctggactataatgc.....atgtgccttgccacaaaaa 406

Scoring table:

IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	403	99.3	1046	17	US-10-302-172-332
2	403	99.3	1065	9	US-09-877-065-5
3	403	99.3	1658	9	US-09-989-722-290
4	403	99.3	1658	9	US-09-989-723-290
5	403	99.3	1658	9	US-09-989-729-290
6	403	99.3	1658	9	US-09-989-727-290
7	403	99.3	1658	9	US-09-989-731-290
8	403	99.3	1658	9	US-09-989-732-290
9	403	99.3	1658	9	US-09-991-073-290
10	403	99.3	1658	9	US-09-990-442-290
11	403	99.3	1658	9	US-09-991-163-290

12	403	99.3	1658	9	US-09-993-604-290	Sequence 290, App
13	403	99.3	1658	9	US-09-990-456-290	Sequence 290, App
14	403	99.3	1658	9	US-09-989-721-290	Sequence 290, App
15	403	99.3	1658	9	US-09-992-598-290	Sequence 290, App
16	403	99.3	1658	9	US-09-989-293A-290	Sequence 290, App
17	403	99.3	1658	9	US-09-989-735-290	Sequence 290, App
18	403	99.3	1658	9	US-09-990-444-290	Sequence 290, App
19	403	99.3	1658	9	US-09-991-181-290	Sequence 290, App
20	403	99.3	1658	9	US-09-989-730-290	Sequence 290, App
21	403	99.3	1658	9	US-09-990-436-290	Sequence 290, App
22	403	99.3	1658	9	US-09-993-687-290	Sequence 290, App
23	403	99.3	1658	10	US-09-989-734-290	Sequence 290, App
24	403	99.3	1658	10	US-09-997-653-290	Sequence 290, App
25	403	99.3	1658	10	US-09-989-724-290	Sequence 290, App
26	403	99.3	1658	10	US-09-989-728-290	Sequence 290, App
27	403	99.3	1658	10	US-09-990-441-290	Sequence 290, App
28	403	99.3	1658	10	US-09-993-667-290	Sequence 290, App
29	403	99.3	1658	10	US-09-997-428-290	Sequence 290, App
30	403	99.3	1658	10	US-09-997-666-290	Sequence 290, App
31	403	99.3	1658	10	US-09-990-438-290	Sequence 290, App
32	403	99.3	1658	10	US-09-990-562-290	Sequence 290, App
33	403	99.3	1658	10	US-09-990-711-290	Sequence 290, App
34	403	99.3	1658	10	US-09-989-726-290	Sequence 290, App
35	403	99.3	1658	10	US-09-998-156-290	Sequence 290, App
36	403	99.3	1658	10	US-09-990-437-290	Sequence 290, App
37	403	99.3	1658	10	US-09-991-157-290	Sequence 290, App
38	403	99.3	1658	10	US-09-997-514-290	Sequence 290, App
39	403	99.3	1658	10	US-09-997-573-290	Sequence 290, App
40	403	99.3	1658	10	US-09-991-172-290	Sequence 290, App
41	403	99.3	1658	10	US-09-990-726-290	Sequence 290, App
42	403	99.3	1658	10	US-09-997-559-290	Sequence 290, App
43	403	99.3	1658	10	US-09-997-601-290	Sequence 290, App
44	403	99.3	1658	10	US-09-990-443-290	Sequence 290, App
45	403	99.3	1658	10	US-09-929-769-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-10-302-172-332
Sequence 332, Application US/10302172
Publication No. US20040053250A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids a
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803_1CNDP
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pt_Fl_genes Version 2.0
SEQ ID NO 332
LENGTH: 1046
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (4) ..(888)
US-10-302-172-332
Query Match 99.3%; Score 403; DB 17; Length 1046;
Best Local Similarity 99.3%; Pred. No. 1.1e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGACCTGAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 60
DB 505 GTGAATGTGACTATTAATGCGACCTGAGAGACCTTGCGGTGTGAGGCTCCCGATGTTTC 564
QY 61 CCCGACCCCAAGTGTCTGGGATTCGCAAGTTGACGAGGAGCCAACTTTTCGGAAGTC 120
DB 565 CCCGACCCCAAGTGTCTGGGATTCGCAAGTTGACGAGGAGCCAACTTTTCGGAAGTC 624
QY 121 TCCAAATACGAGCTTTGAGGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 180
DB 625 TCCAAATACGAGCTTTGAGGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 684
QY 181 TACAAATGTACGATCAACAACACATACCTGTATGATTTGAAATGACATTGCAAAAGA 240
DB 685 TACAAATGTACGATCAACAACACATACCTGTATGATTTGAAATGACATTGCAAAAGA 744
QY 241 ACAGGGGATNTCAAATGACAAATGGAGATCAAAAGGCGAGTACCTTACAGCTGCTA 300
DB 745 ACAGGGGATNTCAAATGACAAATGGAGATCAAAAGGCGAGTACCTTACAGCTGCTA 804
QY 301 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATCAGCTGGGCACTTGTGCT 360
DB 805 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATCAGCTGGGCACTTGTGCT 864
QY 361 CTCAGCCCTTACCTGATGCTAANAATATGTGCTTGCCCAAAAA 406
DB 865 CTCAGCCCTTACCTGATGCTAANAATATGTGCTTGCCCAAAAA 910

RESULT 2

US-09-877-065-5
; Sequence 5, Application US/09877065
; Patent No. US20020051990A1
; GENERAL INFORMATION:
; APPLICANT: OPLE, ERIC
; APPLICANT: MCLACHLAN, KAREN
; APPLICANT: HEARD, CHERYL J.
; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR
; FILE REFERENCE: 037003-0280631
; CURRENT APPLICATION NUMBER: US/09/877,065
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,451
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-065-5

Query Match 99.3%; Score 403; DB 9; Length 1065;
Best Local Similarity 99.3%; Pred. No. 1,1e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATTAATGCGACCTGAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 60
DB 534 GTGAATGTGACTATTAATGCGACCTGAGAGACCTTGCGGTGTGAGGCTCCCGATGTTTC 593
QY 61 CCCGACCCCAAGTGTCTGGGATTCGCAAGTTGACGAGGAGCCAACTTTTCGGAAGTC 120
DB 594 CCCGACCCCAAGTGTCTGGGATTCGCAAGTTGACGAGGAGCCAACTTTTCGGAAGTC 653
QY 121 TCCAAATACGAGCTTTGAGGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 180
DB 654 TCCAAATACGAGCTTTGAGGCTGAACTCTGAGAAATGTGACCATGAAAGTTGTGTGCTC 713
QY 181 TACAAATGTACGATCAACAACACATACCTGTATGATTTGAAATGACATTGCAAAAGA 240
DB 714 TACAAATGTACGATCAACAACACATACCTGTATGATTTGAAATGACATTGCAAAAGA 773
QY 241 ACAGGGGATNTCAAATGACAAATGGAGATCAAAAGGCGAGTACCTTACAGCTGCTA 300

DB 774 ACAGGGGATNTCAAATGACAAATGGAGATCAAAAGGCGAGTACCTTACAGCTGCTA 833
QY 301 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATCAGCTGGGCACTTGTGCT 360
DB 834 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTCCATCAGCTGGGCACTTGTGCT 893
QY 361 CTCAGCCCTTACCTGATGCTAANAATATGTGCTTGCCCAAAAA 406
DB 894 CTCAGCCCTTACCTGATGCTAANAATATGTGCTTGCCCAAAAA 939

RESULT 3

US-09-989-722-290
; Sequence 290, Application US/0989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827

1	PRIOR FILING DATE: 1998-06-03
2	PRIOR APPLICATION NUMBER: 60/088021
3	PRIOR FILING DATE: 1998-06-04
4	PRIOR APPLICATION NUMBER: 60/088025
5	PRIOR FILING DATE: 1998-06-04
6	PRIOR APPLICATION NUMBER: 60/088026
7	PRIOR FILING DATE: 1998-06-04
8	PRIOR APPLICATION NUMBER: 60/088028
9	PRIOR FILING DATE: 1998-06-04
10	PRIOR APPLICATION NUMBER: 60/088029
11	PRIOR FILING DATE: 1998-06-04
12	PRIOR APPLICATION NUMBER: 60/088030
13	PRIOR FILING DATE: 1998-06-04
14	PRIOR APPLICATION NUMBER: 60/088033
15	PRIOR FILING DATE: 1998-06-04
16	PRIOR APPLICATION NUMBER: 60/088326
17	PRIOR FILING DATE: 1998-06-04
18	PRIOR APPLICATION NUMBER: 60/088157
19	PRIOR FILING DATE: 1998-06-05
20	PRIOR APPLICATION NUMBER: 60/088202
21	PRIOR FILING DATE: 1998-06-05
22	PRIOR APPLICATION NUMBER: 60/088212
23	PRIOR FILING DATE: 1998-06-05
24	PRIOR APPLICATION NUMBER: 60/088217
25	PRIOR FILING DATE: 1998-06-05
26	PRIOR APPLICATION NUMBER: 60/088555
27	PRIOR FILING DATE: 1998-06-09
28	PRIOR APPLICATION NUMBER: 60/088734
29	PRIOR FILING DATE: 1998-06-10
30	PRIOR APPLICATION NUMBER: 60/088738
31	PRIOR FILING DATE: 1998-06-10
32	PRIOR APPLICATION NUMBER: 60/088742
33	PRIOR FILING DATE: 1998-06-10
34	PRIOR APPLICATION NUMBER: 60/088810
35	PRIOR FILING DATE: 1998-06-10
36	PRIOR APPLICATION NUMBER: 60/088824
37	PRIOR FILING DATE: 1998-06-10
38	PRIOR APPLICATION NUMBER: 60/088826
39	PRIOR FILING DATE: 1998-06-10
40	PRIOR APPLICATION NUMBER: 60/088858
41	PRIOR FILING DATE: 1998-06-11
42	PRIOR APPLICATION NUMBER: 60/088861
43	PRIOR FILING DATE: 1998-06-11
44	PRIOR APPLICATION NUMBER: 60/088876
45	PRIOR FILING DATE: 1998-06-11
46	PRIOR APPLICATION NUMBER: 60/089105
47	PRIOR FILING DATE: 1998-06-12
48	PRIOR APPLICATION NUMBER: 60/089440
49	PRIOR FILING DATE: 1998-06-16
50	PRIOR APPLICATION NUMBER: 60/089512
51	PRIOR FILING DATE: 1998-06-16
52	PRIOR APPLICATION NUMBER: 60/089514
53	PRIOR FILING DATE: 1998-06-16
54	PRIOR APPLICATION NUMBER: 60/089514
55	PRIOR FILING DATE: 1998-06-16
56	PRIOR APPLICATION NUMBER: 60/089532
57	PRIOR FILING DATE: 1998-06-17
58	PRIOR APPLICATION NUMBER: 60/089538
59	PRIOR FILING DATE: 1998-06-17
60	PRIOR APPLICATION NUMBER: 60/089558
61	PRIOR FILING DATE: 1998-06-17
62	PRIOR APPLICATION NUMBER: 60/089599
63	PRIOR FILING DATE: 1998-06-17
64	PRIOR APPLICATION NUMBER: 60/089600
65	PRIOR FILING DATE: 1998-06-17
66	PRIOR APPLICATION NUMBER: 60/089633
67	PRIOR FILING DATE: 1998-06-17
68	PRIOR APPLICATION NUMBER: 60/089801
69	PRIOR FILING DATE: 1998-06-18
70	PRIOR APPLICATION NUMBER: 60/089907
71	PRIOR FILING DATE: 1998-06-18
72	PRIOR APPLICATION NUMBER: 60/089908
73	PRIOR FILING DATE: 1998-06-18
74	PRIOR APPLICATION NUMBER: 60/089947
75	PRIOR FILING DATE: 1998-06-19

1	PRIOR APPLICATION NUMBER: 60/089948
2	PRIOR FILING DATE: 1998-06-19
3	PRIOR APPLICATION NUMBER: 60/089952
4	PRIOR FILING DATE: 1998-06-19
5	PRIOR APPLICATION NUMBER: 60/090246
6	PRIOR FILING DATE: 1998-06-22
7	PRIOR APPLICATION NUMBER: 60/090252
8	PRIOR FILING DATE: 1998-06-22
9	PRIOR APPLICATION NUMBER: 60/090254
10	PRIOR FILING DATE: 1998-06-22
11	PRIOR APPLICATION NUMBER: 60/090349
12	PRIOR FILING DATE: 1998-06-23
13	PRIOR APPLICATION NUMBER: 60/090355
14	PRIOR FILING DATE: 1998-06-23
15	PRIOR APPLICATION NUMBER: 60/090429
16	PRIOR FILING DATE: 1998-06-24
17	PRIOR APPLICATION NUMBER: 60/090431
18	PRIOR FILING DATE: 1998-06-24
19	PRIOR APPLICATION NUMBER: 60/090435
20	PRIOR FILING DATE: 1998-06-24
21	PRIOR APPLICATION NUMBER: 60/090444
22	PRIOR FILING DATE: 1998-06-24
23	PRIOR APPLICATION NUMBER: 60/090445
24	PRIOR FILING DATE: 1998-06-24
25	PRIOR APPLICATION NUMBER: 60/090540
26	PRIOR FILING DATE: 1998-06-24
27	PRIOR APPLICATION NUMBER: 60/090542
28	PRIOR FILING DATE: 1998-06-24
29	PRIOR APPLICATION NUMBER: 60/090557
30	PRIOR FILING DATE: 1998-06-24
31	PRIOR APPLICATION NUMBER: 60/090676
32	PRIOR FILING DATE: 1998-06-25
33	PRIOR APPLICATION NUMBER: 60/090678
34	PRIOR FILING DATE: 1998-06-25
35	PRIOR APPLICATION NUMBER: 60/090690
36	PRIOR FILING DATE: 1998-06-25
37	PRIOR APPLICATION NUMBER: 60/090694
38	PRIOR FILING DATE: 1998-06-25
39	PRIOR APPLICATION NUMBER: 60/090695
40	PRIOR FILING DATE: 1998-06-25
41	PRIOR APPLICATION NUMBER: 60/090696
42	PRIOR FILING DATE: 1998-06-25
43	PRIOR APPLICATION NUMBER: 60/090862
44	PRIOR FILING DATE: 1998-06-26
45	PRIOR APPLICATION NUMBER: 60/090863
46	PRIOR FILING DATE: 1998-06-26
47	PRIOR APPLICATION NUMBER: 60/091360
48	PRIOR FILING DATE: 1998-07-01
49	PRIOR APPLICATION NUMBER: 60/091478
50	PRIOR FILING DATE: 1998-07-02
51	PRIOR APPLICATION NUMBER: 60/091544
52	PRIOR FILING DATE: 1998-07-01
53	PRIOR APPLICATION NUMBER: 60/091519
54	PRIOR FILING DATE: 1998-07-02
55	PRIOR APPLICATION NUMBER: 60/091626
56	PRIOR FILING DATE: 1998-07-02
57	PRIOR APPLICATION NUMBER: 60/091633
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091978
60	PRIOR FILING DATE: 1998-07-07
61	PRIOR APPLICATION NUMBER: 60/091982
62	PRIOR FILING DATE: 1998-07-07
63	PRIOR APPLICATION NUMBER: 60/092182
64	PRIOR FILING DATE: 1998-07-09

Query Match	99.3%	Score 403;	DB 9;	Length 1658;
Best Local Similarity	99.3%;	Pred. No. 1.4e-125;		
Matches 403; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 GTGAATGTGAGTAAATATATGAGCCAGATCCAGANACCTTGCGGTGTGAGGCTCCCGATGTTTC 60
DB 523 GTGAATGTGAGTAAATATATGAGCCAGATCCAGATCCCTTGCGGTGTGAGGCTCCCGATGTTTC 582
QY 61 CCCCGAGCCAGATGTGTCTGGGATGCCAGTTGACAGGAGCCAACTTTCGGAAATC 120
DB 583 CCCCGAGCCAGATGTGTCTGGGATGCCAGTTGACAGGAGCCAACTTTCGGAAATC 642
QY 121 TCCAAATACAGCTTTGAGCTGGAATCTGAGAAATGTGACCATGAGGTTGTGTGCTC 180
DB 643 TCCAAATACAGCTTTGAGCTGGAATCTGAGAAATGTGACCATGAGGTTGTGTGCTC 702
QY 181 TACAAATGTATACGATCAACAACATCTCTGTATGATTGAAATGACATTGCCAAAGA 240
DB 763 ACAGGGGATATCAAAATGTGACAGATCGAGATCAAAAAGCGAGTACCTACAGCTGCTA 822
QY 241 ACAGGGGATATCAAAATGTGACAGATCGAGATCAAAAAGCGAGTACCTACAGCTGCTA 300
DB 301 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTGGCATCAGCTGGCACTTGTGCTT 360
QY 823 AACTCAAGGCTTCTGTGTGTCTCTTCTTTTGGCATCAGCTGGCACTTGTGCTT 882
QY 361 CTCAGCCTTACTGATGCTAANAATATGTCCTTGCCCAAAAA 406
DB 883 CTCAGCCTTACTGATGCTAANAATATGTCCTTGCCCAAAAA 928

RESULT 4

US-09-989-723-290

Sequence 290, Application US/09989723

Patent No. US20020072092A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538

;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01

;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1.4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGACTATATATGCGACCTCAGANACCTTCGGTGTGAGGCTCCCGATGGTTC 60
|||
DB 523 GTGAATGTGACTATATATGCGACCTCAGAGACCTTCGGTGTGAGGCTCCCGATGGTTC 582
|||
QY 61 CCCAGCCCACTGTGCTGGGATCCCAAGTTGACCGAGGACCACTTCTGGAAATC 120
|||
DB 583 CCCAGCCCACTGTGCTGGGATCCCAAGTTGACCGAGGACCACTTCTGGAAATC 642
|||
QY 121 TCCATATCCAGCTTTGAGCTGGAAGTGAATGACCAATGAAGGTGTGCTGCTC 180
|||
DB 643 TCCATATCCAGCTTTGAGCTGGAAGTGAATGACCAATGAAGGTGTGCTGCTC 702
|||
QY 181 TACATGTTACGATCAACAACACATCTCTGTATGTAATGAATGACATTTGCCAAGCA 240
|||
DB 703 TACATGTTACGATCAACAACACATCTCTGTATGTAATGAATGACATTTGCCAAGCA 762
|||
QY 241 ACAGGGGATATCAAGTGTGACAGATGAGATCAAAAAGCGGAGTCACTTACGCTGCTA 300
|||
DB 763 ACAGGGGATATCAAGTGTGACAGATGAGATCAAAAAGCGGAGTCACTTACGCTGCTA 822
|||
QY 301 AACTCAAGGCTTCTGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
|||
DB 823 AACTCAAGGCTTCTGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 882
|||
QY 361 CTCAGCCCTTACCTGATGCTAANATATGCTCTTGGCCCAAAAA 406
|||
DB 883 CTCAGCCCTTACCTGATGCTAANATATGCTCTTGGCCCAAAAA 928
|||

RESULT 5
US-09-989-279-290
; Sequence 290, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089807
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089808
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690

```

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

```

Query Match 99.3%; Score 403; DB 9; Length 1658;

Best Local Similarity 99.3%; Pred. No. 1,4e-125; Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GTGAAATGTGACTATAATATGACAGCTCAGANACCTTGGGTGTGAGGCTCCCGATGTTTC 60
DB 523 GTGAAATGTGACTATAATATGACAGCTCAGAGACCTTGGGTGTGAGGCTCCCGATGTTTC 582
QY 61 CCCCAGGCCAGTGTGTGTGGGCAATCCCAAGTTGACCAAGGAGCACTTCTGGAAGTTC 120
DB 583 CCCCAGGCCAGTGTGTGTGGGCAATCCCAAGTTGACCAAGGAGCACTTCTGGAAGTTC 642
QY 121 TCCAAATCCAGCTTTGAGTGAAGTCTGAGAAATGTCAGTGAAGGTTGTGTCTGTC 180
DB 643 TCCAAATCCAGCTTTGAGTGAAGTCTGAGAAATGTCAGTGAAGGTTGTGTCTGTC 702
QY 181 TACAATTTTACGATCAACAACAACATCTCTGTATGATTGAAATGACATTTGCCAAAGCA 240
DB 703 TACAATTTTACGATCAACAACAACATCTCTGTATGATTGAAATGACATTTGCCAAAGCA 762
QY 241 ACAGGGGNTATCAAGTGAAGAAATGCGAATCAAAAGCGGAGTCACTTCAAGTCTCTA 300
DB 763 ACAGGGGNTATCAAGTGAAGAAATGCGAATCAAAAGCGGAGTCACTTCAAGTCTCTA 822
QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTCTTTCTTTGCGCATGCTGGGCACTTCTGCTCT 360
DB 823 AACTCAAAAGGCTTCTGTGTGTCTCTCTTTCTTTGCGCATGCTGGGCACTTCTGCTCT 882
QY 361 CTCAGCCCTTACCTGATGATTAANATATGCTTGGCCCAAAAA 406
DB 883 CTCAGCCCTTACCTGATGATTAANATATGCTTGGCCCAAAAA 928

```

RESULT 6

US-09-989-727-290
; Sequence 290, Application US/09989727
; Patent No. US20020072497A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

```

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212

```

PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/0088217
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/008655
PRIOR FILING DATE:	1998-06-09
PRIOR APPLICATION NUMBER:	60/008734
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/008738
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/008742
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/008810
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/008824
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/008826
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/008858
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/008861
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/008876
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/008910
PRIOR FILING DATE:	1998-06-12
PRIOR APPLICATION NUMBER:	60/008940
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/008952
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/008954
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/008953
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/008958
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/008959
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/008960
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/008963
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/008980
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/008907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/008908
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/008947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/008948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/008952
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/009024
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090252
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090254
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090355
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090431
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444

1	PRIOR APPLICATION NUMBER: 60/090445
2	PRIOR FILING DATE: 1998-06-24
3	PRIOR APPLICATION NUMBER: 60/090472
4	PRIOR FILING DATE: 1998-06-24
5	PRIOR APPLICATION NUMBER: 60/090535
6	PRIOR FILING DATE: 1998-06-24
7	PRIOR APPLICATION NUMBER: 60/090540
8	PRIOR FILING DATE: 1998-06-24
9	PRIOR APPLICATION NUMBER: 60/090542
10	PRIOR FILING DATE: 1998-06-24
11	PRIOR APPLICATION NUMBER: 60/090557
12	PRIOR FILING DATE: 1998-06-24
13	PRIOR APPLICATION NUMBER: 60/090676
14	PRIOR FILING DATE: 1998-06-25
15	PRIOR APPLICATION NUMBER: 60/090678
16	PRIOR FILING DATE: 1998-06-25
17	PRIOR APPLICATION NUMBER: 60/090690
18	PRIOR FILING DATE: 1998-06-25
19	PRIOR APPLICATION NUMBER: 60/090694
20	PRIOR FILING DATE: 1998-06-25
21	PRIOR APPLICATION NUMBER: 60/090695
22	PRIOR FILING DATE: 1998-06-25
23	PRIOR APPLICATION NUMBER: 60/090682
24	PRIOR FILING DATE: 1998-06-26
25	PRIOR APPLICATION NUMBER: 60/090863
26	PRIOR FILING DATE: 1998-06-26
27	PRIOR APPLICATION NUMBER: 60/091360
28	PRIOR FILING DATE: 1998-07-01
29	PRIOR APPLICATION NUMBER: 60/091478
30	PRIOR FILING DATE: 1998-07-02
31	PRIOR APPLICATION NUMBER: 60/091544
32	PRIOR FILING DATE: 1998-07-01
33	PRIOR APPLICATION NUMBER: 60/091519
34	PRIOR FILING DATE: 1998-07-02
35	PRIOR APPLICATION NUMBER: 60/091626
36	PRIOR FILING DATE: 1998-07-02
37	PRIOR APPLICATION NUMBER: 60/091633
38	PRIOR FILING DATE: 1998-07-02
39	PRIOR APPLICATION NUMBER: 60/091978
40	PRIOR FILING DATE: 1998-07-07
41	PRIOR APPLICATION NUMBER: 60/091982
42	PRIOR FILING DATE: 1998-07-07
43	PRIOR APPLICATION NUMBER: 60/092182
44	PRIOR FILING DATE: 1998-07-09

Query Match	99.3%	Score 403;	DB 9;	Length 1658;
Best Local Similarity	99.3%	Pred. No. 1.4e-125;		
Matches 403; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Oy	1	TTGATATGAGACTATTAAGCCAGCTCAAMNCTTGCGGTGAGAGCTCCCGATGGTTC	60
Db	523	GTGATGTGGACTATTAATGCCAGCTCAAGACCTTGCGGTGAGAGCTCCCGATGGTTC	582
Oy	61	CCCGAGCCCAAGTGGTCTGGGCATCCCAAGTTGAACAAGGAGCCAACTTCTCGAAGTTC	120
Db	583	CCCGAGCCCAAGTGGTCTGGGCATCCCAAGTTGAACAAGGAGCCAACTTCTCGAAGTTC	642
Oy	121	TTCATATCAGCTTTGAGCTGAACTCTGAGATGTGACATGAAAGTTGTCTGTGCTTC	180
Db	643	TTCATATCAGCTTTGAGCTGAACTCTGAGATGTGACATGAAAGTTGTCTGTGCTTC	702
Oy	181	TACATGTTAGATCAACAACATACCTCGTATGATGAAAAATGACATTGSCAAAGCA	240
Db	703	TACATGTTAGATCAACAACATACCTCGTATGATGAAAAATGACATTGSCAAAGCA	762
Oy	241	ACAGGGGATATCAAAAGTGACAGAAATCGAGATCAAAAGGCGGAGTCACTTACAGCTGCTA	300
Db	763	ACAGGGGATATCAAAAGTGACAGAAATCGAGATCAAAAGGCGGAGTCACTTACAGCTGCTA	822
Oy	301	AACTCAAAGGCTTCTGTGTGTCTTCTTTCTTGCCATCAGCTGGGCACTTCTGCTT	360

Db	823	AACCTCAAAGGCTCTCTGTCGTCTCTTCTTTCTTTGCGATACGCTGGGCACTTCTGCTT	882
Q7	361	CTGAGCCCTTACCTGATGCTAATAATATGTGCTTGGCCACAAAA	406
D6	883	CTGAGCCCTTACCTGATGCTAATAATATGTGCTTGGCCACAAAA	928

RESULT 7

Sequence 290, Application US/09889731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertslen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989, 731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-26
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04

[illegible]

PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAATGTGAGCATTAATGCGAGCTCAGANACCTTGCGGTGAGGCTCCCGATGATTC 60
DB 523 GGAATGTGAGCATTAATGCGAGCTCAGANACCTTGCGGTGAGGCTCCCGATGATTC 582
QY 61 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACAGGAGCCAACTTCTCGAAGTC 120

DB 583 CCCAGCCCAAGTGTCTGGGATCCCAAGTTGACAGGAGCCCAACTTCTCGAAGTC 642
QY 121 TCCATATACAGCTTTAGCTGAACCTGAGATGACCATGAGGTTGTGTGCTC 180
DB 643 TCCATATACAGCTTTAGCTGAACCTGAGATGACCATGAGGTTGTGTGCTC 702
QY 181 TACATGTTAGATCAACACATACCTCTGATATGATTTGAAATGACATTGCCAAGCA 240
DB 703 TACATGTTAGATCAACACATACCTCTGATATGATTTGAAATGACATTGCCAAGCA 762
QY 241 ACAGGGATATCAAAAGTACAGATCGAATCAAAAGCGGAGTCACTTACAGTGTCTA 300
DB 763 ACAGGGATATCAAAAGTACAGATCGAATCAAAAGCGGAGTCACTTACAGTGTCTA 822
QY 301 AACTCAAAAGGCTCTCTGATGCTCTTCTTCTTGCATCAGCTGGGCACTTGTGCT 360
DB 823 AACTCAAAAGGCTCTCTGATGCTCTTCTTCTTGCATCAGCTGGGCACTTGTGCT 882
QY 361 CTCAGCCCTTACCTGATCTAATATATATGCTTGGCCACAAAA 406
DB 883 CTCAGCCCTTACCTGATCTAATATATATGCTTGGCCACAAAA 928

RESULT 8
US-09-989-732-290
Sequence 290, Application US/09989732
Patent No. US20020123463A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gueney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC57

CURRENT APPLICATION NUMBER: US/09/989,732

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/087106
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087607
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087609
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087759
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087827
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/088021
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088025
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088026
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088028
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088029
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088030
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088326
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088167
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088202
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088212
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088217
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088655
PRIOR FILING DATE:	1998-06-09
PRIOR APPLICATION NUMBER:	60/088734
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088738
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088742
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088810
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088824
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088826
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088858
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/088861
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/088876
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/089105
PRIOR FILING DATE:	1998-06-12
PRIOR APPLICATION NUMBER:	60/089440
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089512
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089514
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089532
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089538
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089598
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/091626
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02

/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGTGAACTAATAATCCAGCTCAGANACCTTGCGGTGAGGCTCCCGAGTGTTC 60
DB 523 GTGAATGTGAACTAATAATCCAGCTCAGAGACCTTGCGGTGAGGCTCCCGAGTGTTC 582
QY 61 CCCCGCCCAAGTGTGTGGGATCCCAAGTTGACAGAGGCGCCAACTTCTCGGAAGTC 120
DB 583 CCCCGCCCAAGTGTGTGGGATCCCAAGTTGACAGAGGCGCCAACTTCTCGGAAGTC 642
QY 121 TCCAAATACCACTTGTAGCTGAATCTGTGAATGTGAGGCTGAGGCTGCTGCTC 180
DB 643 TCCAAATACCACTTGTAGCTGAATCTGTGAATGTGAGGCTGAGGCTGCTGCTC 702
QY 181 TACAAATGTACATCAACAACATCTCTGTATGATGAAATGACATTGCCAAGCA 240
DB 703 TACAAATGTACATCAACAACATCTCTGTATGATGAAATGACATTGCCAAGCA 762
QY 241 ACAGGGGATCAAGATGACAGATGGAGTCAAAAGGCGAGTACCTACAGCTGCTA 300
DB 763 ACAGGGGATCAAGATGACAGATGGAGTCAAAAGGCGAGTACCTACAGCTGCTA 822
QY 301 AACTCAAGGCTTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
DB 823 AACTCAAGGCTTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 882
QY 361 CTCAGCCCTTACTGATGCTTAANATATGTGCTTGCCGCCACAAAA 406
DB 883 CTCAGCCCTTACTGATGCTTAANATATGTGCTTGCCGCCACAAAA 928

RESULT 9

US-09-991-073-290
/ Sequence 290, Application US/09991073
/ Patent No. US20020127576A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnovers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerltisen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gueney, Austin L.
/ APPLICANT: Kijavini, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C15

/ CURRENT APPLICATION NUMBER: US/09/991,073
/ CURRENT FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/049787
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/065186
/ PRIOR FILING DATE: 1997-11-12
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066770
/ PRIOR FILING DATE: 1997-11-24
/ PRIOR APPLICATION NUMBER: 60/075945
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/083322
/ PRIOR FILING DATE: 1998-04-28
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/087106
/ PRIOR FILING DATE: 1998-05-28
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087609
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087759
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087827
/ PRIOR FILING DATE: 1998-06-03
/ PRIOR APPLICATION NUMBER: 60/088021
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088025
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088026
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088028
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088029
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088030
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088033
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088326
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088167
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088202
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088212
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088217
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088655
/ PRIOR FILING DATE: 1998-06-09
/ PRIOR APPLICATION NUMBER: 60/088734
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088738
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088742
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088810
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088824
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088826
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088858
/ PRIOR FILING DATE: 1998-06-11
/ PRIOR APPLICATION NUMBER: 60/088861
/ PRIOR FILING DATE: 1998-06-11
/ PRIOR APPLICATION NUMBER: 60/088876

;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGAATGTGACATATATATGCTGAGTGAACCTTGCGTGTGAGGCTCCCGATGATTC 60
Db 523 GTGAATGTGACATATATATGCTGAGTGAACCTTGCGTGTGAGGCTCCCGATGATTC 582

Qy 61 CCCAGCCCAACAGTGTCTGGGCTCCCAAGTTGACCAAGGAGCCAACTTTCGAAATC 120
Db 583 CCCAGCCCAACAGTGTCTGGGCTCCCAAGTTGACCAAGGAGCCAACTTTCGAAATC 642

Qy 121 TCCAAATACCACTTTAGCTGAACTCTGAAATGTAACAATGAAAGTTGTGTGCTC 180
Db 643 TCCAAATACCACTTTAGCTGAACTCTGAAATGTAACAATGAAAGTTGTGTGCTC 702

Qy 181 TACAATGTACGATCAACAACATCTCTGTATGTAATGACATTTGCCAAGCA 240
Db 703 TACAATGTACGATCAACAACATCTCTGTATGTAATGTAATGACATTTGCCAAGCA 762

Qy 241 ACAGGGATATCAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 300
Db 763 ACAGGGATATCAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 822

Qy 301 AACTCAAGGCTTCTGTGTGTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCT 360
Db 823 AACTCAAGGCTTCTGTGTGTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCT 882

Qy 361 CTCAGCCCTTACCTGATGCTAANAATATGATGCTGGCCACAAA 406
Db 883 CTCAGCCCTTACCTGATGCTAANAATATGATGCTGGCCACAAA 928

RESULT 10
US-09-990-442-290
Sequence 290, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerltisen, Mary E.
;; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09

PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535

```

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

```

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1.4e-125; Indels 0; Gaps 0;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GTGAATGTGACTATATATATGCGAGCTGAGANACCTTGGGTGAGGCTCCCGATGTTT 60
DB 523 GTGAATGTGACTATATATGCGAGCTGAGANACCTTGGGTGAGGCTCCCGATGTTT 582
QY 61 CCCGAGCCCACTGCTGCTGGGATCCCAAGTTGACCGAGGACCACTTCTGGAAGTC 120
DB 583 CCCGAGCCCACTGCTGCTGGGATCCCAAGTTGACCGAGGACCACTTCTGGAAGTC 642
QY 121 TCCCAATACAGCTTTGAGCTGAGACTCTGAGATGTGACCATGAAGTTGCTGCTGTC 180
DB 643 TCCCAATACAGCTTTGAGCTGAGACTCTGAGATGTGACCATGAAGTTGCTGCTGTC 702
QY 181 TACAAATGTTAGCATCAACAACACATATCTCTGTATGATTTGAAATGACATTTGCCAAGA 240
DB 703 TACAAATGTTAGCATCAACAACACATATCTCTGTATGATTTGAAATGACATTTGCCAAGA 762
QY 241 ACAAGGGATATCAAAATGACAGAAATGGAGATCAAAAAGGCGAGTCACTTACAGCTGCTA 300
DB 763 ACAAGGGATATCAAAATGACAGAAATGGAGATCAAAAAGGCGAGTCACTTACAGCTGCTA 822
QY 301 AACTCAAAAGCTTCTGCTGCTGCTCTTCTTTCTTTGCCATGAGTGGGCACTTCTGCTT 360
DB 823 AACTCAAAAGCTTCTGCTGCTGCTCTTCTTTCTTTGCCATGAGTGGGCACTTCTGCTT 882
QY 361 CTCAGCCCTTACCTGATGCTAANAATATGCTTGGCCACAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAANAATATGCTTGGCCACAAA 928

```

```

RESULT 11
US-09-991-163-290
; Sequence 290, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Rong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/06770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029

```


Dh 643 TCCAATACGACGCTTGAGCTGAACCTGAGAAATGACATGAAGGTTGTGTCTGCTC 702
Qy 181 TACAAATGTCGATCAACAACATCTCTCTGTATGATTTGAAATGATTCGCAAGCA 240
Db 703 TACAAATGTCGATCAACAACATCTCTCTGTATGATTTGAAATGATTCGCAAGCA 762
Qy 241 ACAGGGGNTTCAAGGAGCAAGATCGAGATCAAAAGGGGAGTCACTACAGCTGCTA 300
Db 763 ACAGGGGATTCAAAGTACAGAGATCGAGATCAAAAGGGGAGTCACTACAGCTGCTA 822
Qy 301 AACTCAAGGCTTCTCTGTGTGTCTCTTCTTCTTCCATCAAGCTGGGACCTTCTGCT 360
Db 823 AACTCAAGGCTTCTCTGTGTGTCTCTTCTTCTTCCATCAAGCTGGGACCTTCTGCT 882
Qy 361 CTGAGCCTTACTGATGCTTAATATGTGCTTGGCCACAAAA 406
Db 883 CTCAGCCTTACTGATGCTTAATATGTGCTTGGCCACAAAA 928

RESULT 12
US-09-933-604-290
; Sequence 290, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801

;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1.4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGAATGTGACATATAATGCGACCTCAGANACCTTGCGGTGTGAGCTCCCGATGTTC 60
DB 523 GTGAATGTGACATATAATGCGACCTCAGAGACTTGCGGTGTGAGCTCCCGATGTTC 582
QY 61 CCCGAGCCCAAGTGTCTGGGCATCCCAAGTTGACGAGGAGCCCACTTCTCGAAGTC 120
DB 583 CCCGAGCCCAAGTGTCTGGGCATCCCAAGTTGACGAGGAGCCCACTTCTCGAAGTC 642
QY 121 TCCATATACAGCTTTGAGGTGAACCTGAGATGAGACCATGAGGTTGTCTGTGCTC 180
DB 643 TCCATATACAGCTTTGAGGTGAACCTGAGATGAGACCATGAGGTTGTCTGTGCTC 702
QY 181 TACAATGTTACGATCAACAACATATCTCTGTATGATTAATGACATTCGCAAGCA 240
DB 703 TACAATGTTACGATCAACAACATATCTCTGTATGATTAATGACATTCGCAAGCA 762
QY 241 ACAGGGGATATCAAGTGCAGATCGAGATCAAAAGGCGAGTCACTTACAGCTGCTA 300
DB 763 ACAGGGGATATCAAGTGCAGATCGAGATCAAAAGGCGAGTCACTTACAGCTGCTA 822
QY 301 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTGCGATCAGCTGGGCACTTGTGCT 360
DB 823 AACTCAAAAGGCTTCTGTGTGTCTCTTCTTTGCGATCAGCTGGGCACTTGTGCT 882
QY 361 CTCAGCCCTTACCTGATGCTAATATATGTGCTTGCCCAAAAA 406
DB 883 CTCAGCCCTTACCTGATGCTAATATATGTGCTTGCCCAAAAA 928
RESULT 13
US-09-990-456-290
; Sequence 290, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250

;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1,4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Dy 1 GTGAATGTGACTATATATATGACAGTCAAGACCTTCGCTGAGGCTCCCGATGATGTC 60
523 GTGAATGTGACTATATATATGACAGTCAAGACCTTCGCTGAGGCTCCCGATGATGTC 582
Qy 61 CCCAGCCCAAGTGTGCTGCGCATCCCAAGTTGACCGAGGACCACTTTCGAAATC 120
583 CCCAGCCCAAGTGTGCTGCGCATCCCAAGTTGACCGAGGACCACTTTCGAAATC 642
Qy 121 TCCAAATACCAAGCTTTGAGCTGAACTGTGAAATGTGACCATGAAAGTTGTGTGCTC 180
643 TCCAAATACCAAGCTTTGAGCTGAACTGTGAAATGTGACCATGAAAGTTGTGTGCTC 702
Dy 181 TACAAATGTTACGATCAACAACACATATCTCTGTATGATTTGAATGACATTTGCCAAAGCA 240
703 TACAAATGTTACGATCAACAACACATATCTCTGTATGATTTGAATGACATTTGCCAAAGCA 762
Qy 241 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAAGGCGAGTCACTTACAGCTGTCTA 300
763 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAAGGCGAGTCACTTACAGCTGTCTA 822
Dy 301 AACTCAAAAGCTTCTGTGTGTCTCTTCTTTTTCGATCAAGCTGGGACATTTGCGCT 360
823 AACTCAAAAGCTTCTGTGTGTCTCTTCTTTTTCGATCAAGCTGGGACATTTGCGCT 882
Qy 361 CTCAGCCCTTACCTGATGCTAATATATATGATGCTTGGCCCAAAA 406
883 CTCAGCCCTTACCTGATGCTAATATATATGATGCTTGGCCCAAAA 928
Dy

RESULT 15
US-09-992-598-290
; Sequence 290, Application US/09992598

Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaev, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429

```

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

```

Query Match 99.3%; Score 403; DB 9; Length 1658;
Best Local Similarity 99.3%; Pred. No. 1.4e-125;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GTGAATGTGACTATAATGTCAGAGCTTGCGGTGTGAGGCTCCCGATGGTTC 60
Db 523 GTGAATGTGACTATAATGTCAGAGCTTGCGGTGTGAGGCTCCCGATGGTTC 582
QY 61 CCCGAGCCCAAGTGTGTGCGCATCCCAAGTTGACAGGAGCACTTCTGGAAGTC 120
Db 583 CCCGAGCCCAAGTGTGTGCGCATCCCAAGTTGACAGGAGCACTTCTGGAAGTC 642
QY 121 TCCAAATCCAGCTTTGAGCTGAACTGAGAAATGTGACATGAAGGTTGTGTGCTC 180
Db 643 TCCAAATCCAGCTTTGAGCTGAACTGAGAAATGTGACATGAAGGTTGTGTGCTC 702
QY 181 TACAATGTGATGATCAACCAACATCTCTGTATGATGAAAATGACATTTGCCAAGCA 240
Db 703 TACAATGTGATGATCAACCAACATCTCTGTATGATGAAAATGACATTTGCCAAGCA 762

```

```

QY 241 ACAGGGGNTATCAAGTGAACAGATGGAGATCAAAAAGGCGAGTCACTAGACTGTCTA 300
Db 763 ACAGGGGNTATCAAGTGAACAGATGGAGATCAAAAAGGCGAGTCACTAGACTGTCTA 822
QY 301 AACTCAAGGCTTCTGTGTGTCTCTTTTTCATGCACTGGGCACTTGTGCTT 360
Db 823 AACTCAAGGCTTCTGTGTGTCTCTTTTTCATGCACTGGGCACTTGTGCTT 882
QY 361 CTCAGCCCTTACTGATGCTAANATATGTGCTTGGCCACAAA 406
Db 883 CTCAGCCCTTACTGATGCTAANATATGTGCTTGGCCACAAA 928

```

Search completed: May 31, 2005, 10:07:39
Job time : 279.562 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:48:09 ; Search time 1579.08 Seconds
(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978B-12

Perfect score: 406
Sequence: 1 gtcgactgtgactcataatgc.....atgtgctctgcccacaaaaa 406

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb est1:*
2: gb est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403	99.3	595	5	BU680630 UI-CF-DUI
2	403	99.3	925	5	BX368964 BX368964
3	401.4	98.9	655	7	CN259811 170006000
4	401.4	98.9	751	5	BM981657 UI-CF-EN1
5	401.4	98.9	2431	3	CR603772 full-len
6	384	94.6	849	9	AY405846 Homo sapi
7	379.2	93.4	849	9	AY405847 Pan trogl
8	315	77.6	443	1	AI799522 tr49b02.x
9	308.8	76.1	436	8	AQ479831 RPI1-11-2
10	282	69.5	852	8	AY405848 Mus muscu
11	219	53.9	830	4	BG172919 602337353
12	216.2	53.3	767	5	BX358434 BX358434
13	215	53.1	714	7	CN259813 170006000
14	211.6	52.0	698	7	CN259812 170006001
15	186.8	46.0	757	7	BI454643 603170538
16	173	42.6	324	6	CB306900 UI-CF-FNO
17	166	40.9	686	2	BB551556 BB551556
18	164	40.4	779	6	CA311913 UI-CF-FNO
19	119.2	29.4	917	2	BE573890 603331875
20	118	29.1	487	7	CN259818 170006000
21	108.8	26.8	702	6	BY736335 BY736335
22	99.6	24.5	827	6	CV079354 AGENCCOURT
23	70	17.2	604	5	BX499180 DKRP779B
24	69	17.0	670	2	BB666051 BB666051

25	63	15.5	681	2	BE741325	BE741325 601594166
26	51	12.6	584	5	BP255229	BP255229 BP255229
27	48	11.8	583	5	BP255264	BP255264 BP255264
28	47.2	11.6	639	2	BE381883	BE381883 601272421
29	47	11.6	712	5	BU471021	BU471021 603364509
30	47	11.6	792	5	BU458718	BU458718 603367659
31	46	11.3	172	1	AI370413	AI370413 qv77d03.x
32	42.2	10.4	932	7	CR439118	CR439118 CR439118
33	41.6	10.2	689	7	CR424164	CR424164 CR424164
34	41.6	10.2	882	7	CF238625	CF238625 AGENCCOURT
35	41	10.1	419	5	BY217767	BY217767 BY217767
36	40	9.9	1101	9	CNS0178M	AL107728 Drosophila
37	38	9.4	549	7	CN288086	CN288086 170005328
38	38	9.3	603	6	CB928916	CB928916 ABA1 38 C
39	37.6	9.3	395	2	BE427973	BE427973 MTD001-I.
40	37.6	9.3	666	2	AM212469	AM212469 u089a12.x
41	37.2	9.2	357	1	AA821479	AA821479 v59a10.r
42	37.2	9.2	443	2	BE982875	BE982875 UI-M-CGDP
43	37.2	9.2	499	2	BE852674	BE852674 u426903.x
44	37.2	9.2	592	2	AW761877	AW761877 u026h05.y
45	37.2	9.2	615	2	BE334708	BE334708 u082912.y

ALIGNMENTS

RESULT 1
BU680630/c 595 bp mRNA linear EST 07-OCT-2002
LOCUS
DEFINITION
UI-CF-DUI-aaz-1-18-0-UI.s1 UI-CF-DUI Homo sapiens cDNA clone
BU680630
ACCESSION
UI-CF-DUI-aaz-1-18-0-UI 3', mRNA sequence.
VERSION
BU680630.1 GI:23529752
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CDNA Distribution: Researchers may obtain clones from Research
Genetics (www.researchgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Source
Location/Qualifiers
1..595
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-DUI-aaz-1-18-0-UI"
/issue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="PH10B (life Technologies) (T1 phage resistant)"
/clone_id="UI-CF-DUI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;

UI-CF-DU1 is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTZ19-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGGTGTAGGC.

TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368

TAG_LIB=UI-CF-DU1

TAG_SEQ=GGGTGTAGGC"

ORIGIN

Query Match 99.3%; Score 403; DB 5; Length 595;
Best Local Similarity 99.3%; Pred. No. 8.2e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GTGAATGTGACTATATATGCTGAGAACCTTGCGTGTGAGGCTCCCGATGTTTC 60
|||||
539 GTGAATGTGACTATATATGCTGAGAACCTTGCGTGTGAGGCTCCCGATGTTTC 480
|||||
61 CCCGAGCCACAGTGTCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 120
|||||
479 CCCGAGCCACAGTGTCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 420
|||||
121 TCCAAATACCAAGCTTTGAGCTGAATCTTGAGATGTGACCAATGAGTTGTGTGCTC 180
|||||
419 TCCAAATACCAAGCTTTGAGCTGAATCTTGAGATGTGACCAATGAGTTGTGTGCTC 360
|||||
181 TCCAAATGTGATGATCAACAACATCTCTGTATGATTTGAATAATGATGCAAGCA 240
|||||
359 TCCAAATGTGATGATCAACAACATCTCTGTATGATTTGAATAATGATGCAAGCA 300
|||||
241 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGCTGCTA 300
|||||
299 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGCTGCTA 240
|||||
301 AACTCAAAAGCTTCTGTGTGTCTTTCTTTCTTTGCAATCAAGTGGCACTTGTGCT 360
|||||
239 AACTCAAAAGCTTCTGTGTGTCTTTCTTTCTTTGCAATCAAGTGGCACTTGTGCT 180
|||||
361 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGGCCACAAA 406
|||||
179 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGGCCACAAA 134

RESULT 2
BX369964 925 bp mRNA linear EST 26-APR-2004
LOCUS BX369964 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION Clone CS0D1039YG21 5-PRIME, mRNA sequence.
ACCESSION BX369964
VERSION BX369964.1 GI:30449865
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 925)
Li W.B., Gruber C., Jesse J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr; Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 742.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BAG030ZA11_CS02865_1&c=742.r.

Location/Qualifiers

FEATURES

source

1..925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/cissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 99.3%; Score 403; DB 5; Length 925;
Best Local Similarity 99.3%; Pred. No. 9.3e-109;
Matches 403; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GTGAATGTGACTATATATGCTGAGAACCTTGCGTGTGAGGCTCCCGATGTTTC 60
|||||
140 GTGAATGTGACTATATATGCTGAGAACCTTGCGTGTGAGGCTCCCGATGTTTC 199
|||||
61 CCCGAGCCACAGTGTCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 120
|||||
200 CCCGAGCCACAGTGTCTGGGATCCCAAGTTGACCAAGGAGCCAACTTCTCGAAGTC 259
|||||
121 TCCAAATACCAAGCTTTGAGCTGAATCTTGAGATGTGACCAATGAGTTGTGTGCTC 180
|||||
260 TCCAAATACCAAGCTTTGAGCTGAATCTTGAGATGTGACCAATGAGTTGTGTGCTC 319
|||||
181 TCCAAATGTGATGATCAACAACATCTCTGTATGATTTGAATAATGATGCAAGCA 240
|||||
320 TCCAAATGTGATGATCAACAACATCTCTGTATGATTTGAATAATGATGCAAGCA 379
|||||
241 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGCTGCTA 300
|||||
380 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGCTGCTA 439
|||||
301 AACTCAAAAGCTTCTGTGTGTCTTTCTTTCTTTGCAATCAAGTGGCACTTGTGCT 360
|||||
440 AACTCAAAAGCTTCTGTGTGTCTTTCTTTCTTTGCAATCAAGTGGCACTTGTGCT 499
|||||
361 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGGCCACAAA 406
|||||
500 CTCAGCCCTTACCTGATGCTAATATATGAGCTTGGCCACAAA 545

RESULT 3
CN259811 655 bp mRNA linear EST 16-MAY-2004
LOCUS CN259811 1700600059341 GRN_PRENUE Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN259811
ACCESSION CN259811
VERSION CN259811.1 GI:47276225
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 655)
Li F., Xu C., Fang R., Guejler K., Rao M.S., Mandelam R.,
Lebkowski J. and Stanton L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Genon Corporation

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@gen.com
Insert Length: 655 Std Error: 0.00.
Location/Qualifiers

FEATURES

source

1. .655
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN PRENEU"
/note="oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."

ORIGIN

Query Match

98.9%; Score 401.4; DB 7; Length 655;
Best Local Similarity 99.0%; Pred. No. 2.5e-108;

Matches 402; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 GTGAATGTGACTATAATGCGCAGTCCAGANACCTTGCGTGTGAGCTCCCGCATGCTTC 60
DB 136 GTGAATGTGACTATAATGCGCAGTCCAGACCTTGCGTGTGAGCTCCCGCATGCTTC 195
QY 61 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTCTTCGGAAGTC 120
DB 196 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTCTTCGGAAGTC 255
QY 121 TCCAAATACAGCTTTGAGTGAAGTCTGAGATGTGACATGAAGTGTGTGCTGCTC 180
DB 256 TCCAAATACAGCTTTGAGTGAAGTCTGAGATGTGACATGAAGTGTGTGCTGCTC 315
QY 181 TACAAATGTTCAGTCAACAACACACTACTCTGTATGATTAATGAATGACATTGCAAAAGCA 240
DB 316 TACAAATGTTCAGTCAACAACACACTACTCTGTATGATTAATGAATGACATTGCAAAAGCA 375
QY 241 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 300
DB 376 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 435
QY 301 AACCTCAAGGCTCTCTGTGTGTCTCTTCTTTTGGCCATCAGTGGGCACTTCGGCT 360
DB 436 AACCTCAAGGCTCTCTGTGTGTCTCTTCTTTTGGCCATCAGTGGGCACTTCGGCT 495
QY 361 CTCAGCCCTTACCTGATGTAAATATATGCTTGGCCACAAAAA 406
DB 496 CTCAGCCCTTACCTGATGTAAATATATGCTTGGCCACAAAAA 541

```

RESULT 4

BM981657/c

LOCUS BM981657 751 bp mRNA linear EST 21-FEB-2003
DEFINITION UI-CF-EN1-adi-m-02-0-UI s1 UI-CF-EN1 Homo sapiens cDNA clone

UI-CF-EN1-adi-m-02-0-UI 3', mRNA sequence.

ACCESSION BM981657 GI:19604370
VERSION EST.

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 751)
Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477
PUBMED 8889548

COMMENT Contact: McCray, PB
McCray Lab

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171

Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Gene Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).

Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source

1. .751
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-adi-m-02-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"

/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dt primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=human Lung Epithelial Cell lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match

98.9%; Score 401.4; DB 5; Length 751;
Best Local Similarity 99.0%; Pred. No. 2.6e-108;

Matches 402; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 GTGAATGTGACTATAATGCGCAGTCCAGANACCTTGCGTGTGAGCTCCCGCATGCTTC 60
DB 549 GTGAATGTGACTATAATGCGCAGTCCAGACCTTGCGTGTGAGCTCCCGCATGCTTC 490
QY 61 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTCTTCGGAAGTC 120
DB 489 CCCGAGCCCAAGTGTGCTGGGCACTCCCAAGTTGACAGGAGCAACTCTTCGGAAGTC 430
QY 121 TCCAAATACAGCTTTGAGTGAAGTCTGAGATGTGACATGAAGTGTGTGCTGCTC 180
DB 429 TCCAAATACAGCTTTGAGTGAAGTCTGAGATGTGACATGAAGTGTGTGCTGCTC 370
QY 181 TACAAATGTTCAGTCAACAACACACTACTCTGTATGATTAATGAATGACATTGCAAAAGCA 240
DB 369 TACAAATGTTCAGTCAACAACACACTCTGTATGATTAATGAATGACATTGCAAAAGCA 310
QY 241 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 300
DB 309 ACAGGGGATATCAAAAGTGAAGATCGAATCAAAAGGCGAGTCACTTACAGTGTCTA 250
QY 301 AACCTCAAGGCTCTCTGTGTGTCTCTTCTTTTGGCCATCAGTGGGCACTTCGGCT 360
DB 249 AACCTCAAGGCTCTCTGTGTGTCTCTTCTTTTGGCCATCAGTGGGCACTTCGGCT 190

```

Oy 361 CTGAGCCCTTACCTGATGCTAANATAATGTGCCCTTGCGCCACAACAAA 406
Db 189 CTCAGCCTTACTGATGCTAAATAATGTGCCTCGGCCACAAAA 144

RESULT 5	CR603772	2431 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR603772				
DEFINITION	Full-length cDNA clone CS0DI039YG21 of Placenta Cot 25-normalized of Homo sapiens (human).				
ACCESSION	CR603772				
VERSION	CR603772.1	GI:50484579			
KEYWORDS	HTC; CNSLT_cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 2431)
AUTHORS	Li W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL :

REFERENCE 2 (bases 1 to 2431)

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage

COMMENT 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primer end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES	Location/Qualifiers
source	1. .2431

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1039YG21"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT 6"

```

ORIGIN

Query Match	98.9%	Score 401.4;	DB 3;	Length 2431;
Best Local Similarity	99.0%	Pred. No. 3.7e-108;		
Matches 402; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY 1 GTGAATGTGGACATATTAATGCGAGCTCAGANAACTTTGGCGGTGTGAGGCTCCCCGATGGTTT 60

Db 394 GTGATGTGGACATATTAATGCGAGCTCAGAGAACTTGGCGGTGTGAGGCTCCCCGATGGTTT 453

61 CCCAGCCCAAGTGGTCTGGSCATCCCAAGTGGACCAAGGAGCCCACTTCTCGAATC 120

121 TCC AAT A C C A G C T T T G A G C T T G A A C T C T T G A G A A T G T G A C C A T G A A G C T T G T G T C T G T G C T T C 180

Db 514 TCCAATACCAGCTTTGAGCTGAACCTGAGAATGTGACCATGAAGTTGTGTCTGTGCTC 573

241 ACAGGGTATCAAGTGACAGAATCGAGATCAAAAGCGGAGTCACCTACAGCTGCTA 300

DB 634 ACAGGGGATATCAAAGTGCAGGAATCGAGATCAAAGCGGAGTCACTTACGCTGCTA 693

[illegible][illegible]

RESULT 6	849 bp	DNA	linear	GSS 12-DEC-2003
AY405846				
LOCUS				
DEFINITION				
AY405846 Homo sapiens HCM2360 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence.				

KEYWORDS GSS.

ORGANISM	Homo sapiens
-----------------	--------------

REFERENCE
1 (bases 1 to 849)
AUTHORS
Clark, A.G., Glinowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Adams, M.D. and Cargill, M.

JOURNAL
Science 302 (5652), 1960-1963 (2003)

AUTHORS
Clark, A.G., GJanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Ferreira, S., Wang, G., Zheng, A.H., Miller, R.O., Sultany, O.O., Adams, M.D. and Cargill, M.

JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

Source

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<!.>849
/locus_tag="HCM2360"
gene

```

ORIGIN

Query Match	94.6%	Score 384	DB 9	Length 849
Best Local Similarly	99.2%	Pred. No.	4.2e-103	
Matches 384	Conservative	0	Mismatches 3	Indels 0
				Gaps 0

QY 1 GTGATATGGACATAATAGCCAGCTCAGANACCTTGGCGTGTAGGCTCCCCATGGTTC 60
DB 463 GTGATATGGACATAATAGCCAGCTCAGACCTTGGCGTGTAGGCTCCCCATGGTTC 522

61 CCCAGCCACAGTGGCTGGCACTCCAGTTCACCAAGGAGCCATCTCTGGATGTC 120

121 TCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCATGAAAGCTTGTGTCTGTGCTC 180

Db 583 TCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTC 642

[illegible]

241 ACAGGGNTATCAAGTGACAGAATCGGAGATCAAAAGGGGAGTCACCTACAGCTGCTA 300

UD /03 ACAGGGGAIAT CATTAGT GACACGGAA CCGAGAT CATTACCGCGGAGT CATTACCGCGGAGT /02

Dh 763 AACTTCAAAGGCTTTCTGTGTCATCTTTCTTTGCCATCAGCGTGCCACCTCTGCGCT 822

OY		361	CTCAGGCCTTACGTATGCTAATAATPA	387	
Dd		823	CTCAGCCCTTACTGAATGCTAAATPA	849	
RESULT 7					
LOCUS	Ay405847	849 bp	DNA	linear	GSS 12-DEC-2003
DEFINITION	Pan troglodytes HCM2360 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	Ay405847				
VERSION	Ay405847.1	GI:39761821			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan. 1 (bases 1 to 849) Clark,A.G., Gnanowskri,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrieres,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.				
TITLE	Interferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL PUBMED REFERENCE AUTHORS	Science 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 849) Clark,A.G., Gnanowskri,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrieres,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES SOURCE	Location/Qualifiers 1..849 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" <.1.>849 locus_tag="HCM2360"				
gene					
ORIGIN					
Query Match	93.4%; Score 379.2;	DB 9;	Length 849;		
Best Local Similarity	98.4%;	Pred. No. 1.1e-101;			
Matches 381;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;	
OY	1	GTGAATGGAGCTAATATGCCAGTCACAAMNCTTGCGGTTGAGGCCCCCAATTGCTC	60		
Dd	463	GTAATGTGGACTATATATGCCAGTCTCAAGACCTTGCGGTTGAGGCCCCCAATTGCTC	522		
OY	61	CCCCAGCCACAGTGGTGTGGCATCCCAGAATTGACAGGAGCCAATTCTCGGAAGTTC	120		
Dd	523	CCCCAGCCACAGTGGTGTGGCATCCCAGAATTGACAGGAGCCAATTCTCGGAAGTTC	582		
OY	121	TCCATATACCAGCTTTGAGCTGAATCTCTGAGAATGTGACCAATGAAGTTGTGTCTGCTC	180		
Dd	583	TCCATATACCAGCTTTGAGCTGAATCTCTGAGAATGTGACCAATGAAGTTGTGTCTGCTC	642		
OY	181	TACATGTTTAGATCAATCAACACATACCTCCGTATGATTTGAATTTGACATTGCCAAAAGCA	240		
Dd	643	TACATGTTTAGATCAATCAACACATACCTCCGTATGATTTGAATTTGACATTGCCAAAAGCA	702		
OY	241	ACAGGGATATCAAAGTGACAGAAATCTGAGATCAAAAAAGCGGAGTCACTTCAAGTGTCTA	300		
Dd	703	ACAGGGATATCAAAGTGACAGAAATCTGAGATCAAAAAAGCGGAGTCACTTCAAGTGTCTA	762		
OY	301	AACCTCAAGGCTCTCTGTTGTTCTCTTCTTTTGGCACACAGCTGGGCACTTCTGCTT	360		
Dd	763	AACCTCAAGGCTCTCTGTTGTTCTCTTCTTTTGGCACACAGCTGGGCACTTCTGCTT	822		

OY	361	CTCAGCCCTTACCTGATGCTTAANATAA	387
Dd	823	CTCAGCCCTTACTGATGCTAAATAAA	849
<hr/>			
RESULT 8			
AI799522/c			
LOCUS	AI799522	443 bp	mRNA linear EST 06-JUL-1999
DEFINITION	U49b02.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2221611 3'		
ACCESSION	AI799522		
VERSION	AI799522.1 GI:5364994		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 443) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.llnl.gov/bdir/image/image.html Seq primer: -40UP from Gldco High quality sequence stop: 418.		
FEATURES	Location/Qualifiers		
SOURCE	1..443		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2221611"		
	/tissue_type="tumor, 5 pooled (see description)"		
	/_lab_host="DH10B"		
	/_clone_id="NCI_CGAP_Ov23"		
	/_note="Organ: ovary; Vector: pCMV-SportE; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"		
ORIGIN			
Query Match	77.6%	Score 315;	DB 1; Length 443;
Best Local Similarity	99.4%	Pred. NO. 1.3e-82;	
Matches 315;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
OY	90	AGTTGACCAGGAGCACTTCGGAAGTCTCCAATACCAAGCTTGAGCTGA	149
Dd	443	AGTGGACCAAGGAGCAACTTCTCGAAGTCTCCAATACCAAGCTTGAGCTGA	384
OY	150	GAAATGACCATGGAAGGTGTGTCTGCTCTACAATGTTACGATCAACACATAC	209
Dd	383	GAAATGACCATGGAAGGTGTGTCTGCTCTACAATGTTACGATCAACACATAC	324
OY	210	CTGTATGATTGAAATGATGCAATGCAAGAACAAGGGGATCAAGTGAACAAGTGA	269
Dd	323	CTGTATGATTGAAATGATGCAATGCAAGAACAAGGGGATCAAGTGAACAAGTGA	264
OY	270	GATCAAAAAGGCGAGTCACTACAGCTGCTAACTCAAAGGCTTCTGTGTCTCTTC	329
Dd	263	GATCAAAAAGGCGAGTCACTACAGCTGCTAACTCAAAGGCTTCTGTGTCTCTTC	204
OY	330	TTCCTTTGCCATCAAGCTGGGCATCTTGCTCTCAGCCCTTACCTGATGCTAANATATG	389

Db 203 TTTCTTTCATCAGCTGGGCACTTCCTGCTCTCAGCCCTTACGTAGCTAAATATG 144

QY 390 TGCCTTGGCCACAAAA 406

Db 143 TGCCTTGGCCACAAAA 127

RESULT 9
LOCUS AQ479831/c 436 bp DNA linear GSS 23-APR-1999

DEFINITION RPCI-11-269N1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-269N1, genomic survey sequence.

ACCESSION AQ479831

VERSION AQ479831.1 GI:4661950

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 436)

AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building (1997)

JOURNAL Unpublished (1997)

COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html. Seq primer: T7

Class: BAC ends.

FEATURES

source Location/Qualifiers

1..436

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="GDB:7603224"

/db_xref="taxon:9606"

/clone="RPCI-11-269N1"

/sex="Male"

/cell_type="Lymphocytes"

/clone_lib="RPCI-11"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN

Query Match 76.1%; Score 308.8; DB 8; Length 436;

Best Local Similarity 91.8%; Pred. No. 9.3e-81;

Matches 336; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 40 TGTGAGGCTCCCGAGTCTTCCCGACCGACAGTGTCTGGGCAATCCCAAGTGAACG 99

Db 435 TGTGAGGCTCCCTTAATGAGGTCTCTCAGCCACAGTGTATGAAGATCCCTAGTGAACG 376

QY 100 GGAGCAACTTCTCGAAGTCTCCAAATACAGCTTTGAGTGAAGTGAATGAGC 159

Db 375 GGAGCAAAATTTCTCAAGTCTTCAATACCACTTTGGGTGAAGTCTGAAGATGGCC 316

QY 160 ATGAAGTTGTGTCTGTGCTTCAATGTTACGATCAACAACATCTCTGTATGATT 219

Db 315 ATTAAGTTGTGTGTGTGCTCTCAATGTTACGATCAACAACATCTCTGTATGATT 256

QY 220 GAAATGACATTTGCCAAGCAAGGGGATTAAGTGAAGATCGAAGATCAAAAG 279

Db 255 GAAATGACATTTGCCAAGCAAGGGGATTAAGTGAAGATCGAAGATCAAAAG 197

QY 280 CGAGTCACTTACAGCTGTCTAACTCAAGGCTTCTGTGTGTCTCTTCTTTTCC 339

Db 196 CGAGTCACTTACAGCTGTCTAACTCAAGGCTTCTGTGTGTCTCTTCTTTTCC 137

QY 340 ATCAGCTGGGCACTTCTGCTCTGAGCCCTTACCTGATGCTAATATATGCGCTGGCC 399

Db 136 ATCAGCTGGGCACTTCTGCTCTTGGCCCTTACCTGATGCTAATATATGACTGGCC 77

QY 400 ACAAAA 405

Db 76 ACAAAA 71

RESULT 10
LOCUS AY405848 852 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM2360 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY405848

VERSION AY405848.1 GI:39761822

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 852)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 852)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source Location/Qualifiers

1..852

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>852

/locus_tag="HCM2360"

ORIGIN

Query Match 69.5%; Score 282; DB 9; Length 852;

Best Local Similarity 84.3%; Pred. No. 1.1e-72;

Matches 328; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

QY 2 TGAATGTGACATATATGCGACGCTCAGANACCTTGGGTGAGGCTCCCGATGGTCC 61

Db 464 TGAATGTGACATATATGCGACGCTCAGAGAGTTTACGCTCGAGGCTCTCGGTGTTCC 523

QY 62 CCAGCCCAAGTGTCTGGGATCCCAAGTTGACCAAGGACCAACTTCTGGAAGTCT 121

Db 524 CCCAGCCCAAGTGTCTGGGATCTCAAGTGAACCAAGGACCAACTTCTGGAAGTCT 583

QY 122 CCAATACAGCTTTGAGCTGAAGCTTGGAATGTACCATGAAGTGTGTGTGCTCT 181

Db 584 CCAATACAGCTTTGAGCTGAAGCTTGGAATGTACCATGAAGTGTGTGTGCTCT 643

QY 182 ACAATGTTACGATCAACAACATATCTCTGTATGATTGAAATGACATTTGCCAAGCA 241

Db 644 ACAATGTTACGATCAACAACATATCTCTGTATGATTGAAATGACATTTGCCAAGCA 703

```

QY 242 CAGGGGNTATCAAGTGACAGATCGAGATCAAAAGGCGAGTACCTACCTACCTGCTAA 301
DB 704 CCGGGGACATCAAGTATGACAGATTCAGAGTCAAAAGGCGAGTACCTACCTGCTCA 763
QY 302 ACTCAAGGCTTCTCTGTGTG--TCTCTTCTTCTTCTTTCGCATCAGCTGGGCACTTTCG 358
DB 764 ACTCCGGGCTTCCCGCTGTGTGTCTTCTCTGCTTGGCGGCTGGCGGCTGCTCTAT 823
QY 359 CTCTCAGCCCTTACCTATGCTAATATA 387
DB 824 CTCTCTCTCTGCTGCTATGATGAATGA 852

RESULT 11
BG172919 830 bp mRNA linear EST 06-FEB-2001
LOCUS 60233735.F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4460268.5,
DEFINITION mRNA sequence.
ACCESSION BG172919
VERSION BG172919.1 GI:12679609
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:
http://image.llnl.gov
Plate: LML0261 row: j column: 13
High quality sequence stop: 674.
Location/Qualifiers
1. 830
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4460268"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam1"
/note="Organ: mammary; Vector: pCMV-Sport6; Site: 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 53.9%; Score 219; DB 4; Length 830;
Best Local Similarity 89.7%; Pred. No. 6.8e-54;
Matches 234; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 TGAATGTGACTTAATGCGACGCTCAGANACTTGGCGGTGAGGCTCCCGATGTTCC 61
DB 98 TAAATGTGACTTAATGCGACGCTCAGANACTTGGCGGTGAGGCTCCCGATGTTCC 157
QY 62 CCCAGCCCAAGTGTGTGGGATCCCAAGTTGACGAGGAGCAACTTCTCGGAAGTC 121
DB 158 CCCAGCCCAAGTGTGTGGGATCCCAAGTTGACGAGGAGCAACTTCTCGGAAGTC 217
QY 122 CCAATACCAAGCTTGAAGCTGAGATGTGACCATGAAGTTGTGTGTCT 181
DB 218 CCAACACCAAGCTTGAAGCTGAGATGTGACCATGAAGTTGTGTGTCT 277

```

```

QY 182 ACAATGTTACGATCAACACACATACCTCTGTATGATTGAATGACATTTGCCAAGCAA 241
DB 278 ACAATGTTACGATCAACACACATACCTCTGTATGATTGAATGACATTTGCCAAGCAA 337
QY 242 CAGGGGNTATCAAGTGACAG 262
DB 338 CCGGGGACATCAAGTGACAG 358

RESULT 12
BX358434 767 bp mRNA linear EST 08-APR-2004
LOCUS BX358434 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS001039G21 5'-PRIME, mRNA sequence.
ACCESSION BX358434
VERSION BX358434.2 GI:46285747
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
AUTHORS Full-length cDNA libraries and normalization
TITLE Unpublished (2001)
JOURNAL On May 5, 2003 this sequence version replaced gi:30366215.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS001039AD110P1c=742.r.
Location/Qualifiers
1. 767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001039G21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 53.3%; Score 216.2; DB 5; Length 767;
Best Local Similarity 79.9%; Pred. No. 4.5e-53;
Matches 215; Conservative 36; Mismatches 17; Indels 1; Gaps 1;

QY 1 GTGAATGTGACTTAATGCGACGCTCAGANACTTGGCGGTGAGGCTCCCGATGTTCC 60
DB 497 KTGAAATGTGACTTAATGCGACGCTCAGANACTTGGCGGTGAGGCTCCCGATGTTCC 556
QY 61 CCCAGCCCAAGTGTGTGGGATCCCAAGTTGACGAGGAGCAACTTCTCGGAAGTC 120
DB 557 CCCAGCCCAAGTGTGTGGGATCCCAAGTTGACGAGGAGCAACTTCTCGGAAGTC 616
QY 121 TCCATACCAAGCTTGAAGCTGAGATGTGACCATGAAGTTGTGTGTCT 180
DB 617 TCCATACCAAGCTTGAAGCTGAGATGTGACCATGAAGTTGTGTGTCT 676
QY 181 TACATGTTACGATCAACACACATACCTCTGTATGATTGAATGACATTTGCCAAGCAA 240
DB 677 TACATGTTACGATCAACACACATACCTCTGTATGATTGAATGACATTTGCCAAGCAA 736

```

```

Oy      241 ACAG-GGGNTATCAAAGTGACAGATCCG 268
          ||| ||| : ||||| : |||||
Db      737 ACAGTGGGATATTWAAGTGACAGATCCG 765

```

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
(pages 1 to 714)	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murgu, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J and Stanton, L.W.	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation	Nat. Biotechnol. 22 (6), 707-716 (2004)	Contact: Brandenberger R

```

FEATURES
  source      Email: rbrandenberger@geron.com
              Insert Length: 714 Std Error: 0.00.
              Location/Qualifiers
                1. .714

```

```

1. . . 714
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
   /clone_idb="GRN PREHEP"
   /note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hns cell line H9 (p22) maintained in
feeder-free conditions"

```

ORIGIN	
Query Match	53.0%;
Best Local Similarity	98.8%;
Best Local	Pred. No. 1e-52;
Matches 237; Conservative	0; Indels 1; Gaps 2

QY	1	2	3	4	5	6
QY	1	2	3	4	5	6
Db	475	476	477	478	479	480
QY	61	62	63	64	65	66
Db	535	536	537	538	539	540
QY	121	122	123	124	125	126
Db	595	596	597	598	599	600
QY	180	181	182	183	184	185
Db	655	656	657	658	659	660

RESULT	14		
LOCUS	CN259812	698 bp	mRNA
DEFINITION	17006000177307 GRN_PREHEP Homo sapiens CDNA 5', mRNA EST.	linear	EST 16-MAY-2004
ACCESSION	CN259812		
VERSION	CN259812.1	GI:47276226	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		

ORGANISM	<i>Homo sapiens</i>
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 698)
AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraue, J., Flak, G. J.,

TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R

```

230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: zbrandenberger@geron.com
Insert Length: 698 Std Error: 0.00.
Location/Qualifiers
1. .698

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clonote_11b="GKN_PRENHP"
/clonote="oligo dt primed, full-length enriched cDNA library from DMSO-treated h9s cell line H9 (p22) maintained in feeder-free conditions"

```

ORIGIN

Query Match	52.1%	Score 211.6	DB 7	Length 698
Best Local Similarity	97.3%	Pred. No. 1e-51		
Matches 214; Conservative	0	Mismatches	6	Indels 0; Gaps 0

Qy	187	GTTTGCATTAACAACAACATCTCTCTGTATGTTTAAAAATGACATTGGCAAGGAAGG	246
Db	4	GTCCGGATTAAACAACAATCTCTCTGTATGTTTAAAAATGACATTGGCAAGGAAGG	63
Qy	247	GNTATCAAAAGTACACAGAATCGGAGATCAAAAAGGCGGAGTCACTTACAGCTGTAAACTCA	306
Db	64	GATATCAAAAGTACACAGAATCGGAGATCAAAAAGGCGGAGTCACTTACAGCTGTAAACTCA	123
Qy	307	AAGGCTTCTGTGTGTCTCTTCTTTTCCATCACTGGGCACTTCTGCTCTCAGC	366
Db	124	AAGGCTTCTGTGTGTCTCTTCTTTTCCATCACTGGGCACTTCTGCTCTCAGC	183
Qy	367	CCTTACACAGTACTTAATTAATATGACCTTGGGCACAAAAA	406
Db	184	CCTTACTGTATCTTAATTAATATGACCTTGGGCACAAAAA	223

LOCUS	DEFINITION	EST 21-AUG-2001
BI454643	757 bp mRNA	linear
BI454643	60317053BP1 NCI CGAP Mams Mus musculus CDNA clone IMAGE:5250177 5' ,	
	mRNA sequence.	

SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
Mus musculus (house mouse)				
Mus musculus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;				
1 (bases 1 to 757)				
NIH-WGC http://mgc.ncl.nih.gov/ .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgabbs-r@mail.nih.gov				
Tissue Procurement: lothar Hennighausen Ph.D., Robin Humphreys				
cDNA Library Preparation: Life Technologies, Inc.				
cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)				

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>

Plate: L1AM1631 row: k column: 10
 High quality sequence stop: 742.
 Location/Qualifiers

FEATURES

```

source
1..757
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5250177"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_1b="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by life technologies. Investigators
providing samples: Lotnar Hemmighaenen/Robin Humphreys,
NIH"

```

ORIGIN

```

Query Match      46.0%; Score 186.8; DB 4; Length 757;
Best Local Similarity 89.7%; Pred. No. 2.7e-44;
Matches 200; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      2 TGAATGTGACTATTAATGCCAGCTCAGANACCTTGCGGTGTGAGGCTCCCGATGTTCC 61
Db      535 TAAATGTGACTATTAATGCCAGTTCAAGAGTTTACGCTCGAGGCTCCTCGGTGTTCC 594

QY      62 CCCAGCCCAAGAGTGTGGGCAATCCCAAGTTGACCAAGGACCACTTCTCGAAGTCT 121
Db      595 CCCAGCCCAAGAGTGTGGGCAATCCCAAGTTGACCAAGGACCACTTCTCAGAACTCT 654

QY      122 CCAATACAGCTTGTGAGCTGAGCTGTGAATGTGACCATGAAGTTGTGTGTGCTCT 181
Db      655 CCAACACAGCTTGTGAGCTGTGAATGTGACCATGAAGTTGTGTGTGCTCT 714

QY      182 ACAATGTTACGATCAACACATACCTCTGTATGATTGAAA 224
Db      715 ACAATGTACATCAACACATACCTCTGTATGATTGACAA 757

```

Search completed: May 31, 2005, 00:10:55
 Job time : 1582.08 secs

THIS PAGE LEFT BLANK

FEATURES	Location/Qualifiers
SOURCE	1..462
ORGANISM	"Homo sapiens"
mol_type	"genomic DNA"
db_xref	"taxon:9606"
ORIGIN	
Query Match	100.0%; Score 462; DB 6; Length 462

Best Local Similarity 100.0%; Pred. No. 2.7e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy	1	GGAAAGGACAGCGACACTCCATCTCACCCAGTACCCAGATACGCTGGAAACCTTCCCGAGCC	60
Db	1	GGAAAGCAGCGGACACTCCACTCACCCAGTACCCAGATACGCTGGAAACCTTCCCGAGCC	60
Qy	61	ATGCGTTCCTGGGGCAGATCCCTCTTCTGGAGCATTAATTAAGCATCATTAATTCGGCT	120
Db	61	ATGCGTTCCTGGGGCAGATCCCTCTTCTGGAGCATTAATTAAGCATCATTAATTCGGCT	120
Qy	121	GGAGCAATTGCACTCATATTGGCTTTGGTATTTACGAGGACATCCATCACTCACT	180
Db	121	GGAGCAATTGCACTCATATTGGCTTTGGTATTTACGAGGACATCCATCACTCACT	180
Qy	181	ACTGTGCGCTCAGCTGGGAAACAATTGGGGAGATGGAATCCTGAGCTGCACATTTGAACT	240
Db	181	ACTGTGCGCTCAGCTGGGAAACAATTGGGGAGATGGAATCCTGAGCTGCACATTTGAACT	240
Qy	241	GACATCAAACTTTTCGTATATCTGTATACAATGGCTGAAGAAAGGTGTTTATAGGCTTGGTC	300
Db	241	GACATCAAACTTTTCGTATATCTGTGTATACAAATGGCTGAAGAAAGGTGTTTATAGGCTTGGTC	300
Qy	301	CATGAGTTCAAAGAAAGGCAAGATAGCTGTGGAGCAAGATGAATGTTTCAGAGGCCGG	360
Db	301	CATGAGTTCAAAGAAAGGCAAGATAGCTGTGGAGCAAGATGAATGTTTCAGAGGCCGG	360
Qy	361	ACAGCAGTGTGTCGTATCAAGTATAGTGTGGCAATGCTCTTTGCGGCTGAAAAACGTG	420
Db	361	ACAGCAGTGTGTCGTATCAAGTATAGTGTGGCAATGCTCTTTGCGGCTGAAAAACGTG	420
Qy	421	CAACTCAGAGATGCTGGGACCTACAAAGTTATATATCAATCACT	462
Db	421	CAACTCAGAGATGCTGGGACCTACAAAGTTATATATCAATCACT	462

RESULT 2	AX375858	1065 bp	DNA	linear	PAT 01-MAR-2002
LOCUS	AX375858				
DEFINITION	Sequence 5 from Patent WO0194641.				
ACCESSION	AX375858				
VERSION	AX375858.1	GI:19170330			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE					
AUTHORS	Ople,E., McIachlan,K. and Heard,C.				
TITLE	Gene targets and ligands that bind thereto for treatment and				
	diagnosis of ovarian carcinomas				
JOURNAL	Patent: WO 0194641-A 5 13-DEC-2001;				
	Idec Pharmaceuticals Corporation (US)				
FEATURES					
source	location/Qualifiers				
	1..1065				
	/Organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					

Query Match	100.0%	Score 462;	DB 6;	Length 1065;
Best Local Similarity	100.0%	Pred. No. 3e-133;		
Matches 462;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	GGAAGGCGAGCGAGCTCCATCTACAGCCAGTACCAGATACGCTGTGGAACTTCCCCAGCC	60	
Db	12	GGAAGGCGAGCGAGCTCCATCTACAGCCAGTACCAGATACGCTGTGGAACTTCCCCAGCC	71	
Qy	61	ATGGCTTCCTGGGGCAGATCCTCTTTCGAGCATTAATTAGCATCATTAATTTCGCT	120	
Db	72	ATGGCTTCCTGGGGCAGATCCTCTTTCGAGCATTAATTAGCATCATTAATTTCGGCT	131	
Qy	121	GGAGCAATTGACATCATTTGGCTTTGGTATTTTCAGGAGACATCCATCAGACTACT	180	

Db	1332	GGAGCAATTGCAC	CTCAT	CATTGGCTTTGGTA	TTTCAGGGAGAC	CTCCAT	CACAGTC	ACT	191	
Qy	181	ACTGTGCGCTCA	GCTGGGA	CA	TTGGGGAGAT	GGAA	TCTGAGCTG	CACTTTGAA	CTT	240
Db	192	ACTGTGCGCTCA	GCTGGGA	CA	TTGGGGAGAT	GGAA	TCTGAGCTG	CACTTTGAA	CTT	251
Qy	241	GACATCAAACTT	TCGATATG	CTGTAT	TCAAATGGCTG	GAAGGATG	TTTAAAGCTT	GGTC	300	
Db	252	GACATCAAACTT	TCGATATG	CTGTAT	TCAAATGGCTG	GAAGGATG	TTTAAAGCTT	GGTC	311	
Qy	301	CATGAGTTCAAA	GAGCAAGAT	GAGCTGT	CGGAGCAGAT	GTAAATGTT	CAGAGGCGG	360		
Db	312	CATGAGTTCAAA	GAGCAAGAT	GAGCTGT	CGGAGCAGAT	GTAAATGTT	CAGAGGCGG	371		
Qy	361	ACAGCAGT	TTTTGCTGAT	TCAAAGTGA	TAGTTGGCA	TGCTCTTTTGGCGG	CTGAAAAAC	GTG	420	
Db	372	ACAGCAGT	TTTTGCTGAT	TCAAAGTGA	TAGTTGGCA	TGCTCTTTTGGCGG	CTGAAAAAC	GTG	431	
Qy	421	CAACTCAGAGAT	CGTGGGAC	CTCA	CAAAATGTA	TATATCA	TCACT	462		
Db	432	CAACTCAGAGAT	CGTGGGAC	CTCA	CAAAATGTA	TATATCA	TCACT	473		

[illegible]

QY 1 GGAAGGAGGCGGAGCTCCACTGAGCAGTACCCAGATGCGCTGGGAACCTTCCCGAGCC 60
DB 1 GGAAGGAGGCGGAGCTCCACTGAGCAGTACCCAGATGCGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGAGCAATTAATAGCATCATATTATTCGGCT 120
DB 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGAGCAATTAATAGCATCATATTATTCGGCT 120
QY 121 GGAGCAATTGCACTCATCATATTGGCTTGGTATTTTCAGGGAGACATCCCATCAGTCACT 180
DB 121 GGAGCAATTGCACTCATCATATTGGCTTGGTATTTTCAGGGAGACATCCCATCAGTCACT 180
QY 181 ACTGTGCGCTCAGCTGGGAAACATTGGGGAGAGATGGAAATCCGAGCTGACATTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGGAAACATTGGGGAGAGATGGAAATCCGAGCTGACATTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATACAAATGCGCTGAAGAGAGGTGTTTAAAGCTTGGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATACAAATGCGCTGAAGAGAGGTGTTTAAAGCTTGGTC 300
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGCGCGG 360
DB 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGCGCGG 360
QY 361 ACAGCAGTGTGCTGATCAAGTATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
DB 361 ACAGCAGTGTGCTGATCAAGTATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
QY 421 CAACTCAGAGATGCTGGACCTCAAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATGCTGGACCTCAAAATGTTATATCATCACT 462

RESULT 4
LOCUS CO875680 1658 bp DNA linear PAT 27-SEP-2004
DEFINITION Sequence 3 from Patent EPI445317.
ACCESSION CO875680
VERSION CO875680.1 GI:52748533

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: EP 1445317-A 3 11-AUG-2004;
Genentech Inc. (US)

FEATURES
Location/Qualifiers

1..1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGAGGCGGAGCTCCACTGAGCAGTACCCAGATGCGCTGGGAACCTTCCCGAGCC 60
DB 1 GGAAGGAGGCGGAGCTCCACTGAGCAGTACCCAGATGCGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGAGCAATTAATAGCATCATATTATTCGGCT 120
DB 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGAGCAATTAATAGCATCATATTATTCGGCT 120
QY 121 GGAGCAATTGCACTCATCATATTGGCTTGGTATTTTCAGGGAGACATCCCATCAGTCACT 180
DB 121 GGAGCAATTGCACTCATCATATTGGCTTGGTATTTTCAGGGAGACATCCCATCAGTCACT 180

QY 181 ACTGTGCGCTCAGCTGGGAAACATTGGGGAGAGATGGAAATCCGAGCTGACATTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGGAAACATTGGGGAGAGATGGAAATCCGAGCTGACATTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATACAAATGCGCTGAAGAGAGGTGTTTAAAGCTTGGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATACAAATGCGCTGAAGAGAGGTGTTTAAAGCTTGGTC 300
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGCGCGG 360
DB 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGCGCGG 360
QY 361 ACAGCAGTGTGCTGATCAAGTATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
DB 361 ACAGCAGTGTGCTGATCAAGTATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
QY 421 CAACTCAGAGATGCTGGACCTCAAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATGCTGGACCTCAAAATGTTATATCATCACT 462

RESULT 5
LOCUS AR252569 1658 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 290 from patent US 6478825.
ACCESSION AR252569
VERSION AR252569.1 GI:27300477

KEYWORDS
SOURCE Unknown.

ORGANISM
Unknown.

REFERENCE
1 (bases 1 to 1658)
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 290 12-NOV-2002;
Location/Qualifiers

1..1658
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGAGGCGGAGCTCCACTGAGCAGTACCCAGATGCGCTGGGAACCTTCCCGAGCC 60
DB 1 GGAAGGAGGCGGAGCTCCACTGAGCAGTACCCAGATGCGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGAGCAATTAATAGCATCATATTATTCGGCT 120
DB 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGAGCAATTAATAGCATCATATTATTCGGCT 120
QY 121 GGAGCAATTGCACTCATCATATTGGCTTGGTATTTTCAGGGAGACATCCCATCAGTCACT 180
DB 121 GGAGCAATTGCACTCATCATATTGGCTTGGTATTTTCAGGGAGACATCCCATCAGTCACT 180
QY 181 ACTGTGCGCTCAGCTGGGAAACATTGGGGAGAGATGGAAATCCGAGCTGACATTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGGAAACATTGGGGAGAGATGGAAATCCGAGCTGACATTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATACAAATGCGCTGAAGAGAGGTGTTTAAAGCTTGGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATACAAATGCGCTGAAGAGAGGTGTTTAAAGCTTGGTC 300
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGCGCGG 360
DB 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGAGAGAGATGAATGTTTCAGAGCGCGG 360
QY 361 ACAGCAGTGTGCTGATCAAGTATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
DB 361 ACAGCAGTGTGCTGATCAAGTATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420

Db 361 ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTTGGCGCTGAAAAACGTG 420
QY 421 CAACCTCAGAGTGTGGGACCTTACAAATGTTATATCATCACT 462
Db 421 CAACCTCAGAGTGTGGGACCTTACAAATGTTATATCATCACT 462

RESULT 6
AX092328 1658 bp DNA linear PAT 23-MAR-2001
LOCUS Sequence 59 from Patent WO0116318.
DEFINITION AX092328
ACCESSION AX092328 GI:1344478
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Baker, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 59 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source 1.1658
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGACGCGGACGCTCCAGCTCAGCAGTACCCAGATACGCTGGAACTTCCCGACCC 60
Db 1 GGAGGACGCGGACGCTCCAGCTCAGCAGTACCCAGATACGCTGGAACTTCCCGACCC 60
QY 61 ATGGCTTCCCTGGGCGAGATCCTCTTCTGGAGCATATTAGCATCATCTATTCTGGCT 120
Db 61 ATGGCTTCCCTGGGCGAGATCCTCTTCTGGAGCATATTAGCATCATCTATTCTGGCT 120
QY 121 GGAGCAATTGCACTATCATCTGCTTGGATTTTCAAGGAGACATCCACCTCAGCACT 180
Db 121 GGAGCAATTGCACTATCATCTGCTTGGATTTTCAAGGAGACATCCACCTCAGCACT 180
QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
Db 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATACAAATGCTGAAGGAGTGTTTAGGCTTGGTC 300
Db 241 GACATCAAACTTTCTGATATCGTATACAAATGCTGAAGGAGTGTTTAGGCTTGGTC 300
QY 301 CATGAGTTCAAAAGAGGCAAGATGAGCTGTGGAGCAGGATGAATGTTCAAGGCGCG 360
Db 301 CATGAGTTCAAAAGAGGCAAGATGAGCTGTGGAGCAGGATGAATGTTCAAGGCGCG 360
QY 361 ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTTGGCGCTGAAAAACGTG 420
Db 361 ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTTGGCGCTGAAAAACGTG 420
QY 421 CAACCTCAGAGTGTGGGACCTTACAAATGTTATATCATCACT 462
Db 421 CAACCTCAGAGTGTGGGACCTTACAAATGTTATATCATCACT 462

RESULT 7
AX376150 1658 bp DNA linear PAT 01-MAR-2002
LOCUS AX376150

DEFINITION Sequence 217 from Patent WO0168848.
ACCESSION AX376150
VERSION AX376150.1 GI:19170467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 217 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source 1.1658
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGACGCGGACGCTCCAGCTCAGCAGTACCCAGATACGCTGGAACTTCCCGACCC 60
Db 1 GGAGGACGCGGACGCTCCAGCTCAGCAGTACCCAGATACGCTGGAACTTCCCGACCC 60
QY 61 ATGGCTTCCCTGGGCGAGATCCTCTTCTGGAGCATATTAGCATCATCTATTCTGGCT 120
Db 61 ATGGCTTCCCTGGGCGAGATCCTCTTCTGGAGCATATTAGCATCATCTATTCTGGCT 120
QY 121 GGAGCAATTGCACTATCATCTGCTTGGATTTTCAAGGAGACATCCACCTCAGCACT 180
Db 121 GGAGCAATTGCACTATCATCTGCTTGGATTTTCAAGGAGACATCCACCTCAGCACT 180
QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
Db 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATACAAATGCTGAAGGAGTGTTTAGGCTTGGTC 300
Db 241 GACATCAAACTTTCTGATATCGTATACAAATGCTGAAGGAGTGTTTAGGCTTGGTC 300
QY 301 CATGAGTTCAAAAGAGGCAAGATGAGCTGTGGAGCAGGATGAATGTTCAAGGCGCG 360
Db 301 CATGAGTTCAAAAGAGGCAAGATGAGCTGTGGAGCAGGATGAATGTTCAAGGCGCG 360
QY 361 ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTTGGCGCTGAAAAACGTG 420
Db 361 ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTTGGCGCTGAAAAACGTG 420
QY 421 CAACCTCAGAGTGTGGGACCTTACAAATGTTATATCATCACT 462
Db 421 CAACCTCAGAGTGTGGGACCTTACAAATGTTATATCATCACT 462

RESULT 8
AX395215 1658 bp DNA linear PAT 18-MAY-2002
LOCUS AX395215
DEFINITION Sequence 3 from Patent WO0216429.
ACCESSION AX395215
VERSION AX395215.1 GI:21066246
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakie, P.,

TITLE Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216429-A 3 28-FEB-2002;

FEATURES
source Location/Qualifiers
1.1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCAAGGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCGACCC 60
DB 1 GGAAGGCAAGGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCGACCC 60
QY 61 ATGGCTTCCCTGGGCGAGATCTCTTGAGGCAATATTAGCATCATCATTTATCTGGCT 120
DB 61 ATGGCTTCCCTGGGCGAGATCTCTTGAGGCAATATTAGCATCATCATTTATCTGGCT 120
QY 121 GGAACAAATTCACATCATCATTTGCTTTGATTTCAAGGAGACATCTCCATCAGTCACT 180
DB 121 GGAACAAATTCACATCATCATTTGCTTTGATTTCAAGGAGACATCTCCATCAGTCACT 180
QY 181 ACTGTCCCTCAGCTGGGAAATTTGGAGAGATGGAATCTCGAGCTGCATTTTGAACCT 240
DB 181 ACTGTCCCTCAGCTGGGAAATTTGGAGAGATGGAATCTCGAGCTGCATTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATCAATGCTGAAGAAAGGTGTTTAAAGCTTGCTC 300
DB 241 GACATCAAACTTTCTGATATCGTATCAATGCTGAAGAAAGGTGTTTAAAGCTTGCTC 300
QY 301 CATGAGTTCAAGAAGCAAGATGAGCTGCGAGGAGATGAAATGTTCAAGAGCGG 360
DB 301 CATGAGTTCAAGAAGCAAGATGAGCTGCGAGGAGATGAAATGTTCAAGAGCGG 360
QY 361 ACAGCAGTGTGTTCTGATCAAGATAGTGGCAATCTCTTTGCGGCTGAAAAACGTG 420
DB 361 ACAGCAGTGTGTTCTGATCAAGATAGTGGCAATCTCTTTGCGGCTGAAAAACGTG 420
QY 421 CAACTCAGAGTGTGGACCTTACAATGTTATATCATCACT 462
DB 421 CAACTCAGAGTGTGGACCTTACAATGTTATATCATCACT 462

RESULT 9
AX403403 1658 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 290 from Patent WO0073454.
DEFINITION AX403403
ACCESSION AX403403.1 GI:21436923
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 Ahkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Bacon, D.,
Ferrara, N., Gerber, H., Gerltzen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kijavlin, I., Napier, M.A., Pan, J.,
Proni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 290 07-DEC-2000;

FEATURES
source Location/Qualifiers
1.1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:9606"

Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCAAGGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCGACCC 60
DB 1 GGAAGGCAAGGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCGACCC 60
QY 61 ATGGCTTCCCTGGGCGAGATCTCTTGAGGCAATATTAGCATCATCATTTATCTGGCT 120
DB 61 ATGGCTTCCCTGGGCGAGATCTCTTGAGGCAATATTAGCATCATCATTTATCTGGCT 120
QY 121 GGAACAAATTCACATCATCATTTGCTTTGATTTCAAGGAGACATCTCCATCAGTCACT 180
DB 121 GGAACAAATTCACATCATCATTTGCTTTGATTTCAAGGAGACATCTCCATCAGTCACT 180
QY 181 ACTGTCCCTCAGCTGGGAAATTTGGAGAGATGGAATCTCGAGCTGCATTTTGAACCT 240
DB 181 ACTGTCCCTCAGCTGGGAAATTTGGAGAGATGGAATCTCGAGCTGCATTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATCAATGCTGAAGAAAGGTGTTTAAAGCTTGCTC 300
DB 241 GACATCAAACTTTCTGATATCGTATCAATGCTGAAGAAAGGTGTTTAAAGCTTGCTC 300
QY 301 CATGAGTTCAAGAAGCAAGATGAGCTGCGAGGAGATGAAATGTTCAAGAGCGG 360
DB 301 CATGAGTTCAAGAAGCAAGATGAGCTGCGAGGAGATGAAATGTTCAAGAGCGG 360
QY 361 ACAGCAGTGTGTTCTGATCAAGATAGTGGCAATCTCTTTGCGGCTGAAAAACGTG 420
DB 361 ACAGCAGTGTGTTCTGATCAAGATAGTGGCAATCTCTTTGCGGCTGAAAAACGTG 420
QY 421 CAACTCAGAGTGTGGACCTTACAATGTTATATCATCACT 462
DB 421 CAACTCAGAGTGTGGACCTTACAATGTTATATCATCACT 462

RESULT 10
AX468680 1658 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 4 from Patent WO0216581.
DEFINITION AX468680
ACCESSION AX468680
VERSION AX468680.1 GI:21901458
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 Gao, W.Q., Polak, P., Shou, J., Smith, V., Soriano, R., Williams, P.M.,
Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216581-A 4 28-FEB-2002;

FEATURES
source Location/Qualifiers
1.1658
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 1658;
Best Local Similarity 100.0%; Pred. No. 3.1e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCAAGGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCGACCC 60
DB 1 GGAAGGCAAGGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGAAACCTTCCCGACCC 60
QY 61 ATGGCTTCCCTGGGCGAGATCTCTTGAGGCAATATTAGCATCATCATTTATCTGGCT 120

```

Db      61  ATGGCTCCCTGGGGGAGATCCCTCTCTGGAGCATATATAGCATCATCTATTATTCGGCT 120
      121  GGAGCAATTGCACTCATCTATGCTTTGGTATTTTCAGGAGACACCTCCATCCAGCACT 180
      121  GGAGCAATTGCACTCATCTATGCTTTGGTATTTTCAGGAGACACCTCCATCCAGCACT 180
      181  ACTGTCGCTCAGCTGAGGAACATTTGGGAGAGATGGAATCCTGAGCTGACCTTTGAACCT 240
      181  ACTGTCGCTCAGCTGAGGAACATTTGGGAGAGATGGAATCCTGAGCTGACCTTTGAACCT 240
      241  GACATCAAACTTTCTGATATCTGATATCAATGCTGGAAGAGCTTTTATGAGCTTGGTC 300
      241  GACATCAAACTTTCTGATATCTGATATCAATGCTGGAAGAGCTTTTATGAGCTTGGTC 300
      301  CATGAGTTCAAGAGAGCAAGATGAGCTGCTGGAGACAGATGAATGTTTCAGAGGCCGG 360
      301  CATGAGTTCAAGAGAGCAAGATGAGCTGCTGGAGACAGATGAATGTTTCAGAGGCCGG 360
      361  ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTGGCGCTGAAAAACGTG 420
      361  ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTGGCGCTGAAAAACGTG 420
      421  CAACCTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
      421  CAACCTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462

```

RESULT 11
 AY358352 1658 bp mRNA linear PRI 03-OCT-2003
 LOCUS Homo sapiens clone DNAS9610 B7h.5 (UN0659) mRNA, complete cds.
 DEFINITION AY358352.1 GI:37181828
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE

AUTHORS
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.B.,
 Heldens,S., Huang,A., Kim,H.S., Kilmowski,L., Jin,Y., Johnson,S.,
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
 Schoenfeld,J., Seebagiri,S., Simmons,L., Singh,J., Smith,V.,
 Stinson,J., Vagter,A., Vandlen,R., Watanabe,C., Wleand,D., Woods,K.,
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PubMed 12975309
 2 (bases 1 to 1658)
 Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES

source
 1. 1658
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DNAS9610"
 1. 1658
 /locus_tag="UN0659"
 61..909
 /locus_tag="UN0659"
 /note="PRO1291"
 /codon_start=1
 /product="B7h.5"
 /protein_id="AA08718.1"

```

/db_xref="GI:37181829"
/translation="MASLGGQILFMSIISIIILAGALALIGFGISGRHSITVTVAS
AGNIGEDGILISTCEPDIKLSDIVQMLKEVLGIVHFKEKDELSEODEMFRRTA
VPADQIVGNASLRLKPNVOLDAGYKCYIITSKKGANAEYKGAFSMEVANDYN
ASSSTIRCEARPRPOPVTWASQVDOGANSSEVSNFSPEINSENVTKVSVLVNVT
INMTYSCTENDIAKATQDIVTSEIRSRHLDLNSKASLCVSPFAISMALLPLS
PYLMRK"

```

ORIGIN

Query Match 100.0%; Score 462; DB 9; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 3,1e-133;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

      1  GGAGGACGCGGACGCTCCACTCAGCCAGTACCAGATACGCTGGAACTTTCCAGCC 60
      1  GGAGGACGCGGACGCTCCACTCAGCCAGTACCAGATACGCTGGAACTTTCCAGCC 60
      61  ATGGCTCCCTGGGGGAGATCCCTCTCTGGAGCATATATGATATATATTCGGCT 120
      61  ATGGCTCCCTGGGGGAGATCCCTCTCTGGAGCATATATGATATATATTCGGCT 120
      121  GGAGCAATTGCACTCATCTATGCTTTGGTATTTTCAGGAGACACTCCATCAGACTACT 180
      121  GGAGCAATTGCACTCATCTATGCTTTGGTATTTTCAGGAGACACTCCATCAGACTACT 180
      181  ACTGTCGCTCAGCTGAGGAACATTTGGGAGAGATGGAATCCTGAGCTGACCTTTGAACCT 240
      181  ACTGTCGCTCAGCTGAGGAACATTTGGGAGAGATGGAATCCTGAGCTGACCTTTGAACCT 240
      241  GACATCAAACTTTCTGATATCTGATATCAATGCTGGAAGAGCTTTTATGAGCTTGGTC 300
      241  GACATCAAACTTTCTGATATCTGATATCAATGCTGGAAGAGCTTTTATGAGCTTGGTC 300
      301  CATGAGTTCAAGAGAGCAAGATGAGCTGTCGAGCAGATGAATGTTTCAGAGGCCGG 360
      301  CATGAGTTCAAGAGAGCAAGATGAGCTGTCGAGCAGATGAATGTTTCAGAGGCCGG 360
      361  ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTGGCGCTGAAAAACGTG 420
      361  ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTGGCGCTGAAAAACGTG 420
      421  CAACCTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
      421  CAACCTCAGAGATGCTGGCACTTCAAAATGTTATATCATCACT 462

```

RESULT 12

LOCUS CQ412191 1965 bp DNA linear PAT 23-JAN-2004
 DEFINITION Sequence 19262 from Patent WO0170979.
 ACCESSION CQ412191
 VERSION CQ412191.1 GI:41319972
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE

AUTHORS
 Lee,J. and Lillie,J.
 TITLE Genes, compositions, kits, and method for identification,
 assessment, prevention, and therapy of ovarian cancer
 JOURNAL Patent: WO 0170979-A 19262 27-SEP-2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES

source
 1. 1965
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 1965;
 Best Local Similarity 100.0%; Pred. No. 3.2e-133;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAGATAGCTGGGAACTTCCCGCAGCC 60
DB 20 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAGATAGCTGGGAACTTCCCGCAGCC 79
QY 61 ATGGCTTCCCTGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 120
DB 80 ATGGCTTCCCTGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 139
QY 121 GGAAGCAATTGCATCATCTATTGGCTTTGGTATTTCAGGAGACATCTCCATCAAGTCACT 180
DB 140 GGAAGCAATTGCATCATCTATTGGCTTTGGTATTTCAGGAGACATCTCCATCAAGTCACT 199
QY 181 ACTGTGGCTCAGCTGGGAAACATTTGGGGAGATGGAAATCTGAGCTGCACTTTTGAACCT 240
DB 200 ACTGTGGCTCAGCTGGGAAACATTTGGGGAGATGGAAATCTGAGCTGCACTTTTGAACCT 259
QY 241 GACATCAAACTTTCTGATATCGTATCAAAATGGCTGAGAGAGAGTGTTTTGGCTTGGTC 300
DB 260 GACATCAAACTTTCTGATATCGTATCAAAATGGCTGAGAGAGAGTGTTTTGGCTTGGTC 319
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGAGATGAATGTTCAAGGCGCG 360
DB 320 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGAGATGAATGTTCAAGGCGCG 379
QY 361 ACAGCAGTGTGTTGCTGATCAAGATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
DB 380 ACAGCAGTGTGTTGCTGATCAAGATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 439
QY 421 CAACTCAGAGATGCTGGCACTCAAAATGTTATATCATCACT 462
DB 440 CAACTCAGAGATGCTGGCACTCAAAATGTTATATCATCACT 481

RESULT 13
AX375860 2626 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 7 from Patent WO0194641.
ACCESSION AX375860
VERSION AX375860.1 GI:19170332
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ople,E., McIachlan,K. and Heard,C.
TITLE Gene targets and ligands that bind thereto for treatment and
diagnosis of ovarian carcinomas
JOURNAL Patent: WO 0194641-A 7 13-DEC-2001;
Idex Pharmaceuticals Corporation (US)
FEATURES
source 1. .2626
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 462; DB 6; Length 2626;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAGATAGCTGGGAACTTCCCGCAGCC 60
DB 1 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAGATAGCTGGGAACTTCCCGCAGCC 60
QY 61 ATGGCTTCCCTGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 120
DB 61 ATGGCTTCCCTGGGGAGATCTCTTCTGGAGCAATAATTAGCATCATTAATTTGGCT 120
QY 121 GGAAGCAATTGCATCATCTATTGGCTTTGGTATTTCAGGAGACATCTCCATCAAGTCACT 180
DB 121 GGAAGCAATTGCATCATCTATTGGCTTTGGTATTTCAGGAGACATCTCCATCAAGTCACT 180

QY 181 ACTGTGGCTCAGCTGGGAAACATTTGGGGAGATGGAAATCTGAGCTGCACTTTTGAACCT 240
DB 181 ACTGTGGCTCAGCTGGGAAACATTTGGGGAGATGGAAATCTGAGCTGCACTTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATCAAAATGGCTGAGAGAGATGTTTGGCTTGGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATCAAAATGGCTGAGAGAGATGTTTGGCTTGGTC 300
QY 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGAGATGAATGTTCAAGGCGCG 360
DB 301 CATGAGTTCAAGAAGGCAAAAGATGAGCTGTGGAGAGAGATGAATGTTCAAGGCGCG 360
QY 361 ACAGCAGTGTGTTGCTGATCAAGATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
DB 361 ACAGCAGTGTGTTGCTGATCAAGATGATGTTGGCAATGCTCTTGGCGCTGAAAACGCTG 420
QY 421 CAACTCAGAGATGCTGGCACTCAAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATGCTGGCACTCAAAATGTTATATCATCACT 462

RESULT 14
BD265002 2627 bp DNA linear PAT 17-JUL-2003
LOCUS Compositions and methods for the therapy and diagnosis of ovarian
DEFINITION cancer.
ACCESSION BD265002.1 GI:33074770
VERSION JP 2002532093-A/387.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Mitcham,J.L., King,G.E., Algate,P.A. and Prudakis,T.N.
TITLE 1 (bases 1 to 2627)
JOURNAL Compositions and methods for the therapy and diagnosis of ovarian
Patent: JP 2002532093-A 387 02-OCT-2002;
CORIXA CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002532093-A/387
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681,17-DEC-1998 US 09/215603 PR
23-JUN-1999 US 09/338933,24-SEP-1999 US 09/404879 PI
JENNIFER L MITCHAM,GORDON E KING,PAUL A ALGATE,TONY N PRUDAKIS PC
C12N15/09,A61K31/7115,A61K35/14,A61K35/76,A61K39/00,A61K39/395, PC
A61K39/395,
PC A61K48/00,A61P35/00,A61P37/04,C07K14/82,C07K19/00,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/06,C12N5/10,C1201/68,G01N33/53,G01N33/53,G01N33/ PC
566,
PC G01N33/574,G01N33/577,C12N15/00,C12N5/00,C12N5/00 CC
Compositions and methods for the therapy and diagnosis of CC
ovarian cancer
FH Key Location/Qualifiers
FT source 1. .2627
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 462; DB 6; Length 2627;
Best Local Similarity 100.0%; Pred. No. 3.3e-133;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAGATAGCTGGGAACTTCCCGCAGCC 60
DB 23 GGAAGGAGGAGGAGCTCCAGTACAGGAGTACCAGATAGCTGGGAACTTCCCGCAGCC 82

Qy	61	ATGGCTTCCCGGGGCAATATCTCTTCGAGACAAATTAGATATCATTAATTCGGCT	120
Db	83	ATGGCTTCCCTGGGGCAATCTCTTCGAGACAAATTAGATATCATTAATTCGGCT	142
Qy	121	GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAGACATCCATCACTCACT	180
Db	143	GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAGACATCCATCACTCACT	202
Qy	181	ACTGTGCGCTCAAGCTGGGAACTTTGGGAGGATGGAAATCTCGAGCTGCATTTGAACCT	240
Db	203	ACTGTGCGCTCAAGCTGGGAACTTTGGGAGGATGGAAATCTCGAGCTGCATTTGMAACT	262
Qy	241	GACATCAAACTTTCGATATCTGTATAAATGCGTGAAGGAAAGGCTTTAGCGCTTGCTC	300
Db	263	GACATCAAACTTTCGATATCTGTATAAATGCGTGAAGGAAAGGCTTTAGCGCTTGCTC	322
Qy	301	CATGAGTTCAAGAAGCAAGATAGCTGTGAGCAGAGATGAATGTTCCAGAGCCGG	360
Db	323	CATGAGTTCAAGAAGCAAGATAGCTGTGAGCAGAGATGAATGTTCCAGAGCCGG	382
Qy	361	ACAGCAGTGTTCGTGATCAAGTAGTAAGTTGGCAATGCTCTTTGGCGCTGAAAAAGTGG	420
Db	383	ACAGCAGTGTTCGTGATCAAGTAGTAAGTTGGCAATGCTCTTTGGCGCTGAAAAAGTGG	442
Qy	421	CAACTCAGAGTCTGGGCACTCAAGAAATGTTATATATCACT	482
Db	443	CAACTCAGAGTCTGGGCACTCAAGAAATGTTATATATCACT	484

RESULT 15				
LOCUS	AR238405	2627 bp	DNA	linear
DEFINITION	Sequence 391 from patent US 6468546.			
ACCESSION	AR238405			
VERSION	AR238405.1	GI:27283369		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 2627)			
AUTHORS	Mitcham, J. L., King, G. E. and Algate, P. A.			
TITLE	Compositions and methods for therapy and diagnosis of ovarian cancer			
JOURNAL	Patent: US 6468546-A 391 22-OCT-2002;			
FEATURES	Location/Qualifiers			
source	1..2627			

ORIGIN

Query Match	100.0%;	Score 462;	DB 6;	Length 2627;
Best Local Similarity	100.0%;	Pred. No. 3.3e-133;		
Matches 462;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GGAAAGCAGCGSACAGTCCATCAGCCAGTACCCAGATAGCGCTGGGAAACCTTCCCAGAC	60
Db	23	GGAAGGACAGCGSACAGTCCATCAGCCAGTACCCAGATAGCGCTGGGAAACCTTCCCAGAC	82
Qy	61	ATGCGTTCCCTGGGGCAGATCCTCTTTCGGAGACAAATTAAGATATCATTAATTTGGCT	120
Db	83	ATGCGTTCCCTGGGGCAGATCCTCTTTCGGAGACAAATTAAGATATCATTAATTTGGCT	142
Qy	121	GGAGCAATTTGACATCATCATATTGGCTTTGGTATTTACGGAGACATCTCATCAAGTCACT	180
Db	143	GGAGCAATTTGACATCATCATATTGGCTTTGGTATTTACGGAGACATCTCATCAAGTCACT	202
Qy	181	ACTGTCGCGCTAGCGTGGGAAACATTGGGAGAGATGGAAATCTGAGCTGCACCTTTGAACCT	240
Db	203	ACTGTCGCGCTAGCGTGGGAAACATTGGGAGAGATGGAAATCTGAGCTGCACCTTTGAACCT	262
Qy	241	GACATCAAACTTTCTGATATCGTGATACATGCTGAAGGAAAGGTGTTTTAGGCTTGGTCTC	300

Db	263	GACATCAAACTTTTCGATATCGTATACAAATGCTGAAGAAAGGTGTTTTAGCGTTGGTC	322
Oy	301	CATGAAGTTCAAAAGAAAGCCAAAGATAGCTGTTCGAGCAGATGAAATGTTCAAGAGGCCGG	362
Db	323	CATGAATTCAAAGAAAGGCCAAAGATAGCTGTTCGAGCAGAGTGAATGTTCAAGAGGCCGG	382
Oy	361	ACAGCAGTCTTTGTCGATCAAGTGAATGATGTCGATGCGCAATGCTCTTTGCGCGGTCAAAAACGTG	420
Db	383	ACAGCAGTCTTTGTCGATCAAGTGAATGATGTCGATGCGCAATGCTCTTTGCGCGGTCAAAAACGTG	442
Oy	421	CAACTCAGAGATGCTGGCACTACACAAATGTTATATCATCACT	462
Db	443	CAACTCAGAGATGCTGGCACTACACAAATGTTATATCATCACT	484

Search completed: May 30, 2005, 17:54:08
Job time : 2132.43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: May 30, 2005, 05:15:03 ; Search time 283.354 Seconds
(without alignments)
9651.969 Million cell updates/sec

Title: US-09-763-978B-13

Perfect score: 462

Sequence: 1 ggaagcgcagcgcgcgcctcca.....acaatgttatcatcact 462

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	462	3	AAZ90482
2	462	100.0	1065	6	ABL56580
3	462	100.0	1657	3	AAZ65059
4	462	100.0	1658	4	AAZ46033
5	462	100.0	1658	4	AAZ92087
6	462	100.0	1658	5	AAZ44205
7	462	100.0	1658	6	ABK11744
8	462	100.0	1658	6	ABK11744
9	462	100.0	1658	6	ABK11744
10	462	100.0	1658	6	ABK11091
11	462	100.0	1658	8	ACB89483
12	462	100.0	1658	8	ACA73493
13	462	100.0	1658	8	ACA05808
14	462	100.0	1658	8	ACA66642
15	462	100.0	1658	8	ACA64352
16	462	100.0	1658	8	ACA91193
17	462	100.0	1658	8	ACD81570
18	462	100.0	1658	8	ACF20217
19	462	100.0	1658	8	ACF19603
20	462	100.0	1658	8	ACD21891

21	462	100.0	1658	8	ACD25159
22	462	100.0	1658	8	ACF00208
23	462	100.0	1658	8	ACA60392
24	462	100.0	1658	8	ACA72265
25	462	100.0	1658	8	ACD04789
26	462	100.0	1658	8	ACD18250
27	462	100.0	1658	8	ACD08257
28	462	100.0	1658	8	ACA86691
29	462	100.0	1658	8	ACA70133
30	462	100.0	1658	8	ACD12355
31	462	100.0	1658	8	ACD12355
32	462	100.0	1658	8	ACD15898
33	462	100.0	1658	8	ACD25466
34	462	100.0	1658	8	ACD17943
35	462	100.0	1658	8	ACD82230
36	462	100.0	1658	8	ACD21584
37	462	100.0	1658	8	ACD18651
38	462	100.0	1658	8	ACA58839
39	462	100.0	1658	8	ABX98261
40	462	100.0	1658	8	ACD14012
41	462	100.0	1658	8	ACD09792
42	462	100.0	1658	8	ACD8537
43	462	100.0	1658	8	ACD21277
44	462	100.0	1658	8	ABX75649
45	462	100.0	1658	8	ACA64015

ALIGNMENTS

RESULT 1
AAZ90482
ID AAZ90482 standard; cDNA; 462 BP.
XX
AC AAZ90482;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cancer specific gene (clone ID 16656542) fragment #13.
XX
DS C6G; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KW endometrial; uterine; lung; cytotoxic; ss.
XX
OS Homo sapiens.
XX
PN WO200012758-A1.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99MO-US019655.
XX
PR 02-SEP-1998; 98US-0098880P.
XX
PA (DIAD-) DIADEXUS LLC.
XX
PI Salceda S, Sun Y, Recipon H, Cafferey R;
XX
DR WPI; 2000-256657/22.
XX
PT Diagnosis, staging, monitoring, imaging and treating cancer especially
PT gynecological cancers e.g. breast, ovarian cancer and lung cancer.
PT involves measuring cancer specific gene levels in cells and body fluids.
XX
PS Claim 9; Page 52; 58pp; English.
XX
The invention relates to detecting, diagnosing metastasis and staging
cancer by measuring levels of cancer specific genes (C6G) in cells,
tissues or body fluids. Their remission and progression, decreases and
increases in C6G levels, is also monitored, by periodic sample analysis.
The methods are useful for detecting cancers, especially gynecologic
cancers which include ovarian, breast, endometrial and uterine cancer and
lung cancer. Antibodies against the C6Gs labeled with paramagnetic ions
or a radioisotope is useful for imaging cancer and when conjugated with a

CC cytotoxic agent are useful for treating cancer. The present sequence
 CC represents a CSG (clone ID: 16656542 and gene ID: 234617) fragment
 XX
 SQ Sequence 462 BP; 119 A; 108 C; 119 G; 116 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 3; Length 462;
 Best Local Similarity 100.0%; Pred. No. 7,2e-136;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGCGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAGACCTTCCCGAGCC 60
 DB 1 GGAAGGACGCGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAGACCTTCCCGAGCC 60
 QY 61 ATGGCTTCCCTGGGAGATCCTCTTCTGAGACATTAATGATCATCATTAATTCGGCT 120
 DB 61 ATGGCTTCCCTGGGAGATCCTCTTCTGAGACATTAATGATCATCATTAATTCGGCT 120
 QY 121 GGAGCAATTGCACTCATCTATTTGGCTTTGATTTTCAGGAGACACTCCATCAGCTCACT 180
 DB 121 GGAGCAATTGCACTCATCTATTTGGCTTTGATTTTCAGGAGACACTCCATCAGCTCACT 180
 QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTCTGATATCGTATATCAATGCGCTGGAAGAGTGTTTTAAAGCTTGGTC 300
 DB 241 GACATCAAACTTCTGATATCGTATATCAATGCGCTGGAAGAGTGTTTTAAAGCTTGGTC 300
 QY 301 CATGAGTTCAAGAAGGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 360
 DB 301 CATGAGTTCAAGAAGGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 360
 QY 361 ACAGCAGTGTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGCG 420
 DB 361 ACAGCAGTGTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGCG 420
 QY 421 CAACTCAGAGATGCTGGCACTTCACAATGTTATATCATCACT 462
 DB 421 CAACTCAGAGATGCTGGCACTTCACAATGTTATATCATCACT 462

RESULT 2
 ABL56580
 ID ABL56580 standard; cDNA; 1065 BP.
 XX
 AC ABL56580;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Nucleotide sequence of expressed sequence tag (EST) A1799522.
 XX
 KW Human; gene A: ovarian tumour; gene B: ORO; ovarian cancer;
 KW expressed sequence tag; EST; A1799522; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200194641-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 11-JUN-2001; 2001WO-US018700.
 XX
 PR 09-JUN-2000; 2000US-0210451P.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Ople E, McLachlan K, Heard C;
 XX
 DR WPI; 2002-404365/43.
 XX
 PT New polynucleotide and corresponding antigens from human ovarian cancer
 cells, useful for treatment and diagnosis of ovarian cancer.

XX
 PS Example 4; Fig 4c; 71bp; English.
 XX

CC The present sequence represents expressed sequence tag (EST) A1799522.
 CC This EST was identified as a match to the novel gene B by database
 CC analysis. Gene B was identified by representational difference analysis
 CC (RDA) screening, and is selectively expressed by certain human ovarian
 CC tumours. The specification also describes gene A, identified by the same
 CC method. Gene B is named ORO (Ople RDA of Epithelial Tissue vs. Ovary
 CC tumour). Gene A and B polynucleotides are useful for detecting ovarian
 CC cancer. Their polypeptides are useful for treating ovarian cancer

SQ Sequence 1065 BP; 293 A; 252 C; 257 G; 263 T; 0 U; 0 Other;
 Query Match 100.0%; Score 462; DB 6; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 1.1e-135;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGCGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAGACCTTCCCGAGCC 60
 DB 12 GGAAGGACGCGGAGCTCCAGCTCAGCCAGTACCCAGATCGCTGGAGACCTTCCCGAGCC 71
 QY 61 ATGGCTTCCCTGGGAGATCCTCTTCTGAGACATTAATGATCATCATTAATTCGGCT 120
 DB 72 ATGGCTTCCCTGGGAGATCCTCTTCTGAGACATTAATGATCATCATTAATTCGGCT 131
 QY 121 GGAGCAATTGCACTCATCTATTTGGCTTTGATTTTCAGGAGACACTCCATCAGCTCACT 180
 DB 132 GGAGCAATTGCACTCATCTATTTGGCTTTGATTTTCAGGAGACACTCCATCAGCTCACT 191
 QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 192 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGAGATGGAATCCTGAGCTGCACTTTGAACCT 251
 QY 241 GACATCAAACTTCTGATATCGTATATCAATGCGCTGGAAGAGTGTTTTAAAGCTTGGTC 300
 DB 252 GACATCAAACTTCTGATATCGTATATCAATGCGCTGGAAGAGTGTTTTAAAGCTTGGTC 311
 QY 301 CATGAGTTCAAGAAGGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 360
 DB 312 CATGAGTTCAAGAAGGCAAGATGAGCTGTGGAGCAGATGAATGTTTCAGAGCCGG 371
 QY 361 ACAGCAGTGTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGCG 420
 DB 372 ACAGCAGTGTGCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAACGCG 431
 QY 421 CAACTCAGAGATGCTGGCACTTCACAATGTTATATCATCACT 462
 DB 432 CAACTCAGAGATGCTGGCACTTCACAATGTTATATCATCACT 473

RESULT 3
 AA265059
 ID AA265059 standard; cDNA; 1657 BP.
 XX
 AC AA265059;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1291 encoding cDNA.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIB ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9963088-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-US012252.
 XX
 PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088376P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088722P.
 PR 10-JUN-1998; 98US-0088730P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088741P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089090P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 17-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 19-JUN-1998; 98US-0089947P.
 PR 19-JUN-1998; 98US-0089948P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
 PR 22-JUN-1998; 98US-0090254P.
 PR 23-JUN-1998; 98US-0090349P.
 PR 23-JUN-1998; 98US-0090355P.
 PR 24-JUN-1998; 98US-0090429P.
 PR 24-JUN-1998; 98US-0090431P.
 PR 24-JUN-1998; 98US-0090435P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 24-JUN-1998; 98US-0090455P.
 PR 24-JUN-1998; 98US-0090461P.
 PR 24-JUN-1998; 98US-0090472P.
 PR 24-JUN-1998; 98US-0090535P.
 PR 24-JUN-1998; 98US-0090538P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 24-JUN-1998; 98US-0090557P.
 PR 25-JUN-1998; 98US-0090676P.
 PR 25-JUN-1998; 98US-0090678P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090690P.
 PR 25-JUN-1998; 98US-0090691P.
 PR 25-JUN-1998; 98US-0090694P.
 PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090662P.

PR 26-JUN-1998; 98US-0090863P.
 PR 01-JUL-1998; 98US-0091358P.
 PR 01-JUL-1998; 98US-0091360P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091633P.
 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0091982P.
 PR 09-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 04-AUG-1998; 98US-0095285P.
 PR 04-AUG-1998; 98US-0095301P.
 PR 04-AUG-1998; 98US-0095302P.
 PR 04-AUG-1998; 98US-0095318P.
 PR 04-AUG-1998; 98US-0095321P.
 PR 10-AUG-1998; 98US-0095325P.
 PR 10-AUG-1998; 98US-0095316P.
 PR 10-AUG-1998; 98US-0095329P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 11-AUG-1998; 98US-0096143P.
 PR 11-AUG-1998; 98US-0096146P.
 PR 12-AUG-1998; 98US-00965329P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 17-AUG-1998; 98US-0096766P.
 PR 17-AUG-1998; 98US-0096768P.
 PR 17-AUG-1998; 98US-0096773P.
 PR 17-AUG-1998; 98US-0096791P.
 PR 17-AUG-1998; 98US-0096867P.
 PR 17-AUG-1998; 98US-0096891P.
 PR 17-AUG-1998; 98US-0096894P.
 PR 17-AUG-1998; 98US-0096895P.
 PR 18-AUG-1998; 98US-0096897P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096950P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0096960P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 19-AUG-1998; 98US-0097022P.
 PR 20-AUG-1998; 98US-0097141P.
 PR 20-AUG-1998; 98US-0097218P.
 PR 24-AUG-1998; 98US-0097611P.
 PR 26-AUG-1998; 98US-0097851P.
 PR 26-AUG-1998; 98US-0097952P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 26-AUG-1998; 98US-0097986P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098525P.
 PR 16-SEP-1998; 98US-0100634P.
 PR 12-JUN-1999; 99US-0115565P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX WPI, 2000-072863/06.
 DR P-PSDB; AAY66719.
 XX
 PT Membrane-bound proteins and related nucleotide sequences.
 XX

PS Claim 2; Fig 207; 822bp; English.

XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques

SQ Sequence 1657 BP; 521 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 3; Length 1657;

Best Local Similarity 100.0%; Pred. No. 1,4e-135; Mismatches 0; Indels 0; Gaps 0;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGCGAGCTCCAGCTCAGCCAGATACCGCTGGAACTTCCCGC 60
DB 1 GGAAGGACGCGAGCTCCAGCTCAGCCAGATACCGCTGGAACTTCCCGC 60
QY 61 ATGGCTTCCCTGGGGAGATCCCTCTTCTGAGATATTAAGATCAATTCCTGGCT 120
DB 61 ATGGCTTCCCTGGGGAGATCCCTCTTCTGAGATATTAAGATCAATTCCTGGCT 120
QY 121 GGAGCAATTCGACTCATTCATTCGCTTGGTATTTTCAGGAGACACTCCATCAGTCACT 180
DB 121 GGAGCAATTCGACTCATTCATTCGCTTGGTATTTTCAGGAGACACTCCATCAGTCACT 180
QY 181 ACTGTCGCTCAGCTGGGAAACATTTGGGGAGATGAAATCCTGAGCTGCACTTTGAACCT 240
DB 181 ACTGTCGCTCAGCTGGGAAACATTTGGGGAGATGAAATCCTGAGCTGCACTTTGAACCT 240
QY 241 GACATCAATCTTTCGATATTCGATATCAATGCTGTAAGAAAGCTTTTAAAGCTTGGTGC 300
DB 241 GACATCAATCTTTCGATATTCGATATCAATGCTGTAAGAAAGCTTTTAAAGCTTGGTGC 300
QY 301 CATGATCAATCAAGAAAGCAAGATGAGCTGTCGAGCAGAGATGAATGTTTCAGAGCCCG 360
DB 301 CATGATCAATCAAGAAAGCAAGATGAGCTGTCGAGCAGAGATGAATGTTTCAGAGCCCG 360
QY 361 ACAGCAGTGTTCGATCAAGTATGATGATTTGCGATGCTCTTTGCGGCTGAAAAACGTG 420
DB 361 ACAGCAGTGTTCGATCAAGTATGATGATTTGCGATGCTCTTTGCGGCTGAAAAACGTG 420
QY 421 CAACCTCAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
DB 421 CAACCTCAGATGCTGGCACTTCAAAATGTTATATCATCACT 462

RESULT 4

AA546033 standard; cDNA; 1658 BP.

AA546033;

18-DEC-2001 (first entry)

Human DNA encoding PRO polypeptide sequence #109.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.

OS Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

PF 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000WO-US018720P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189328P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192655P.
XX 29-MAR-2000; 2000US-0193032P.
XX 30-MAR-2000; 2000US-0193053P.
XX 30-MAR-2000; 2000WO-US008439.
XX 04-APR-2000; 2000US-0194443P.
XX 04-APR-2000; 2000US-0194647P.
XX 11-APR-2000; 2000US-0195975P.
XX 11-APR-2000; 2000US-0196000P.
XX 11-APR-2000; 2000US-0196187P.
XX 11-APR-2000; 2000US-0196690P.
XX 11-APR-2000; 2000US-0196820P.
XX 18-APR-2000; 2000US-0198121P.
XX 18-APR-2000; 2000US-0198585P.
XX 25-APR-2000; 2000US-0199397P.
XX 25-APR-2000; 2000US-0199550P.
XX 25-APR-2000; 2000US-0199654P.
XX 03-MAY-2000; 2000US-0201515P.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 05-JUN-2000; 2000US-0209832P.
XX 28-JUL-2000; 2000WO-US020710.
XX 22-AUG-2000; 2000US-00644848.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000WO-US034956.

XX (GENTH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2001-602746/68.
XX P-PSDB; AAU29132.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.

XX Claim 2; Fig 217; 774bp; English.

XX Sequences AA545925-AA546231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also

CC susceptibility to tumour development, particularly adrenal, lung, colon, CC breast, prostate, rectal, cervical, or liver tumours, in mammalian CC subjects. The oligonucleotide probes specific for the PRO nucleic acids CC can be used for genetic analysis of individuals with genetic disorders XX

Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 4; Length 1658;

Best Local Similarity 100.0%; Pred. No. 1.4e-135;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCGGCGGAGCTCCACTGACCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 DB 1 GGAAGGCGGCGGAGCTCCACTGACCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 QY 61 ATGGCTTCCCTGGGCGGAGATCTTCTTGAGAGCATATTAGCATCATATTATTTGGCT 120
 DB 61 ATGGCTTCCCTGGGCGGAGATCTTCTTGAGAGCATATTAGCATCATATTATTTGGCT 120
 QY 121 GGAGCAATTGCACTCATCATTTGGCTTGTATTTCAGGAGACACTGCATCAGATGACT 180
 DB 121 GGAGCAATTGCACTCATCATTTGGCTTGTATTTCAGGAGACACTGCATCAGATGACT 180
 QY 181 ACTGTGCTCCTGAGCTGGAACTTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGCTCCTGAGCTGGAACTTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTTCTGATATCGTGATGATCAATGCTGTAAGAAAGGTTTAAAGCTGTC 300
 DB 241 GACATCAAACTTTCTGATATCGTGATGATCAATGCTGTAAGAAAGGTTTAAAGCTGTC 300
 QY 301 CATGAGTTCAAAAGGCAAGATGAGCTGTCGAGAGAGATGAAAGTTTCAGAGGCGCG 360
 DB 301 CATGAGTTCAAAAGGCAAGATGAGCTGTCGAGAGAGATGAAAGTTTCAGAGGCGCG 360
 QY 361 ACAGCAGTGTCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAAGCTG 420
 DB 361 ACAGCAGTGTCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAAGCTG 420
 QY 421 CAACCTCAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
 DB 421 CAACCTCAGATGCTGGCACTTCAAAATGTTATATCATCACT 462

RESULT 5
 AAF92087 standard; cDNA; 1658 BP.
 ID AAF92087
 AC AAF92087;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Human PRO1291 cDNA.
 XX
 KM Human; PRO protein; mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200116318-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-US023328.
 XX
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-016949P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JUN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.

PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 25-APR-2000; 2000US-019397P.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.

XX (GENTH) GENENTECH INC.

PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi CV, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2001-183260/18.

DR P-PSDB; AAB87555.

XX

PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular

biology, including use as hybridization probes, and in chromosome and

gene mapping.

XX

PS Claim 2; Fig 59; 278pp; English.

XX

CC The present sequence is the coding sequence for a human PRO polypeptide

(secreted and transmembrane). The PRO protein, and PRO agonists, PRO

antagonists or anti-PRO antibodies are useful for preparation of a

medicament useful in the treatment of a condition which is responsive to

the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

protein may also be employed as molecular weight markers for protein

electrophoresis. The PRO coding sequence has applications in molecular

biology, including use as hybridisation probes, and in chromosome and

gene mapping

XX

SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 4; Length 1658;

Best Local Similarity 100.0%; Pred. No. 1.4e-135;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGCGGCGGAGCTCCACTGACCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 DB 1 GGAAGGCGGCGGAGCTCCACTGACCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 QY 61 ATGGCTTCCCTGGGCGGAGATCTTCTTGAGAGCATATTAGCATCATATTATTTGGCT 120
 DB 61 ATGGCTTCCCTGGGCGGAGATCTTCTTGAGAGCATATTAGCATCATATTATTTGGCT 120
 QY 121 GGAGCAATTGCACTCATCATTTGGCTTGTATTTCAGGAGACACTGCATCAGATGACT 180
 DB 121 GGAGCAATTGCACTCATCATTTGGCTTGTATTTCAGGAGACACTGCATCAGATGACT 180
 QY 181 ACTGTGCTCCTGAGCTGGAACTTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGCTCCTGAGCTGGAACTTTGGGAGATGGAATCCTGAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTTCTGATATCGTGATGATCAATGCTGTAAGAAAGGTTTAAAGCTGTC 300
 DB 241 GACATCAAACTTTCTGATATCGTGATGATCAATGCTGTAAGAAAGGTTTAAAGCTGTC 300
 QY 301 CATGAGTTCAAAAGGCAAGATGAGCTGTCGAGAGAGATGAAAGTTTCAGAGGCGCG 360
 DB 301 CATGAGTTCAAAAGGCAAGATGAGCTGTCGAGAGAGATGAAAGTTTCAGAGGCGCG 360
 QY 361 ACAGCAGTGTCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAAGCTG 420
 DB 361 ACAGCAGTGTCTGATCAAGTATGATTTGGCAATGCTCTTTGGCGCTGAAAAAGCTG 420
 QY 421 CAACCTCAGATGCTGGCACTTCAAAATGTTATATCATCACT 462
 DB 421 CAACCTCAGATGCTGGCACTTCAAAATGTTATATCATCACT 462

RESULT 6
 AAF44205 standard; cDNA; 1658 BP.
 ID AAF44205

XX AAF44205;
 AC
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1291 (UNQ659) nucleotide sequence SEQ ID NO:290.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytosolic; cell death;
 KW cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US008439.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000375.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 XX
 PA (GENENTECH INC.)
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DI;
 PI Ferrara N, Fong S, Gettier H, Gerltzen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.
 DR P-PSDB; AAB65242.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target bioactive
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX
 PS Claim 2; Fig 207; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to

CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 XX SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
 Query Match 100.0%; Score 462; DB 5; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 1,4e-135;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAAGGACGGGAGCTCCAGCTCAGCTGAGTCCGAGATGAGTGGAGACCTTCCACACC 60
 Db 1 GGAAGGACGGGAGCTCCAGCTCAGCTGAGTCCGAGATGAGTGGAGACCTTCCACACC 60
 QY 61 ATGGCTTCCCTGGGAGATCCTCTTCTGAGCATATATAGCATCATATATCTGCT 120
 Db 61 ATGGCTTCCCTGGGAGATCCTCTTCTGAGCATATATAGCATCATATATCTGCT 120
 QY 121 GGAGCAATTGCACTCATATGCTTGGTGTATTTTGAAGGAGACACTCATCACTACT 180
 Db 121 GGAGCAATTGCACTCATATGCTTGGTGTATTTTGAAGGAGACACTCATCACTACT 180
 QY 181 ACTGTCGCTCAGCTGGGACATTTGGGAGATGAGTGAATCCTGAGTGCATTTGAACT 240
 Db 181 ACTGTCGCTCAGCTGGGACATTTGGGAGATGAGTGAATCCTGAGTGCATTTGAACT 240
 QY 241 GACATCAAACTTTCATATGCTGATATACATATGCTGAAGAGGTGTTTAAAGCTTGTG 300
 Db 241 GACATCAAACTTTCATATGCTGATATACATATGCTGAAGAGGTGTTTAAAGCTTGTG 300
 QY 301 CATGATTCAAAGAGGCAAAAGATGAGTGTGCGAGCATGAAATGTTTCAAGAGCCGG 360
 Db 301 CATGATTCAAAGAGGCAAAAGATGAGTGTGCGAGCATGAAATGTTTCAAGAGCCGG 360
 QY 361 ACAGCAGTGTGCTGATCAAGTGAATGATGAGCAATGCTCTTTCGCGCTGAAAAACGTG 420
 Db 361 ACAGCAGTGTGCTGATCAAGTGAATGATGAGCAATGCTCTTTCGCGCTGAAAAACGTG 420
 QY 421 CAACTCAGATGCTGGGACCTTACCAATGTTATATCATCTACT 462
 Db 421 CAACTCAGATGCTGGGACCTTACCAATGTTATATCATCTACT 462
 RESULT 7
 ABR11744
 ID ABR11744 standard; cDNA; 1658 BP.
 XX
 AC ABR11744;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE DNA encoding tumour associated antigenic target polypeptide (TAT) 136.
 XX
 KW Tumour associated antigenic target polypeptide; TAT; cancer;
 KW breast cancer; colorectal cancer; lung cancer; ovarian cancer;
 KW central nervous system cancer; liver cancer; bladder cancer;
 KW pancreatic cancer; cervical cancer; melanoma; leukaemia; TAT136; gene;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH CDS 61..909
 FT /*tag= b
 FT /product= "TAT136"
 FT /note= "Tumour associated antigenic target polypeptide"
 FT sig_peptide 61..144
 FT /*tag= a
 FT mat_peptide 145..906
 FT /*tag= c
 FT /*label= Mature_TAT136
 XX
 PN WO200216581-A2.
 XX

Pd		28-FEB-2002.
Pf		
Xx		14-AUG-2001; 2001WO-US025464.
Px		
Px		24-AUG-2000; 2000WO-US02328.
Pr		28-FEB-2001; 2001WO-US006520.
Pr		22-JUN-2001; 2001US-00888257.
Pr		22-JUN-2001; 2001WO-US020118.
Xx		(GENTH) GENENTECH INC.
Xx		
Pa	Gao W,	Polakis P, Shou J, Smith V, Soriano R, Williams PM;
Pi	Mu TD,	Zhang Z;
Dx		
Dr	WPI;	2002-280928/32.
Xx		P-PsDB; AAU77766.
Pt		
Pt		Novel isolated antibody which binds to tumor-associated antigenic target
Pt		polypeptide useful for killing cancer cells expressing the polypeptide
Pt		and for treating tumor comprising cells that expresses the polypeptide.
Xx		
Ps	Claim 2;	Fig 4; 123pb; English.
Cc		
Cc		The invention describes an isolated antibody which binds to a tumour-
Cc		associated antigenic target (TAT) polypeptide. The antibody is useful
Cc		for: Killing a cancer cell (such as a breast, colorectal, lung, ovarian,
Cc		central nervous system, liver, bladder, pancreatic, cervical, melanoma or
Cc		leukaemia cell) that expresses a polypeptide with at least 80% identity
Cc		to the TAT polypeptide sequence; treating a tumour comprising cells that
Cc		express a polypeptide with at least 80% identity to the TAT polypeptide
Cc		sequence; determining the presence of a polypeptide having at least 80 %
Cc		identity to the TAT polypeptide sequence in a sample suspected of
Cc		containing the polypeptide; diagnosing the presence of a tumour in a
Cc		mammal, and for antibody dependent enzyme mediated prodrug therapy
Cc		(ADPPT). This sequence encodes the tumour associated antigenic target
Cc		polypeptide (TAT) 136, described in the invention
SQ	Sequence	1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
	Query Match	100.0%; Score 462; DB 6; Length 1658;
	Best Local Similarity	100.0%; Pred. No. 1,4e-115;
	Matches	462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1	GGAAGGCAAGCGGCAGCTTCCTACTCAGCCAGTACCGTAGATACGTGGAACTTTCCCACC 60
Db	1	GGAAAGCAAGCGGCAGCTTCCTACTCAGCCAGTACCGTAGATACGTGGAACTTTCCCACC 60
Oy	61	ATGCTTCCTCCCTGGGGCAGATCTCTTTTGAGACATAATTAGCATATCATTTTGGCT 120
Db	61	ATGCTTCCTCCCTGGGGCAGATCTCTTTTGAGACATAATTAGCATATCATTTTGGCT 120
Oy	121	GGAGCAATTGGCATCTCATCTATGGCTTGGTATTTTGAAGGAGACACTCATCACAGTACT 180
Db	121	GGAGCAATTGGCATCTCATCTATGGCTTGGTATTTTGAAGGAGACACTCATCACAGTACT 180
Oy	181	ACTGTGCGCTCAGCTGGGAACAATTGGGAGATGGAATCTGAGCTGACATTTTGAACCT 240
Db	181	ACTGTGCGCTCAGCTGGGAACAATTGGGAGATGGAATCTGAGCTGACATTTTGAACCT 240
Oy	241	GACATCAAACCTTTCTGATATCTGTATTAACAATGGCTGAAGAAGGTGTTTTAGCTTGGTC 300
Db	241	GACATCAAACCTTTCTGATATCTGTATTAACAATGGCTGAAGAAGGTGTTTTAGCTTGGTC 300
Oy	301	CATGAGTTCAAAAGAGGCAAGAGATAGCTGTGGAGCAAGATGAATGTTCAGAGGCCGG 360
Db	301	CATGAGTTCAAAAGAGGCAAGAGATAGCTGTGGAGCAAGATGAATGTTCAGAGGCCGG 360
Oy	361	ACAGCAGTGTGCTGATCAAGATGATGATTTGGCAATGCTCTTTGCGGCTGAAAAACGTG 420
Db	361	ACAGCAGTGTGCTGATCAAGATGATGATTTGGCAATGCTCTTTGCGGCTGAAAAACGTG 420
Oy	421	CACTCAACAGATGCTGGCACTTACCAATGTTATATCATCACT 462
Db	421	CACTCAACAGATGCTGGCACTTACCAATGTTATATCATCACT 462

Db	421	CNACTCAGACATGCTGGACACTTCAAAATGTATATCATCACT	462
RESULT 8			
AB574407			
ID	AB574407	standard; cDNA; 1658 BP.	
XX			
AC	AB574407;		
XX			
DT	10-DEC-2002	(first entry)	
XX			
DE	Human cDNA encoding secreted/transmembrane protein PRO1291.		
XX			
KW	Human; <i>se</i> ; gene; secreted protein; transmembrane protein; antirheumatic;		
KW	antiarthritic; osteopathic; sports-related joint problem;		
KW	articular cartilage defect; osteoarthritis; rheumatoid arthritis.		
XX			
OS	Homo sapiens.		
XX			
PN	US2002119130-A1.		
XX			
PD	29-AUG-2002.		
XX			
PF	06-DEC-2001; 2001US-00006867.		
XX			
PR	29-OCT-1997;	97US-0063435P.	
PR	29-OCT-1997;	97US-0064215P.	
PR	22-APR-1998;	98US-0082797P.	
PR	29-APR-1998;	98US-0083495P.	
PR	15-MAY-1998;	98US-0085579P.	
PR	02-JUN-1998;	98US-0087759P.	
PR	04-JUN-1998;	98US-0088021P.	
PR	04-JUN-1998;	98US-0088029P.	
PR	10-JUN-1998;	98US-0088734P.	
PR	10-JUN-1998;	98US-0088740P.	
PR	10-JUN-1998;	98US-0088811P.	
PR	10-JUN-1998;	98US-0088824P.	
PR	10-JUN-1998;	98US-0088825P.	
PR	11-JUN-1998;	98US-0088863P.	
PR	12-JUN-1998;	98US-0089105P.	
PR	16-JUN-1998;	98US-0089514P.	
PR	17-JUN-1998;	98US-0089653P.	
PR	19-JUN-1998;	98US-0089952P.	
PR	22-JUN-1998;	98US-0090446P.	
PR	24-JUN-1998;	98US-0090444P.	
PR	25-JUN-1998;	98US-0090688P.	
PR	25-JUN-1998;	98US-0090696P.	
PR	26-JUN-1998;	98US-0090862P.	
PR	02-JUL-1998;	98US-0091628P.	
PR	10-AUG-1998;	98US-0096012P.	
PR	17-AUG-1998;	98US-0096575P.	
PR	18-AUG-1998;	98US-0096949P.	
PR	18-AUG-1998;	98US-0096959P.	
PR	26-AUG-1998;	98US-0097954P.	
PR	26-AUG-1998;	98US-0097971P.	
PR	26-AUG-1998;	98US-0097979P.	
PR	01-SEP-1998;	98US-0098749P.	
PR	10-SEP-1998;	98US-0099741P.	
PR	10-SEP-1998;	98US-0099763P.	
PR	10-SEP-1998;	98US-0099792P.	
PR	10-SEP-1998;	98US-0099812P.	
PR	10-SEP-1998;	98US-0099815P.	
PR	16-SEP-1998;	98US-0100627P.	
PR	16-SEP-1998;	98US-0100662P.	
PR	16-SEP-1998;	98US-0100663P.	
PR	17-SEP-1998;	98US-0100683P.	
PR	17-SEP-1998;	98US-0100684P.	
PR	17-SEP-1998;	98US-0100930P.	
PR	22-SEP-1998;	98US-0101279P.	
PR	23-SEP-1998;	98US-0101475P.	
PR	24-SEP-1998;	98US-0101738P.	
PR	24-SEP-1998;	98US-0101743P.	

PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 22-DEC-1999; 99WO-US021194.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

PI Baton Dr., Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;

XX WPI; 2002-731348/79.
 DR P-PSDB; ABG95880.

PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 2; Fig 59; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95881-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis

CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the
 CC invention

XX SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 6; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 1,4e-135; Indels 0; Gaps 0;
 Matches 462; Conservative 0; Mismatches 0;

QY 1 GGAAAGGAGCGGACAGCTCACTCAAGCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 DB 1 GGAAGGAGCGGAGCGGACGCTCACTCAAGCCAGTACCAGATACGCTGGAACTTCCCGACCC 60
 QY 61 ATGGCTTCCCTGGGCGCAATCTCTTCTGGAGCATTAATTAGCATATATATCTGGCT 120
 DB 61 ATGGCTTCCCTGGGCGCAATCTCTTCTGGAGCATTAATTAGCATATATATCTGGCT 120
 QY 121 GGAGCAATTGGACATCATGATGGCTTTGGTATTTTCAGGGAGACACTCCATCAAGTCACT 180
 DB 121 GGAGCAATTGGACATCATGATGGCTTTGGTATTTTCAGGGAGACACTCCATCAAGTCACT 180
 QY 181 ACTGTGCGCTCAGCTGGAGAACATTGGGGAGGAGATGGAATCTGAGCTGCATTTTGAACCT 240
 DB 181 ACTGTGCGCTCAGCTGGAGAACATTGGGGAGGAGATGGAATCTGAGCTGCATTTTGAACCT 240
 QY 241 GACATCAAACTTCTGATATGCTATACAAATGCTGAAGAGGCTTTTGGCTGGTC 300
 DB 241 GACATCAAACTTCTGATATGCTATACAAATGCTGAAGAGGCTTTTGGCTGGTC 300
 QY 301 CATGAGTTCAAAAGAGGAAAGATGAGCTGTGAGAGCAGATGAAATGTCAGAGCCGG 360
 DB 301 CATGAGTTCAAAAGAGGAAAGATGAGCTGTGAGAGCAGATGAAATGTCAGAGCCGG 360
 QY 361 ACAGCAGTGTTCCTGATCAAGTGATAGTGGCAATGCTTTGGGCTGAAAAACGTG 420
 DB 361 ACAGCAGTGTTCCTGATCAAGTGATAGTGGCAATGCTTTGGGCTGAAAAACGTG 420
 QY 421 CAATCACAAGATGCTGGCACTTACAAATGTTATATCATCACT 462
 DB 421 CAATCACAAGATGCTGGCACTTACAAATGTTATATCATCACT 462

RESULT 9

ABK11091
 ID ABK11091 standard; cDNA; 1658 BP.

XX ABK11091;

XX 05-JUN-2002 (first entry)

DE cDNA encoding tumour-associated antigenic target protein, TAT136.

XX TAT136; Tumour-associated Antigenic Target; tumour; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer;

KW central nervous system cancer; liver cancer; bladder cancer; melanoma;

XX pancreatic cancer; leukemia; gene therapy; gene; ss.

XX Homo sapiens.

FT Key Location/Qualifiers
 FT CDS 61..909
 FT /*tag= a
 FT /product= "TAT136"

FT /note= "Tumour-associated antigenic target"
 XX
 PN W0200216429-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-JUN-2001; 2001WO-US020118.
 XX
 PR 24-AUG-2000; 2000WO-US023328.
 PR 26-SEP-2000; 2000US-0235451P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,
 PI Wood WI, Wu TD, Zhang Z;
 XX
 DR WPI: 2002-280917/32.
 DR P-PSDB; AAU76536.
 XX
 PT Novel isolated tumor-associated antigenic target polypeptides which are
 PT useful as targets for cancer therapy and diagnosis in mammals.
 XX
 PS Claim 1; Fig 3; 121pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigenic target
 CC polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the
 CC polynucleotides (II) encoding them. (II) is useful for diagnosing the
 CC presence of a tumour in a mammal, where the level of expression of (II)
 CC is indicative of the presence of tumour in the mammal from which the test
 CC sample was obtained. Antibody to (I) is useful for killing a cancer cell,
 CC (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
 CC an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
 CC liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
 CC melanoma cell or a leukemia cell) that expresses (I). Oligonucleotides
 CC hybridizing to (II) are useful as diagnostic probes, antisense
 CC oligonucleotide probes or for encoding fragments of full length TAT
 CC polypeptide. (II) is also useful in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA probes, for constructing
 CC hybridisation probes for mapping the gene encoding TAT and for genetic
 CC analysis of individuals with genetic disorders. (II) is also useful for
 CC generating either transgenic animals or knockout animals, and in gene
 CC therapy. The TAT polypeptides and nucleic acids may also be used for
 CC tissue typing and the TAT polypeptides are useful for screening compounds
 CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
 CC polypeptide (antagonist). The antibody is useful for staging TAT
 CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT
 CC polypeptide from cells, for detection and quantitation of TAT polypeptide
 CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
 CC Western blot. The antibodies are also useful for treating a TAT-
 CC expressing cancer or alleviating one or more symptoms of cancer in a
 CC mammal. The present sequence represents the coding sequence of TAT136
 XX
 XX
 SO Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 6; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 1.4e-135;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCCAGTCAAGCAATACCAATAGCTGGAACTTCCCGGCC 60
 DB 1 GGAAGGAGGAGGAGCTCCAGTCAAGCAATACCAATAGCTGGAACTTCCCGGCC 60
 QY 61 ATGGCTTCCCTGGGGAGATCTCTTCTGGAGCAATATAGCATCATTTATTTGGCT 120
 DB 61 ATGGCTTCCCTGGGGAGATCTCTTCTGGAGCAATATAGCATCATTTATTTGGCT 120
 QY 121 GGAAGCAATTCATCATTCATTTGGCTTTGGATTTTCAAGGAGACATCTCATCAAGTCACT 180
 DB 121 GGAAGCAATTCATCATTCATTTGGCTTTGGATTTTCAAGGAGACATCTCATCAAGTCACT 180

QY 181 ACTGTGCGCTCAGCTGGGAAATTTGGGGAGATGATGATCGTAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGCGCTCAGCTGGGAAATTTGGGGAGATGATGATCGTAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTTCTGATATCGTATACATAGCTGAGAGAGGTGTTTAAAGCTTGCT 300
 DB 241 GACATCAAACTTTCTGATATCGTATACATAGCTGAGAGAGGTGTTTAAAGCTTGCT 300
 QY 301 CATGAGTTCAAGAGGCAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGGCCGG 360
 DB 301 CATGAGTTCAAGAGGCAAGATGAGCTGTCCGAGCAGATGAAATGTTCAAGGCCGG 360
 QY 361 ACAGAGTGTGTTCTGATCAAGATAGTGTGGCAATGCCCTTTGGGGCTGAAAAACGTC 420
 DB 361 ACAGAGTGTGTTCTGATCAAGATAGTGTGGCAATGCCCTTTGGGGCTGAAAAACGTC 420
 QY 421 CAACTCAGAGATGCTGCACTTCAAAATGTTATATCATCACT 462
 DB 421 CAACTCAGAGATGCTGCACTTCAAAATGTTATATCATCACT 462

RESULT 10
 ID ACA89483
 ACA89483 standard; cDNA; 1658 BP.
 XX
 AC ACA89483;
 XX
 DT 09-JUL-2003 (first entry)
 XX
 DE cDNA encoding human PRO polypeptide #109.
 XX
 KW Human; PRO polypeptide; secreted protein; transmembrane protein;
 KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
 KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
 KW tumour necrosis factor-alpha; proliferation; differentiation;
 KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
 KW arthritis; cystostatic; antiarthritic; osteopathic; gene therapy; gene;
 KW 88.
 XX
 OS Homo sapiens.
 XX
 PN US2003036141-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 01-JUL-2002; 2002US-00187597.
 XX
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 20-MAR-1998; 98US-0078866P.
 PR 20-MAR-1998; 98US-0078939P.

PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085582P.
PR 18-MAY-1998; 98US-0086023P.
PR 18-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088826P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089922P.
PR 19-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.

PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090789P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 04-JUL-1998; 98US-0094066P.
PR 10-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095598P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098173P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.

PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1,4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGAGGCGGCGCTCCACTGAGCAATGATCCGATGCGTGGAACTTCCCGAGCC 60
DB 1 GGAAGGAGGCGGCGCTCCACTGAGCAATGATCCGATGCGTGGAACTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGCGAGATCTCTTGGAGCAATATTTGACATCATATTTCTGGCT 120
DB 61 ATGGCTTCCCTGGGCGAGATCTCTTGGAGCAATATTTGACATCATATTTCTGGCT 120
QY 121 GGAAGCAATTCATCATATTTGCTTGTATTTCAAGGAGACATCCATCAGTCACT 180
DB 121 GGAAGCAATTCATCATATTTGCTTGTATTTCAAGGAGACATCCATCAGTCACT 180
QY 181 ACTGTCCCTCAGCTGGAAATTGGGAGAGATGAAATCTGAGCTGCACTTTGAACCT 240
DB 181 ACTGTCCCTCAGCTGGAAATTGGGAGAGATGAAATCTGAGCTGCACTTTGAACCT 240
QY 241 GACATCAACTTCTGATATGATATCAATGCTGAAGAGGTTTAAAGCTTGGCTC 300
DB 241 GACATCAACTTCTGATATGATATCAATGCTGAAGAGGTTTAAAGCTTGGCTC 300
QY 301 CATGAGTTCAAGAGCAAGATGAGCTGCGAGAGAGATGAATGTTCAAGAGCCGG 360
DB 301 CATGAGTTCAAGAGCAAGATGAGCTGCGAGAGAGATGAATGTTCAAGAGCCGG 360
QY 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGGTAAGAAAGCTG 420
DB 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGGTAAGAAAGCTG 420
QY 421 CAATCAAGATGCTGACCTCAATGTTATTCATCCT 462
DB 421 CAATCAAGATGCTGACCTCAATGTTATTCATCCT 462
RESULT 11
ID ACA73493 standard; cDNA; 1658 BP.
AC ACA73493;
XX 01-JUL-2003 (first entry)
DE Human secreted/transmembrane protein (PRO) cDNA #109.
XX Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KM tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036146-A1.
PD 20-FEB-2003.
XX
XX 02-JUL-2002; 2002US-00187603.
XX
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98MO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98MO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98MO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99MO-US005028.

PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99MO-US028301.
PR 02-DEC-1999; 99MO-US028551.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 15-MAR-2000; 2000MO-US006884.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000MO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001MO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001MO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332034/31.
XX P-PSDB; AB086301.
XX
XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
PT gene therapy, chromosome identification, tissue typing, and for detecting
the presence of tumor in a mammal.
XX
XX Claim 2; Fig 217; 707pp; English.
XX
XX The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to

CC them, or encoding a PRO polypeptide lacking its associated signal peptide
CC or an extracellular domain of the PRO polypeptide, with or lacking its
CC associated signal peptide. Also included are the encoded PRO proteins,
CC PRO expression vectors, host cells transformed with the vector (used to
CC produce PRO proteins), a chimeric molecule comprising the PRO
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, a method for stimulating the release of tumor necrosis factor
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
CC PRO827, PRO1791, PRO1331, PRO1336, PRO1183, PRO1760, PRO1567 or
CC PRO8333), a method for stimulating the proliferation or differentiation
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
CC a method for detecting the presence of tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a cDNA encoding a PRO
CC protein
XX
XX

SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAAGCAGCGGAGGAGCTCCAGCTCAGCCAGTACCAGATCGCTGGGAACTTCCCGAGCC 60
DB 1 GGAAAGCAGCGGAGGAGCTCCAGCTCAGCCAGTACCAGATCGCTGGGAACTTCCCGAGCC 60
QY 61 ATGGCTTCCTGGGGAGATCTCTTCTGGAGCATTAATTAGCATCATTAATTCTGGCT 120
DB 61 ATGGCTTCCTGGGGAGATCTCTTCTGGAGCATTAATTAGCATCATTAATTCTGGCT 120
QY 121 GGAAGCAATTGCATCATCTATGCTTTGGTATTTCGAGGAGACATCCATCAGATCACT 180
DB 121 GGAAGCAATTGCATCATCTATGCTTTGGTATTTCGAGGAGACATCCATCAGATCACT 180
QY 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGATGAATCCTGAGCTGCATTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGGAAACATTTGGGAGATGAATCCTGAGCTGCATTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATACAATGGCTGAAGAAAGTGTTTAAGCTTGGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATACAATGGCTGAAGAAAGTGTTTAAGCTTGGTC 300
QY 301 CATGATTTCAAGAAAGCAAAAGATGAGCTGTCCGAGCAGATGAATAATGTTCAAGGCCGG 360
DB 301 CATGATTTCAAGAAAGCAAAAGATGAGCTGTCCGAGCAGATGAATAATGTTCAAGGCCGG 360
QY 361 ACAGCAGTGTGTTGCTGATCAAGTATGTTGGCAATGCCCTTTGGCGCTGAAAAACGCG 420
DB 361 ACAGCAGTGTGTTGCTGATCAAGTATGTTGGCAATGCCCTTTGGCGCTGAAAAACGCG 420
QY 421 CAACTCAGATGCTGGCACTTAACAATGTTATATCATCACT 462
DB 421 CAACTCAGATGCTGGCACTTAACAATGTTATATCATCACT 462

RESULT 12
ACA05808

ID ACA05808 standard; cDNA, 1658 BP.
XX
AC ACA05808;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #109.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
PN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194423.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 25-AUG-1999; 99US-00380139.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.

PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WT, Zhang Z;
XX
XX WPI; 2003-332039/31.
DR P-PSDB; ABU67514.
XX
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.
XX
XX
XX Claim 2; Fig 217; 706pp; English.

CC The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumor necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in AC05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention
XX
XX

XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGAGGAGGAGCTCCAGTCCAGTACCAATGAGTGGGAACTTCCCGGCC 60
DB 1 GGAAGGAGGAGGAGCTCCAGTCCAGTACCAATGAGTGGGAACTTCCCGGCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCAATTAATGATCATCATTTTGGCT 120
DB 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGGAGCAATTAATGATCATCATTTTGGCT 120
QY 121 GGAGCAATTCATCATTCATTTGGTCTTGTATTTGAGGAGACATCTCCACAGTCACT 180
DB 121 GGAGCAATTCATCATTCATTTGGTCTTGTATTTGAGGAGACATCTCCACAGTCACT 180
QY 181 ACTGTGCGCTCAGCTGGAACATTTGGGAGATGAACTCTGAGCTGCACTTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGAACATTTGGGAGATGAACTCTGAGCTGCACTTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCTGATGCAATGCTGAGAGAGAGCTTTTAAAGCTTGGCT 300
DB 241 GACATCAAACTTTCTGATATCTGATGCAATGCTGAGAGAGAGCTTTTAAAGCTTGGCT 300

QY 301 CATGAGTTCAAGAAGGCAAGATGAGCTCTCGAGACAGGATGAATGTTTCAGAGCGCGG 360
DB 301 CATGAGTTCAAGAAGGCAAGATGAGCTCTCGAGACAGGATGAATGTTTCAGAGCGCGG 360
QY 361 ACAGCAGTGTGTTCTGATCATGATGATGTTGCAATGCCCTTTGGCGGCTGAATAACGTC 420
DB 361 ACAGCAGTGTGTTCTGATCATGATGATGTTGCAATGCCCTTTGGCGGCTGAATAACGTC 420
QY 421 CAACTCAGAGATCTGGCACCTTACAAATGTTATATCATCACT 462
DB 421 CAACTCAGAGATCTGGCACCTTACAAATGTTATATCATCACT 462

RESULT 13

ACA66642
ID ACA66642 standard; cDNA; 1658 BP.
XX
XX ACA66642;
AC
AC 23-JUN-2003 (first entry)
DT
XX
XX cDNA encoding human PRO protein #109.
DE
XX
XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
KW liver; PRO; gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX US2003036137-A1.
PN
XX
PD 20-FEB-2003.
XX
XX 27-JUN-2002; 2002US-00184640.
PF
XX
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028351.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000MO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 XX
 PA (GENTH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR MPI: 2003-142038/32.
 DR P-PSDB; AB080542.

XX Three hundred and five nucleic acids encoding secreted and transmembrane
 PT PRO polypeptides, useful for the diagnosis, prevention and/or treatment
 PT of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 PT cervical or liver tumors.

XX Claim 2; Fig 217; 708bp; English.

XX The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane). Methods and compositions
 CC of the present invention are useful for the diagnosis, prevention and/or
 CC treatment of tumors, such as adrenal, lung, colon, breast, prostate,
 CC rectal, cervical or liver tumors. The PRO polypeptides are also useful
 CC as molecular weight markers, or for chromosome identification. The PRO
 CC genes are useful as hybridisation probes, or for screening libraries of
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. The present
 CC sequence represents a cDNA encoding a human PRO polypeptide of the
 CC invention

XX Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 462; DB 8; Length 1658;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-135;
 XX Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCAGCAGCAGCTCCAGTCCAGCAGCAGATACGCTGGGAACTTCCAGCC 60
 DB 1 GGAAGCAGCAGCAGCTCCAGTCCAGCAGCAGATACGCTGGGAACTTCCAGCC 60
 QY 61 ATGGCTTCCTGGGAGATCTCTTCTGAGCATATTAGCATCATCTTTATTCGGCT 120
 DB 61 ATGGCTTCCTGGGAGATCTCTTCTGAGCATATTAGCATCATCTTTATTCGGCT 120
 QY 121 GGAGCAATGCACTATCTATTTGGTGTATTTTCAGGAGACATCCCACTCAAGTCACT 180
 DB 121 GGAGCAATGCACTATCTATTTGGTGTATTTTCAGGAGACATCCCACTCAAGTCACT 180

QY 181 ACTGCGCTCAGCTGGGAACTTGGGAGAGTGAATCTTGACCTGCATCTTTGAACCT 240
 DB 181 ACTGCGCTCAGCTGGGAACTTGGGAGAGTGAATCTTGACCTGCATCTTTGAACCT 240
 QY 241 GACATCAACTTTCTGTATGTGTATCAATGCTGGAAGAGTGTATTAGCTGTGTC 300
 DB 241 GACATCAACTTTCTGTATGTGTATCAATGCTGGAAGAGTGTATTAGCTGTGTC 300
 QY 301 CATGATTCAGAAAGGAGAAAGATGAGCTGCGAGAGATGAATGTTGAGAGCCGG 360
 DB 301 CATGATTCAGAAAGGAGAAAGATGAGCTGCGAGAGATGAATGTTGAGAGCCGG 360
 QY 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTCAAAAAGTG 420
 DB 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTCAAAAAGTG 420
 QY 421 CAATCAGATGCTGGCAGCTAGCAAAATGTTATTCATCACT 462
 DB 421 CAATCAGATGCTGGCAGCTAGCAAAATGTTATTCATCACT 462

RESULT 14

ID ACA64352 standard; cDNA; 1658 BP.

XX ACA64352;

DT 17-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1291 cDNA.

XX Human; secreted and transmembrane protein; cytosolic; anti-HIV;
 KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
 KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
 KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukemia;
 KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
 KW drug screening; gene; ss.

OS Homo sapiens.

XX US2003003531-A1.

XX 02-JAN-2003.

XX 19-NOV-2001; 2001US-00389734.

PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087755P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98MO-US019330.
 PR 17-SEP-1998; 98MO-US019437.
 PR 07-OCT-1998; 98MO-US021141.
 PR 01-DEC-1998; 98MO-US025108.
 PR 05-JAN-1999; 99MO-US000106.
 PR 08-MAR-1999; 99MO-US005028.
 PR 02-JUN-1999; 99MO-US012252.
 PR 15-SEP-1999; 99MO-US021097.
 PR 15-SEP-1999; 99MO-US021547.
 PR 30-NOV-1999; 99MO-US028313.
 PR 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030911.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 15-MAY-2000; 2000MO-US013358.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 11-AUG-2000; 2000MO-US022031.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023528.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PR 28-AUG-2001; 2001US-00941992.

XX (GETH) GENENTECH INC.
 XX

PI Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;
 PI Ferreira N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Glimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;
 XX
 DR WPI, 2003-352829/33.
 DR P-PSDB; AB072533.
 XX
 PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
 PT PRO184), useful for treating or diagnosing e.g. ovarian cancer. Kaposi's
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
 PT disease.
 XX
 PS Claim 1; Fig 207; 663pp; English.
 XX

CC The invention describes a new isolated nucleic acid molecule comprising
 CC the full length coding sequence of the DNA deposited with the American
 CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
 CC 209439, 203135, etc) ; or a sequence with at least 80% identity to a DNA
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
 CC are particularly useful for detecting or treating e.g. malignancies or
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
 CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
 CC disease in mammals. The PRO polypeptides are useful in drug screening,
 CC particularly as targets for therapeutic intervention in these diseases,
 CC and in the diagnostic determination of the presence of these diseases.
 CC The PRO polypeptides are also useful as molecular weight markers, or for
 CC chromosome identification. The PRO genes are useful as hybridisation
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
 CC The PRO genes may also be used in gene therapy, particularly for
 CC replacing a defective gene. This sequence encodes a novel human secreted
 CC and transmembrane PRO polypeptide
 XX

SO Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;

Query Match 100.0%; Score 462; DB 8; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 1.4e-135;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGGGAGAGCTCCAGCTGAGCAGTACCCAGATACGCTGGGAACCTTCCCAAGC 60
 DB 1 GGAAGGACGGGAGAGCTCCAGCTGAGCAGTACCCAGATACGCTGGGAACCTTCCCAAGC 60
 QY 61 ATGGCTTCCCTGGGGAGAGATCTCTTCTGAGAGATATTAGCATCATCTATTCTGGCT 120
 DB 61 ATGGCTTCCCTGGGGAGAGATCTCTTCTGAGAGATATTAGCATCATCTATTCTGGCT 120
 QY 121 GGAGCAATTGCACTCATCTATGCTTGGTATTTCAGGAGACATCTCCATCAGTCACT 180
 DB 121 GGAGCAATTGCACTCATCTATGCTTGGTATTTCAGGAGACATCTCCATCAGTCACT 180
 QY 181 ACTGTGGCTCAGCTGAGGAACATTTGGGAGAGATGAATCTGAGCTGCACTTTGAACCT 240
 DB 181 ACTGTGGCTCAGCTGAGGAACATTTGGGAGAGATGAATCTGAGCTGCACTTTGAACCT 240
 QY 241 GACATCAAACTTCTGATATCGGATACATGAGCTGAAGAGTGTATTAGCTTGGCTGTC 300
 DB 241 GACATCAAACTTCTGATATCGGATACATGAGCTGAAGAGTGTATTAGCTTGGCTGTC 300
 QY 301 CATGAGTTCAAGAGGCAAGATGAGCTGTGGAGCAGAGTGAATGTTTCAGAGGCCG 360
 DB 301 CATGAGTTCAAGAGGCAAGATGAGCTGTGGAGCAGAGTGAATGTTTCAGAGGCCG 360
 QY 361 ACAGCAGTGTTCGATGATGAGTGAATGTTGGAAGCTCTTTGGGGCTGAAAAACGTC 420
 DB 361 ACAGCAGTGTTCGATGATGAGTGAATGTTGGAAGCTCTTTGGGGCTGAAAAACGTC 420
 QY 421 CAACTCAGAGTGTGCACTTCAAAATGTTATATCATCACT 462
 DB 421 CAACTCAGAGTGTGCACTTCAAAATGTTATATCATCACT 462

RESULT 15
 ACA91193
 ID ACA91193 standard; cDNA; 1658 BP.

XX ACA91193;
AC
XX
DT 11-JUL-2003 (first entry)
DE Novel human secreted and transmembrane protein PRO1291 cDNA.
XX
XX Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003018173-A1.
XX
XX 23-JAN-2003.
PD
XX
XX 01-MAY-2002; 2002US-00063515.
PF
XX
XX 06-DEC-2001; 2001US-00006867.
PR
XX
XX (GENENTECH INC.
PA
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-401702/38.
XX P-PSDB; ABU90905.
XX
XX
XX New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX
PS Disclosure; Fig 59; 345pp; English.
XX
XX The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostic, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 1658 BP; 522 A; 357 C; 367 G; 412 T; 0 U; 0 Other;
Query Match 100.0%; Score 462; DB 8; Length 1658;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGCGAGCGGAGCTCCAGCTCAGCCAGTACGCCAGATACGCTGGGAACCTTCCCGAGCC 60
DB 1 GGAAGGCGAGCGGAGCTCCAGCTCAGCCAGTACGCCAGATACGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGGAGCATATATTAGCATCATCTTATTCGACT 120
DB 61 ATGGCTTCCCTGGGGGAGATCCTCTTCTGGAGCATATATTAGCATCATCTTATTCGACT 120
QY 121 GGAGCAATTGCACTCATCTATTGGCTTTGATTTTCAGGGAGACATCCATCAAGTCACT 180
DB 121 GGAGCAATTGCACTCATCTATTGGCTTTGATTTTCAGGGAGACATCCATCAAGTCACT 180
QY 181 ACTGTCGCTCAGCTGGGAAACATTTGGGAGATGGAATCTGAGCTGCATTTGAACCT 240
DB 181 ACTGTCGCTCAGCTGGGAAACATTTGGGAGATGGAATCTGAGCTGCATTTGAACCT 240
QY 241 GACATCAACCTTTCGATATCGATATACATGAGCTGAAGAAAGTGTATTAGCTTGCTC 300
DB 241 GACATCAACCTTTCGATATCGATATACATGAGCTGAAGAAAGTGTATTAGCTTGCTC 300

QY 301 CATGAGTTCAAGAAAGGCAAGATGAGCTGTGAGAGCAGATGAATGTTCAAGAGCCCGG 360
DB 301 CATGAGTTCAAGAAAGGCAAGATGAGCTGTGAGAGCAGATGAATGTTCAAGAGCCCGG 360
QY 361 ACAGCAGTGTTCCTGATCAAGTGTATGTCGCAATGCTCTTTCGGGCTGAAAAACGTG 420
DB 361 ACAGCAGTGTTCCTGATCAAGTGTATGTCGCAATGCTCTTTCGGGCTGAAAAACGTG 420
QY 421 CAACTCAGATGCTGCACTTACAAATGTTATATCATCACT 462
DB 421 CAACTCAGATGCTGCACTTACAAATGTTATATCATCACT 462

Search completed: May 30, 2005, 10:27:14
Job time : 284.354 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 ; Search time 65.6262 Seconds
(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-13

Perfect score: 462
Sequence: 1 ggaagcagcagcagcagctcca.....acaatgtatataccact 462

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCUTUS.COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	2627	3	US-09-404-879A-391 Sequence 391, App
2	462	100.0	2627	4	US-09-667-857-391 Sequence 391, App
3	372	80.5	1046	4	US-09-789-451-332 Sequence 332, App
4	43.6	9.4	948	4	US-09-910-174B-27 Sequence 27, App
5	43.6	9.4	948	4	US-09-620-461-27 Sequence 27, App
6	40.6	8.8	1964	4	US-09-949-016-876 Sequence 876, App
7	36.4	7.9	2882	2	US-08-724-394A-12 Sequence 12, App
8	36.2	7.8	601	4	US-09-949-016-20613 Sequence 20613, A
9	36.2	7.8	601	4	US-09-949-016-69029 Sequence 69029, A
10	36.2	7.8	601	4	US-09-949-016-69030 Sequence 69030, A
11	36.2	7.8	11820	4	US-09-949-016-11887 Sequence 11887, A
12	36.2	7.8	11820	4	US-09-949-016-11887 Sequence 11887, A
13	36.2	7.8	11826	4	US-09-949-016-13767 Sequence 13767, A
14	36	7.8	854	4	US-09-270-767-11547 Sequence 11547, A
15	34.8	7.5	3416	2	US-08-724-394A-15 Sequence 15, App
16	34.6	7.5	1645	2	US-08-724-394A-14 Sequence 14, App
17	34.6	7.5	2970	4	US-09-566-921-105 Sequence 105, App
18	34.2	7.4	873	4	US-09-451-291-4 Sequence 4, App
19	34.2	7.4	3593	4	US-09-645-069-22 Sequence 22, App
20	33.6	7.3	518	4	US-09-702-705-1314 Sequence 1314, App
21	33.6	7.3	518	4	US-09-736-457-1314 Sequence 1314, App
22	33.6	7.3	518	4	US-09-614-124B-1314 Sequence 1314, App
23	33.6	7.3	518	4	US-09-671-325-1314 Sequence 1314, App
24	33.6	7.3	518	4	US-09-658-824-1314 Sequence 1314, App
25	33.6	7.3	951	4	US-09-910-174B-23 Sequence 23, App
26	33.6	7.3	951	4	US-09-620-461-23 Sequence 23, App
27	33.6	7.3	1020	3	US-09-651-200-7 Sequence 7, App

28	33.6	7.3	1323	3	US-09-651-200-9 Sequence 9, App
29	33.6	7.3	1602	3	US-09-651-200-11 Sequence 11, App
30	33.6	7.3	2229	3	US-09-651-200-5 Sequence 5, App
31	33.6	7.3	2691	3	US-09-651-200-1 Sequence 1, App
32	33.6	7.3	2885	3	US-09-651-200-3 Sequence 3, App
33	33.6	7.3	3063	4	US-09-620-312D-844 Sequence 844, App
34	33.4	7.2	1284	4	US-09-489-039A-1322 Sequence 1322, App
35	33.4	7.2	10136	1	US-08-353-700-2 Sequence 2, App
36	33.4	7.2	10136	5	PCT-US95-16216-2 Sequence 2, App
37	33	7.1	1399	4	US-09-188-930-198 Sequence 198, App
38	33	7.1	1399	4	US-09-312-283C-198 Sequence 198, App
39	33	7.1	2926	3	US-08-724-394A-13 Sequence 13, App
40	32.6	7.1	5919	4	US-08-875-435B-2 Sequence 2, App
41	32.4	7.0	870	4	US-09-451-291-2 Sequence 2, App
42	32.4	7.0	872	1	US-08-381-280-5 Sequence 5, App
43	32.4	7.0	872	1	US-08-381-280-10 Sequence 10, App
44	32.4	7.0	872	1	US-08-381-280-19 Sequence 19, App
45	32.4	7.0	872	2	US-08-445-533-5 Sequence 5, App

ALIGNMENTS

RESULT 1									
US-09-404-879A-391									
Sequence 391, Application US/09404879A									
Patent No. 6468546									
GENERAL INFORMATION:									
APPLICANT: Mitcham, Jennifer L.									
APPLICANT: King, Gordon E.									
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND									
FILE REFERENCE: 210121.462C2									
CURRENT APPLICATION NUMBER: US/09/404,879A									
CURRENT FILING DATE: 1999-09-24									
NUMBER OF SEQ ID NOS: 393									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 391									
LENGTH: 2627									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-404-879A-391									
Query Match 100.0%; Score 462; DB 3; Length 2627;									
Best Local Similarity 100.0%; Pred. No. 56-146;									
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GGAAGCAGCGGAGCTCCAGCCAGTACGAGTACGCTGGGAACTCCCAAGCC	60						
Db	23	GGAAGCAGCGGAGCTCCAGCCAGTACGAGTACGCTGGGAACTCCCAAGCC	82						
Qy	61	ATAGCTTCCCTGGGAGATCTCTTCTGGAGCATATTAGCATCATTTATTTGGCT	120						
Db	83	ATAGCTTCCCTGGGAGATCTCTTCTGGAGCATATTAGCATCATTTATTTGGCT	142						
Qy	121	GGAAGCAGCTCATCATTCATTCGCTTTGATTTACGGAGACATTCATCAGTCACT	180						
Db	143	GGAAGCAGCTCATCATTCATTCGCTTTGATTTACGGAGACATTCATCAGTCACT	202						
Qy	181	ACGTGCGCCCTGAGTGGGAGATTCGCTTTGATTTACGGAGACATTCATCAGTCACT	240						
Db	203	ACGTGCGCCCTGAGTGGGAGATTCGCTTTGATTTACGGAGACATTCATCAGTCACT	262						
Qy	241	GACATCAAACTTTCTGATATCGTATACATGAGTGGGAGATTCATCAGTCACT	300						
Db	263	GACATCAAACTTTCTGATATCGTATACATGAGTGGGAGATTCATCAGTCACT	322						
Qy	301	CATGAGTTCAAGAGGCAAGTACGCTGTCGAGCAGGATCAAAATTTCAAGGCGG	360						
Db	323	CATGAGTTCAAGAGGCAAGTACGCTGTCGAGCAGGATCAAAATTTCAAGGCGG	382						
Qy	361	ACAGCAGTGTTCGTATCAAGTATGATTTGCAATGCTCTTTGGGGCTGAAGAGCTG	420						

Db 383 ACAGCAGTGTTCGATGATCAAGATGATGGCAAGCCCTTTCGGCGTGAAGAAACGCG 442
QY 421 CAACCTCAGAGTGTGGCGACCTTCAAAATGTTATATATCACT 462
Db 443 CAACCTCAGAGTGTGGCGACCTTCAAAATGTTATATATCACT 484

RESULT 2

US-09-667-857-391
Sequence 391, Application US/09667857
Patent No. 6699664
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Reiter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 391
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
US-09-667-857-391

Query Match 100.0%; Score 462; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. Se-146;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGGGAGGTCCAGTCCAGCAGACCAATGCGTGGGAACCTTCCCGAGCC 60
Db 23 GGAAGGACGGGAGGTCCAGTCCAGCAGACCAATGCGTGGGAACCTTCCCGAGCC 82
QY 61 ATGGCTTCCCTGGGAGATCCCTCTTCTGAGCATATTAAGCATCATTAATTCTGCT 120
Db 83 ATGGCTTCCCTGGGAGATCCCTCTTCTGAGCATATTAAGCATCATTAATTCTGCT 142
QY 121 GGAAGCATTCAGTATCATTTGGCTTGTGATTTTCAAGGAGACATCCATCAGTCACT 180
Db 143 GGAAGCATTCAGTATCATTTGGCTTGTGATTTTCAAGGAGACATCCATCAGTCACT 202
QY 181 ACTGTGCGCTCAGCTGGGAACATTTGGGGAGATGGAATCGTAGCTGCACTTTGAACCT 240
Db 203 ACTGTGCGCTCAGCTGGGAACATTTGGGGAGATGGAATCGTAGCTGCACTTTGAACCT 262
QY 241 GACATCAAACTTTCGATATCGTATATACATGCTGGAAGAGTGTTTAAGCTTGTGTC 300
Db 263 GACATCAAACTTTCGATATCGTATATACATGCTGGAAGAGTGTTTAAGCTTGTGTC 322
QY 301 CATGATTTCAAGAGAGCAAGATGAGCTGTGCGAGCAGATGAATGTTTCAAGGCCCG 360
Db 323 CATGATTTCAAGAGAGCAAGATGAGCTGTGCGAGCAGATGAATGTTTCAAGGCCCG 382
QY 361 ACAGCAGTGTTCGATGATGATGATGGAATGGAATGCTTTGGCGCTGAAGAAACGCG 420
Db 383 ACAGCAGTGTTCGATGATGATGATGGAATGGAATGCTTTGGCGCTGAAGAAACGCG 442
QY 421 CAACCTCAGAGTGTGGCGACCTTCAAAATGTTATATATCACT 462
Db 443 CAACCTCAGAGTGTGGCGACCTTCAAAATGTTATATATCACT 484

RESULT 3

US-09-799-451-332
Sequence 332, Application US/09799451
Patent No. 6783969

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yunging
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No.6783969el Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_Fl_genes Version 2.0
SEQ ID NO 332
LENGTH: 1046
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (4)..(888)
US-09-799-451-332

Query Match 80.5%; Score 372; DB 4; Length 1046;
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGCATATTTAGCATCATATTAATTTGCTGGAGCAATTTGACATCATTTGGCTTTGGT 150
Db 73 AGCATATTTAGCATCATATTAATTTGCTGGAGCAATTTGACATCATTTGGCTTTGGT 132
QY 151 ATTTGAGGAGACATTCATCACTCACTACTGCTGCTGAGCTGGGAAACATTTGGGAG 210
Db 133 ATTTGAGGAGACATTCATCACTCACTACTGCTGCTGAGCTGGGAAACATTTGGGAG 192
QY 211 GATGGAATTCAGTGCATCTTTTGAACCTTGACATCAAACTTCTGATATCGTATACA 270
Db 193 GATGGAATTCAGTGCATCTTTTGAACCTTGACATCAAACTTCTGATATCGTATACA 252
QY 271 TGGCTGAAGAAAGTGTGTTTACGCTTGTGTCATGAGTTCAAGAAAGCAAGATGAGCTG 330
Db 253 TGGCTGAAGAAAGTGTGTTTACGCTTGTGTCATGAGTTCAAGAAAGCAAGATGAGCTG 312
QY 331 TCGAGCAGAGATGAATGTTTCAAGCCGAGACAGAGTGTTCGATATCAAGTATAGTT 390
Db 313 TCGAGCAGAGATGAATGTTTCAAGCCGAGACAGAGTGTTCGATATCAAGTATAGTT 372
QY 391 GGCATGCTCTTTGCGGCTGAAGAAACGTGCAACTCAGAGATGCTGGCACTTCAAAATGT 450
Db 373 GGCATGCTCTTTGCGGCTGAAGAAACGTGCAACTCAGAGATGCTGGCACTTCAAAATGT 432
QY 451 TATATCATCACT 462
Db 433 TATATCATCACT 444

RESULT 4

US-09-910-174B-27

```
; Sequence 27, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-910-174B-27

Query Match          9.4%; Score 43.6; DB 4; Length 948;
Best Local Similarity 63.2%; Pred. No. 0.00037;
Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 357 CCGGACAGCAGTGTCTGATCAAGTAGATTGGCAATGCCCTTTGGCGCTGAATAA 416
DB 273 CCGGACAGCAGCTCTTCCCTGACCTGTGGTGAAGGCAATGCCCTTTGAGGCTGCAGCG 332

QY 417 CGTGCACTCAAGATGCTGGCACCCTCAAAATGTTATATCATCACT 462
DB 333 CGTCCGAGTAACGACAGGCGACCTACCTGCTTTGTAGCACTT 378

RESULT 5
US-09-620-461-27
; Sequence 27, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Mus
US-09-620-461-27

Query Match          9.4%; Score 43.6; DB 4; Length 948;
Best Local Similarity 63.2%; Pred. No. 0.00037;
Matches 67; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 357 CCGGACAGCAGTGTCTGATCAAGTAGATTGGCAATGCCCTTTGGCGCTGAATAA 416
DB 273 CCGGACAGCAGCTCTTCCCTGACCTGTGGTGAAGGCAATGCCCTTTGAGGCTGCAGCG 332

QY 417 CGTGCACTCAAGATGCTGGCACCCTCAAAATGTTATATCATCACT 462
DB 333 CGTCCGAGTAACGACAGGCGACCTACCTGCTTTGTAGCACTT 378
```

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 876
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-876

Query Match          8.8%; Score 40.6; DB 4; Length 1964;
Best Local Similarity 47.5%; Pred. No. 0.006;
Matches 121; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 203 TTGGGGAGATGGAATCTGAGCTGCACTTTGACCTGACATCAAACTTTGATATCG 262
DB 253 TGGGGAGAGCGCGCTGTTCTCTGCTCCTCTTTCTCTGAGACAGTGCAGAGCTATCG 312

QY 263 TGATACATGCTGGAAGGAGGAGTGTGTTAGCTGTGCTCATGAGTCAAGAGGCAAG 322
DB 313 AAGTGGGCTTCTTCAAGAAATCACTTCATGCTGTGTCACCTTACAGAGATGGGGAAG 372

QY 323 ATGAGCTGTGAGCAGCATGAAATGTTACAGAGCGGACAGCAGTGTTCGATCAAG 382
DB 373 ACTGGAAATCTAAGACATGCTCCACAGTATGAGGAGAACTGAGTTGTGAAGACTCCA 432

QY 383 TGATAGTTGCAATGCTCTCTTGGGCTGAAGAAAGGCAACTCAGACATGCTGGCACT 442
DB 433 TTGAGGGGGGCGCTGCTCTTAAAGCTAATAAAATCACTCCTCGACATGCGCTGT 492

QY 443 ACAATGTTATATCA 457
DB 493 ATGGGTGCTGTCTCA 507

RESULT 7
US-08-724-394A-12
; Sequence 12, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```


ORGANISM: Human
US-09-949-016-69029

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 601;
Matches 50; Conservativity 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGCCCGACAGCAGTG 369
DB 488 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 547

QY 370 TTGCTGATCAAG 382
DB 548 TCTGCTGGGGAAG 560

RESULT 11
US-09-949-016-69030

Sequence 69030, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 69030

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-69030

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 601;
Matches 50; Conservativity 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGCCCGACAGCAGTG 369
DB 485 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 544

QY 370 TTGCTGATCAAG 382
DB 545 TCTGCTGGGGAAG 557

RESULT 12
US-09-949-016-11887

Sequence 11887, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11887
LENGTH: 11820

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(11820)

OTHER INFORMATION: n = A,T,C or G

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 11820;
Matches 50; Conservativity 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGCCCGACAGCAGTG 369
DB 5264 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 5323

QY 370 TTGCTGATCAAG 382
DB 5324 TCTGCTGGGGAAG 5336

RESULT 13
US-09-949-016-13767

Sequence 13767, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13767

LENGTH: 11826

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(11826)

OTHER INFORMATION: n = A,T,C or G

Query Match
Best Local Similarity 7.8%; Score 36.2; DB 4; Length 11826;
Matches 50; Conservativity 0; Mismatches 23; Indels 0; Gaps 0;

QY 310 AAGAAGGCAAGATGAGCTGTGAGCAGATGAATGTTTCAGAGCCCGACAGCAGTG 369
DB 5264 AAGAAGGCAAGATGAGGCTGATCGGGGCAATGCCAGAGGGGAAACAGGAAG 5323

QY 370 TTGCTGATCAAG 382
DB 5324 TCTGCTGGGGAAG 5336

RESULT 14
US-09-949-016-11547/C

Sequence 11547, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11547
LENGTH: 854
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-11547

Query Match
Best Local Similarity 55.6%; Score 36; DB 4; Length 854;
Pred. No. 0.13; Mismatches 55; Indels 0; Gaps 0;
Matches 69; Conservative 0;

QY 54 CCAGCATGCTCCCTGGGAGATCCTCTTCTGGAGCATATAGCATCATCATAT 113
DB 628 CTTCTTCACCTTTTCTTCTGAAAATCATCTTTACTGCAAGTTCTTCAATCTTCT 569
QY 114 TCTGCTGAGCAATGCACTCATCATCTTGGTATTGAGGAGACACTGCATCAC 173
DB 568 TATGCTGATTCCTGCAACCTTCACTTGGCTTTCCGTTGGGAGTCTGCTCTCAT 509
QY 174 AGTC 177
DB 508 CCTC 505

RESULT 15
US-08-724-394A-15
Sequence 15, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Teuchihaashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fiteb, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: misc feature
LOCATION: 1..3416
OTHER INFORMATION: /note="cDNA 44"
US-08-724-394A-15

Query Match
Best Local Similarity 46.1%; Score 34.8; DB 2; Length 3416;
Pred. No. 0.78; Mismatches 137; Indels 0; Gaps 0;
Matches 117; Conservative 0;

QY 203 TTGGGAGAGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAAACTTTCTGATATCG 262
DB 490 TGGTGAAAGAGCTGATCTGCTCTGTCACCTGTTCCGACCATGAGTGCAGAGACATGG 549
QY 263 TGATCAATGCTGAGAGAGAGATGTTTAAAGCTTGGTTCATGATTTCAAGAGGCAAG 322
DB 550 AGCTGAAGTGGGTGAGTTCAGAGCTTAAGGCAAGTGTGAAGTGTATGCAATGGAAGG 609
QY 323 ATGAGCTGCGAGCAGATGAATGTTCAAGGCCGAGCAGAGTGTCTGATCAG 382
DB 610 AAGTGAAGACAGAGAGTGCACCGTATCGAGGAGAACTTGAATCTGGCGGATGCA 669
QY 383 TGATAGTTGGCAATGCTCTTTGGGGCTGAAAAGTGCACATGACAGATGCTGGACCT 442
DB 670 TCATGCGAGGAGAGCTCTCTCGAATACCAAGCTCACAGCTTGAACAGTGAAGT 729
QY 443 ACAATGTTATATC 456
DB 730 ACTTGTTATTTT 743

Search completed: May 31, 2005, 00:29:01
Job time : 86.6262 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 17:54:16 ; Search time 316.984 Seconds
(without alignments)
8948.327 Million cell updates/sec

Title: US-09-763-978B-13

Perfect score: 462

Sequence: 1 ggaaggcagcgagctcca.....acaatgtatatacact 462

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 306979757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	1065	9	US-09-877-065-5
2	462	100.0	1658	9	US-09-989-722-290
3	462	100.0	1658	9	US-09-989-723-290
4	462	100.0	1658	9	US-09-989-729-290
5	462	100.0	1658	9	US-09-989-727-290
6	462	100.0	1658	9	US-09-989-731-290
7	462	100.0	1658	9	US-09-989-732-290
8	462	100.0	1658	9	US-09-991-073-290
9	462	100.0	1658	9	US-09-990-442-290
10	462	100.0	1658	9	US-09-991-163-290
11	462	100.0	1658	9	US-09-993-604-290

12	462	100.0	1658	9	US-09-990-456-290	Sequence 290, App
13	462	100.0	1658	9	US-09-989-721-290	Sequence 290, App
14	462	100.0	1658	9	US-09-992-598-290	Sequence 290, App
15	462	100.0	1658	9	US-09-989-293A-290	Sequence 290, App
16	462	100.0	1658	9	US-09-989-735-290	Sequence 290, App
17	462	100.0	1658	9	US-09-990-444-290	Sequence 290, App
18	462	100.0	1658	9	US-09-991-181-290	Sequence 290, App
19	462	100.0	1658	9	US-09-989-130-290	Sequence 290, App
20	462	100.0	1658	9	US-09-990-436-290	Sequence 290, App
21	462	100.0	1658	9	US-09-993-687-290	Sequence 290, App
22	462	100.0	1658	10	US-09-989-734-290	Sequence 290, App
23	462	100.0	1658	10	US-09-997-653-290	Sequence 290, App
24	462	100.0	1658	10	US-09-989-724-290	Sequence 290, App
25	462	100.0	1658	10	US-09-990-441-290	Sequence 290, App
26	462	100.0	1658	10	US-09-990-441-290	Sequence 290, App
27	462	100.0	1658	10	US-09-993-667-290	Sequence 290, App
28	462	100.0	1658	10	US-09-997-428-290	Sequence 290, App
29	462	100.0	1658	10	US-09-997-666-290	Sequence 290, App
30	462	100.0	1658	10	US-09-990-438-290	Sequence 290, App
31	462	100.0	1658	10	US-09-990-562-290	Sequence 290, App
32	462	100.0	1658	10	US-09-990-711-290	Sequence 290, App
33	462	100.0	1658	10	US-09-989-726-290	Sequence 290, App
34	462	100.0	1658	10	US-09-998-156-290	Sequence 290, App
35	462	100.0	1658	10	US-09-990-437-290	Sequence 290, App
36	462	100.0	1658	10	US-09-991-157-290	Sequence 290, App
37	462	100.0	1658	10	US-09-997-514-290	Sequence 290, App
38	462	100.0	1658	10	US-09-997-573-290	Sequence 290, App
39	462	100.0	1658	10	US-09-991-172-290	Sequence 290, App
40	462	100.0	1658	10	US-09-997-559-290	Sequence 290, App
41	462	100.0	1658	10	US-09-997-601-290	Sequence 290, App
42	462	100.0	1658	10	US-09-990-443-290	Sequence 290, App
43	462	100.0	1658	10	US-09-929-764-4	Sequence 290, App
44	462	100.0	1658	10	US-09-991-854-290	Sequence 290, App
45	462	100.0	1658	10	US-09-991-854-290	Sequence 290, App

ALIGNMENTS

RESULT 1
US-09-877-065-5
; Sequence 5, Application US/09877065
; Patent No. US20020051990A1
; GENERAL INFORMATION:
; APPLICANT: OPIE, ERIC
; APPLICANT: MCILACHLAN, KAREN
; APPLICANT: HEARD, CHERYL J.
; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF OVARIAN CARCINOMAS
; FILE REFERENCE: 037003-0280631
; CURRENT APPLICATION NUMBER: US/09/877, 065
; PRIOR FILING DATE: 2001-06-11
; PRIORITY APPLICATION NUMBER: 60/210, 451
; PRIORITY FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-065-5

Query Match 100.0%; Score 462; DB 9; Length 1065;
Best Local Similarity 100.0%; Pred. No. 4.6e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGAGGAGGAGCTCCAGCAGACAGATAGCGTGGAGACCTTCCGAGCC 60
DB 12 GGAAGGAGGAGGAGCTCCAGCAGACAGATAGCGTGGAGACCTTCCGAGCC 71
QY 61 ATGGCTTCCCTGGGAGAGATCTCTTCTGGAGCATATTAGCATCATATTATTCGGCT 120
DB 72 ATGGCTTCCCTGGGAGAGATCTCTTCTGGAGCATATTAGCATCATATTATTCGGCT 131

QY 121 GGAGCAATTGCACTCATTCATTGGCTTTGGTATTTGAGGAGACATCCATCAAGTCACT 180
| | | | |
Db 132 GGAGCAATTGCACTCATTCATTGGCTTTGGTATTTGAGGAGACATCCATCAAGTCACT 191
| | | | |
QY 181 ACTGTCCTCCAGCTGGGAAACATTGGGGAGATGGAATCTTGAGCTGCACCTTTGAACCT 240
| | | | |
Db 192 ACTGTCCTCCAGCTGGGAAACATTGGGGAGATGGAATCTTGAGCTGCACCTTTGAACCT 251
| | | | |
QY 241 GACATAAACCTTTCGATATTCGATACATGGCTGAAGAAAGTCTTTAGGCTTGGTC 300
| | | | |
Db 252 GACATAAACCTTTCGATATTCGATACATGGCTGAAGAAAGTCTTTAGGCTTGGTC 311
| | | | |
QY 301 CATGAGTTCAAGAGAGCAAGATGAGCTGTCGAGCAGATGAATGTTTCAGAGCCCG 360
| | | | |
Db 312 CATGAGTTCAAGAGAGCAAGATGAGCTGTCGAGCAGATGAATGTTTCAGAGCCCG 371
| | | | |
QY 361 ACAGCAGTGTTCGATCAAGTGAATGTTGCAATGCTCTTTGGCGCTGAAAAAGTGC 420
| | | | |
Db 372 ACAGCAGTGTTCGATCAAGTGAATGTTGCAATGCTCTTTGGCGCTGAAAAAGTGC 431
| | | | |
QY 421 CAACCTCAGATGCTGGCACTTCAATGTTATATCATCACT 462
| | | | |
Db 432 CAACCTCAGATGCTGGCACTTCAATGTTATATCATCACT 473
| | | | |
RESULT 2
US-09-989-722-290
Sequence 290, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17

;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGCGAGGCGAGCTCCAGCTACGACGATGACCAATGCGTGGAACTTCCCAACC 60
Db 1 GGAGGCGAGGCGAGCTCCAGCTACGACGATGACCAATGCGTGGAACTTCCCAACC 60

Qy 61 ATGGCTTCCCTGGGGGAGATCCCTCTGGAGCATTAATGACATCATTAATTCGGCT 120
Db 61 ATGGCTTCCCTGGGGGAGATCCCTCTGGAGCATTAATGACATCATTAATTCGGCT 120

Qy 121 GGAGCAATTGCACTCATCATTTGGTATTTCAGGAGACACTCCATCCAGTCACT 180
Db 121 GGAGCAATTGCACTCATCATTTGGTATTTCAGGAGACACTCCATCCAGTCACT 180

Qy 181 ACTGTGCTCCTACGCTGGGAACATTTGGGGAGATGAAATCTGAGCTGCACTTTGAACCT 240
Db 181 ACTGTGCTCCTACGCTGGGAACATTTGGGGAGATGAAATCTGAGCTGCACTTTGAACCT 240

Qy 241 GACATCAAACTTTCTGATATCGATATCAATGCGTGAAGAGGTGTTTAAAGCTGGTC 300
Db 241 GACATCAAACTTTCTGATATCGATATCAATGCGTGAAGAGGTGTTTAAAGCTGGTC 300

Qy 301 CATGACTCAAGAGAGCAAGATGAGCTGTGAGACAGATGAATGTTTCAGAGCCCG 360
Db 301 CATGACTCAAGAGAGCAAGATGAGCTGTGAGAGCAAGATGAATGTTTCAGAGCCCG 360

Qy 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAGAAACGTC 420
Db 361 ACAGCAGTGTGCTGATCAAGTATGTTGGCAATGCTCTTTGGCGCTGAAGAAACGTC 420

Qy 421 CAACTCAGATGCTGGACCTTCAAAATGTTATATCATCACT 462
Db 421 CAACTCAGATGCTGGACCTTCAAAATGTTATATCATCACT 462

RESULT 3
US-09-989-723-290
; Sequence 290, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25

* PRIOR APPLICATION NUMBER: 60/090690
 * PRIOR FILING DATE: 1998-06-25
 * PRIOR APPLICATION NUMBER: 60/090694
 * PRIOR FILING DATE: 1998-06-25
 * PRIOR APPLICATION NUMBER: 60/090695
 * PRIOR FILING DATE: 1998-06-25
 * PRIOR APPLICATION NUMBER: 60/090696
 * PRIOR FILING DATE: 1998-06-25
 * PRIOR APPLICATION NUMBER: 60/090862
 * PRIOR FILING DATE: 1998-06-26
 * PRIOR APPLICATION NUMBER: 60/090863
 * PRIOR FILING DATE: 1998-06-26
 * PRIOR APPLICATION NUMBER: 60/091360
 * PRIOR FILING DATE: 1998-07-01
 * PRIOR APPLICATION NUMBER: 60/091478
 * PRIOR FILING DATE: 1998-07-02
 * PRIOR APPLICATION NUMBER: 60/091544
 * PRIOR FILING DATE: 1998-07-01
 * PRIOR APPLICATION NUMBER: 60/091519
 * PRIOR FILING DATE: 1998-07-02
 * PRIOR APPLICATION NUMBER: 60/091626
 * PRIOR FILING DATE: 1998-07-02
 * PRIOR APPLICATION NUMBER: 60/091633
 * PRIOR FILING DATE: 1998-07-02
 * PRIOR APPLICATION NUMBER: 60/091978
 * PRIOR FILING DATE: 1998-07-07
 * PRIOR APPLICATION NUMBER: 60/091982
 * PRIOR FILING DATE: 1998-07-07
 * PRIOR APPLICATION NUMBER: 60/092182
 * PRIOR FILING DATE: 1998-07-09

Query Match	Score	DB	Length
100.0%	462	9	1658
100.0%	462	9	1658

Best Local Similarity 100.0%; File: NO. 5.2e-14/;
Matches 462; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy	1	GGAGGACACGGGAGCTCCACTCAGGACAGTACCCAGATACGCTGGAACTTTCCCAAGC	60
Db	1	GGAGGACACGGGAGCTCCACTCAGGACAGTACCCAGATACGCTGGAACTTTCCCAAGC	60
Qy	61	ATGCGTTCCCTGGGGGAGATCCTCTTCTGGAGCATATTTAGCATCATATTTCTGGCT	120
Db	61	ATGCGTTCCCTGGGGGAGATCCTCTTCTGGAGCATATTTAGCATCATATTTCTGGCT	120
Qy	121	GGAGCAATTGCACCTATCATATGGCTTTGGTATTTAGGAGAGACCTCATACAGTCACT	180
Db	121	GGAGCAATTGCACCTATCATATGGCTTTGGTATTTAGGAGAGACCTCATACAGTCACT	180
Qy	181	ACTGTGCGCTCAGCTGGGAACTTTGGGGAGATGTGAACTCTAGCTGCACCTTTGAACT	240
Db	181	ACTGTGCGCTCAGCTGGGAACTTTGGGGAGATGTGAACTCTAGCTGCACCTTTGAACT	240
Qy	241	GACATCAAACTTTCTGATATTCGTATPACATGGCTGAAGAGAGGTGTTTAGGCTTGCTC	300
Db	241	GACATCAAACTTTCTGATATTCGTATPACATGGCTGAAGAGAGGTGTTTAGGCTTGCTC	300
Qy	301	CATGAGTTCAAAAGAGGCAAAAGATAGACGTCTGGAGCAGATGGAATTTAGAGGCGCG	360
Db	301	CATGAGTTCAAAAGAGGCAAAAGATAGACGTCTGGAGCAGATGGAATTTAGAGGCGCG	360
Qy	361	ACAGCAGTGTTCCTGATCAAGTGAATGTTGGCAATGCTCTTTTGCGGCTGAAGAAACGTG	420
Db	361	ACAGCAGTGTTCCTGATCAAGTGAATGTTGGCAATGCTCTTTTGCGGCTGAAGAAACGTG	420
Qy	421	CAACTCAGAGATGCTGGCACTTACAAATGTTATATCATCACT	462
Db	421	CAACTCAGAGATGCTGGCACTTACAAATGTTATATCATCACT	462

RESULT 4
US-09-989-279-290
; Sequence 290, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04

1	CURRENT APPLICATION NUMBER: US/09/989,279	
2	CURRENT FILING DATE: 2001-11-19	
3	PRIOR APPLICATION NUMBER: 60/049787	
4	PRIOR FILING DATE: 1997-06-16	
5	PRIOR APPLICATION NUMBER: 60/062250	
6	PRIOR FILING DATE: 1997-10-17	
7	PRIOR APPLICATION NUMBER: 60/065186	
8	PRIOR FILING DATE: 1997-11-12	
9	PRIOR APPLICATION NUMBER: 60/065311	
10	PRIOR FILING DATE: 1997-11-13	
11	PRIOR APPLICATION NUMBER: 60/066770	
12	PRIOR FILING DATE: 1997-11-24	
13	PRIOR APPLICATION NUMBER: 60/075945	
14	PRIOR FILING DATE: 1998-02-25	
15	PRIOR APPLICATION NUMBER: 60/078910	
16	PRIOR FILING DATE: 1998-03-20	
17	PRIOR APPLICATION NUMBER: 60/083322	
18	PRIOR FILING DATE: 1998-04-28	
19	PRIOR APPLICATION NUMBER: 60/084600	
20	PRIOR FILING DATE: 1998-05-07	
21	PRIOR APPLICATION NUMBER: 60/087106	
22	PRIOR FILING DATE: 1998-05-28	
23	PRIOR APPLICATION NUMBER: 60/087607	
24	PRIOR FILING DATE: 1998-06-02	
25	PRIOR APPLICATION NUMBER: 60/087609	
26	PRIOR FILING DATE: 1998-06-02	
27	PRIOR APPLICATION NUMBER: 60/087759	
28	PRIOR FILING DATE: 1998-06-02	
29	PRIOR APPLICATION NUMBER: 60/087827	
30	PRIOR FILING DATE: 1998-06-03	
31	PRIOR APPLICATION NUMBER: 60/088021	
32	PRIOR FILING DATE: 1998-06-04	
33	PRIOR APPLICATION NUMBER: 60/088025	
34	PRIOR FILING DATE: 1998-06-04	
35	PRIOR APPLICATION NUMBER: 60/088026	
36	PRIOR FILING DATE: 1998-06-04	
37	PRIOR APPLICATION NUMBER: 60/088028	
38	PRIOR FILING DATE: 1998-06-04	
39	PRIOR APPLICATION NUMBER: 60/088029	
40	PRIOR FILING DATE: 1998-06-04	
41	PRIOR APPLICATION NUMBER: 60/088030	
42	PRIOR FILING DATE: 1998-06-04	
43	PRIOR APPLICATION NUMBER: 60/088033	
44	PRIOR FILING DATE: 1998-06-04	
45	PRIOR APPLICATION NUMBER: 60/088326	
46	PRIOR FILING DATE: 1998-06-04	

PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5.9e-147; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCAGCGGCGAGCTCCTCACTCAACGAGTACCAGATACGCTGGAACTTTCCCAAGC 60
Db 1 GGAAGCAGCGGCGAGCTCCTCACTCAACGAGTACCAGATACGCTGGAACTTTCCCAAGC 60

QY 61 ATGGCTTCCTGGGCGAGATCTCTTCTGGAGCATATATAGCATATATATTTGGCT 120
Db 61 ATGGCTTCCTGGGCGAGATCTCTTCTGGAGCATATATATAGCATATATATTTGGCT 120

QY 121 GGAGCAATTGACATCATATGGCTTTGGTATTTTCCAGGAGACACTCCATCAAGTCACT 180
Db 121 GGAGCAATTGACATCATATGGCTTTGGTATTTTCCAGGAGACACTCCATCAAGTCACT 180

QY 181 ACTGTGCGCTCACTGAGTGGAGCAATTGGGAGATGGAATCTGAGCTGCATTTTGAACCT 240
Db 181 ACTGTGCGCTCACTGAGTGGAGCAATTGGGAGATGGAATCTGAGCTGCATTTTGAACCT 240

QY 241 GACATCAAACTTTCTGATATCTGTATACATAGGCTGAAGAAAGTGTTTTAGCTTGGTCT 300

Db 241 GACATCAAACTTCTGTATCGTATCAATGGCTGAAGAGGTGTTTAGGCTTGGTC 300
Qy 301 CATGAGTTCAAAGAGCAAAAGATGAGCTGTGGAGCAGATGAATGTTCAAGGCCGG 360
Db 301 CATGAGTTCAAAGAGCAAAAGATGAGCTGTGGAGCAGATGAATGTTCAAGGCCGG 360
Qy 361 ACAGCAGTGTGTTGCTGATCAAGTATGTTGGCAATGCCCTTGGCGGCTGAAGAACGTG 420
Db 361 ACAGCAGTGTGTTGCTGATCAAGTATGTTGGCAATGCCCTTGGCGGCTGAAGAACGTG 420
Qy 421 CAACTCAGATGCTGGCACCCTCAAAATGTTATTCATCACT 462
Db 421 CAACTCAGATGCTGGCACCCTCAAAATGTTATTCATCACT 462

RESULT 5
US-09-989-727-290
; Sequence 290, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kijavlin, Mary A.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609

; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090662
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGGCGGGGAGCTTCACTGAGCCAGTACCCAGATAGCTGGAACTTCCCGGCC 60
DB 1 GGAAGGCGGGGAGCTTCACTGAGCCAGTACCCAGATAGCTGGAACTTCCCGGCC 60
QY 61 ATGGCTTCCCTGGGGAGATCTCTTCTGAGCATTAATTAGCATCATTAATTTCTGGCT 120
DB 61 ATGGCTTCCCTGGGGAGATCTCTTCTGAGCATTAATTAGCATCATTAATTTCTGGCT 120
QY 121 GGAGCAATTCGATCATTCATTGGCTTTGGTATTTTCAGGAGACACTCCATCACTACT 180
DB 121 GGAGCAATTCGATCATTCATTGGCTTTGGTATTTTCAGGAGACACTCCATCACTACT 180
QY 181 ACTGTCGCTCACTGAGCAATTCGGAGATGGAACTTGAAGCTGCACTTTTGAACCT 240
DB 181 ACTGTCGCTCACTGAGCAATTCGGAGATGGAACTTGAAGCTGCACTTTTGAACCT 240
QY 241 GACATCAAACTTCTGATATGCTGATACATGCTGAAGAGTGTAGCTTGCTGCTC 300
DB 241 GACATCAAACTTCTGATATGCTGATACATGCTGAAGAGTGTAGCTTGCTGCTC 300
QY 301 CATGAGTTCAAGAGGCAAGATGAGCTGTGAGAGCATGAATGTTCAAGAGCCGG 360
DB 301 CATGAGTTCAAGAGGCAAGATGAGCTGTGAGAGCATGAATGTTCAAGAGCCGG 360
QY 361 ACAGCAGTTTTCGATCAAGTGAATGTTGGCAATGCTTTTGGCTGAAAGCTG 420
DB 361 ACAGCAGTTTTCGATCAAGTGAATGTTGGCAATGCTTTTGGCTGAAAGCTG 420
QY 421 CAATCAGAGATGCTGCACTCAAAATGTTATATCACTACT 462
DB 421 CAATCAGAGATGCTGCACTCAAAATGTTATATCACTACT 462
RESULT 6
US-09-989-731-290
; Sequence 290, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Grimaldi, U. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

1	PRIOR APPLICATION NUMBER: 1997-10-17
2	PRIOR FILING DATE: 1997-10-17
3	PRIOR APPLICATION NUMBER: 60/065186
4	PRIOR FILING DATE: 1997-11-12
5	PRIOR APPLICATION NUMBER: 60/065311
6	PRIOR FILING DATE: 1997-11-13
7	PRIOR APPLICATION NUMBER: 60/066770
8	PRIOR FILING DATE: 1997-11-24
9	PRIOR APPLICATION NUMBER: 60/075945
10	PRIOR FILING DATE: 1998-02-25
11	PRIOR APPLICATION NUMBER: 60/078910
12	PRIOR FILING DATE: 1998-03-20
13	PRIOR APPLICATION NUMBER: 60/083322
14	PRIOR FILING DATE: 1998-04-28
15	PRIOR APPLICATION NUMBER: 60/084600
16	PRIOR FILING DATE: 1998-05-07
17	PRIOR APPLICATION NUMBER: 60/087106
18	PRIOR FILING DATE: 1998-05-28
19	PRIOR APPLICATION NUMBER: 60/087607
20	PRIOR FILING DATE: 1998-06-02
21	PRIOR APPLICATION NUMBER: 60/087609
22	PRIOR FILING DATE: 1998-06-02
23	PRIOR APPLICATION NUMBER: 60/087759
24	PRIOR FILING DATE: 1998-06-02
25	PRIOR APPLICATION NUMBER: 60/087827
26	PRIOR FILING DATE: 1998-06-03
27	PRIOR APPLICATION NUMBER: 60/088021
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088025
30	PRIOR FILING DATE: 1998-06-04
31	PRIOR APPLICATION NUMBER: 60/088026
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088028
34	PRIOR FILING DATE: 1998-06-04
35	PRIOR APPLICATION NUMBER: 60/088029
36	PRIOR FILING DATE: 1998-06-04
37	PRIOR APPLICATION NUMBER: 60/088030
38	PRIOR FILING DATE: 1998-06-04
39	PRIOR APPLICATION NUMBER: 60/088033
40	PRIOR FILING DATE: 1998-06-04
41	PRIOR APPLICATION NUMBER: 60/088326
42	PRIOR FILING DATE: 1998-06-04
43	PRIOR APPLICATION NUMBER: 60/088157
44	PRIOR FILING DATE: 1998-06-05
45	PRIOR APPLICATION NUMBER: 60/088202
46	PRIOR FILING DATE: 1998-06-05
47	PRIOR APPLICATION NUMBER: 60/088212
48	PRIOR FILING DATE: 1998-06-05
49	PRIOR APPLICATION NUMBER: 60/088217
50	PRIOR FILING DATE: 1998-06-05
51	PRIOR APPLICATION NUMBER: 60/088655
52	PRIOR FILING DATE: 1998-06-09
53	PRIOR APPLICATION NUMBER: 60/088734
54	PRIOR FILING DATE: 1998-06-10
55	PRIOR APPLICATION NUMBER: 60/088738
56	PRIOR FILING DATE: 1998-06-10
57	PRIOR APPLICATION NUMBER: 60/088742
58	PRIOR FILING DATE: 1998-06-10
59	PRIOR APPLICATION NUMBER: 60/088810
60	PRIOR FILING DATE: 1998-06-10
61	PRIOR APPLICATION NUMBER: 60/088824
62	PRIOR FILING DATE: 1998-06-10
63	PRIOR APPLICATION NUMBER: 60/088826
64	PRIOR FILING DATE: 1998-06-10
65	PRIOR APPLICATION NUMBER: 60/088858
66	PRIOR FILING DATE: 1998-06-11
67	PRIOR APPLICATION NUMBER: 60/088861
68	PRIOR FILING DATE: 1998-06-11
69	PRIOR APPLICATION NUMBER: 60/088876
70	PRIOR FILING DATE: 1998-06-11
71	PRIOR APPLICATION NUMBER: 60/089105
72	PRIOR FILING DATE: 1998-06-12
73	PRIOR APPLICATION NUMBER: 60/089440

[illegible]

;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5.9e-147; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGCGAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCGAGCC 60
DB 1 GGAAGGACGCGAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTCCCTGGGAGCATCTCTTCTGGAGCATATTAAGCATCATCTATTCTGGCT 120
DB 61 ATGGCTCCCTGGGAGCATCTCTTCTGGAGCATATTAAGCATCATCTATTCTGGCT 120
QY 121 GGAGCATTCGACTCATCTATGGCTTGGATTTCAGGAGACATCCCATCAGTCACT 180
DB 121 GGAGCATTCGACTCATCTATGGCTTGGATTTCAGGAGACATCCCATCAGTCACT 180
QY 181 ACTGTGCTCCTCAGCTGGGAACAATGGGAGAGATGGAATCTGAGCTGCACTTTGAACT 240
DB 181 ACTGTGCTCCTCAGCTGGGAACAATGGGAGAGATGGAATCTGAGCTGCACTTTGAACT 240
QY 241 GACATCAAACTTTTGATATCTGATATCAATGCTGGAAGAGCTTTAGGCTTGGCT 300
DB 241 GACATCAAACTTTTGATATCTGATATCAATGCTGGAAGAGCTTTAGGCTTGGCT 300
QY 301 CATGAGTTCAAGGAAGGAGGAGTGTGCTGGAGCAGATGAATGTTTCAGAGCGCG 360
DB 301 CATGAGTTCAAGGAAGGAGGAGTGTGCTGGAGCAGATGAATGTTTCAGAGCGCG 360
QY 361 ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTTGGGCTGAAAAACGTG 420
DB 361 ACAGCAGTGTTCCTGATCAAGTATGATGTCGCAATGCTCTTTGGGCTGAAAAACGTG 420
QY 421 CAACTTACAGATGCTGGGACCTTAACAATGTATATATATCTACT 462
DB 421 CAACTTACAGATGCTGGGACCTTAACAATGTATATATCTACT 462

RESULT 7
US-09-989-732-290

;; Sequence 290, Application US/09989732
;; Patent No. US20020123463A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desmoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C57
;; CURRENT APPLICATION NUMBER: US/09/989,732
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09

PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred No.5.9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCAGCGGAGCTCCAGTCCAGTACCAATACGCTGGAACTTCCCGAGCC 60
DB 1 GGAAGCAGCGGAGCTCCAGTCCAGTACCAATACGCTGGAACTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGAGATCCTCTTGTGAGCATATTAATGATCATATTTGGCT 120
DB 61 ATGGCTTCCCTGGGAGATCCTCTTGTGAGCATATTAATGATCATATTTGGCT 120
QY 121 GGAAGCAATGCACTCATCTTGGCTTTGATTTGAGGAGACATCCCATCAGTCACT 180
DB 121 GGAAGCAATGCACTCATCTTGGCTTTGATTTGAGGAGACATCCCATCAGTCACT 180
QY 181 ACTGTGCTCAGCTGGAACATTTGGGAGATGGAATCTAGCTGACCTTTGAACCT 240
DB 181 ACTGTGCTCAGCTGGAACATTTGGGAGATGGAATCTAGCTGACCTTTGAACCT 240
QY 241 GACATCAAACTTTGATATCGTATATCAATGCTGAAGAAAGTGTTTAGGCTTGGTC 300
DB 241 GACATCAAACTTTGATATCGTATATCAATGCTGAAGAAAGTGTTTAGGCTTGGTC 300
QY 301 CATGAGTTCAAGAGGCAAGATAGCTGTGGAGCAGAGAAATGTTGAGAGCCGG 360
DB 301 CATGAGTTCAAGAGGCAAGATAGCTGTGGAGCAGAGAAATGTTGAGAGCCGG 360
QY 361 ACAGCAGTGTGCTGATCAATGATAGTGTGCAATGCTCTTTGGCGGTGAAAAAGCTG 420
DB 361 ACAGCAGTGTGCTGATCAATGATAGTGTGCAATGCTCTTTGGCGGTGAAAAAGCTG 420

PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5, 9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGGGAGCTCCAGTCAGCCAGTACAGTCCGCTGGAGACCTTCCAGCC 60
DB 1 GGAAGGACGGGAGCTCCAGTCAGCCAGTACAGTCCGCTGGAGACCTTCCAGCC 60
QY 61 ATGGCTTCCTGGGAGATCTCTTCTGAGCATATTAGCATCATTTATCTGGCT 120

DB 61 ATGGCTTCCTGGGAGATCTCTTCTGAGCATATTAGCATCATTTATCTGGCT 120
QY 121 GGAAGCAATTGCACTATCATTTGGCTTTGGTATTTACAGGAGACATTCATCAGATCACT 180
DB 121 GGAAGCAATTGCACTATCATTTGGCTTTGGTATTTACAGGAGACATTCATCAGATCACT 180
QY 181 ACTGTGGCTCAGCTGAGGAAATTTGGGGAGATGGAATCTGAGCTGCACTTTTGAACCT 240
DB 181 ACTGTGGCTCAGCTGAGGAAATTTGGGGAGATGGAATCTGAGCTGCACTTTTGAACCT 240
QY 241 GACATCAAACTTTCTGATATCGTATACATGGCTGGAAGAGTGTATTTAGGCTTGGTC 300
DB 241 GACATCAAACTTTCTGATATCGTATACATGGCTGGAAGAGTGTATTTAGGCTTGGTC 300
QY 301 CATGATTTCAAGAGGCAAAAGTGAAGCTGTGGAGCAGAGTAAATTTTCAAGGCCG 360
DB 301 CATGATTTCAAGAGGCAAAAGTGAAGCTGTGGAGCAGAGTAAATTTTCAAGGCCG 360
QY 361 ACAGCAGTGTTCCTGATCAAGTATGATGTTGGCAATGCTCTTTGGGCTGAAAAAGTG 420
DB 361 ACAGCAGTGTTCCTGATCAAGTATGATGTTGGCAATGCTCTTTGGGCTGAAAAAGTG 420
QY 421 CAACTCAGATGCTGGCACTTCAAAATGTTATATCACT 462
DB 421 CAACTCAGATGCTGGCACTTCAAAATGTTATATCACT 462

RESULT 9
US-09-442-290
Sequence 290, Application US/09990442
Patent No. US2002013252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferreira, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/0895939
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/0896000
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/0896533
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/0898001
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/0899070
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/0899008
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/0899477
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/0899488
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/0899522
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/0902466
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/0902522
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/0902544
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/0903499
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/0903555
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/0904299
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0904311
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0904355
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0904444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0904455
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0904720
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0905577
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0905355
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0905040
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0905420
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/0906560
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906594
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906535
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906780
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906500
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906594
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906535
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906566
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/0906822
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/0908633
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/0913600
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/0914780
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/0915444
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/0915199
PRIOR FILING DATE:	1998-07-02

```

; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5, 9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGGACGGGCGAGCTCCACTGAGCCAGTACCAGTACGCTGGGAACCTTCCCGAGCC 60
DB 1 GGAAGGACGGGCGAGCTCCACTGAGCCAGTACCAGTACGCTGGGAACCTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGGGAGATCCTTCTGGAGATATATAGCATCATATTATTCGGCT 120
DB 61 ATGGCTTCCCTGGGGGAGATCCTTCTGGAGATATATAGCATCATATTATTCGGCT 120
QY 121 GGAGCAATTCAGCTCATTCATTCGCTTTGTATTTGAGGAGACATCCATCAGATCACT 180
DB 121 GGAGCAATTCAGCTCATTCATTCGCTTTGTATTTGAGGAGACATCCATCAGATCACT 180
QY 181 ACTGTGCGCTCAGCTGGAAACATTTGGGAGAGATGAAATCTGAGCTGCACTTTGAACCT 240
DB 181 ACTGTGCGCTCAGCTGGAAACATTTGGGAGAGATGAAATCTGAGCTGCACTTTGAACCT 240
QY 241 GACATCAAACTTCTGATATCGATATACATTCGCTGAGGAAGGTGTTTAAAGCTTGGCT 300
DB 241 GACATCAAACTTCTGATATCGATATACATTCGCTGAGGAAGGTGTTTAAAGCTTGGCT 300
QY 301 CATGATTCAAAGAGGCAAGATGAGCTGTCGAGAGAGATGAAATGTTCAAGAGCCGG 360
DB 301 CATGATTCAAAGAGGCAAGATGAGCTGTCGAGAGAGATGAAATGTTCAAGAGCCGG 360
QY 361 ACAGCAGTGTTCCTGATCAAGTATGATGTTGGCAATGCCCTTTGGCGGCTGAAAAAGCTG 420
DB 361 ACAGCAGTGTTCCTGATCAAGTATGATGTTGGCAATGCCCTTTGGCGGCTGAAAAAGCTG 420
QY 421 CAACCTCAGAGATGCTGGACCTCAATGTATATATATCACT 462
DB 421 CAACCTCAGAGATGCTGGACCTCAATGTATATATCACT 462

RESULT 10
US-09-991-163-290
; Sequence 290, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
```

```

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
```

PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090662
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGCGAGCGGAGCTTCACTGACGCAATCCAGATACGCTGGGAACCTTCCACACC 60
DB 1 GGAGGCGAGCGGAGCTTCACTGACGCAATCCAGATACGCTGGGAACCTTCCACACC 60
QY 61 ATGGCTTCCCTGGGGCAATCCTCTTGGAGCAATTAATCATCATATTTGCT 120
DB 61 ATGGCTTCCCTGGGGCAATCCTCTTGGAGCAATTAATCATCATATTTGCT 120
QY 121 GGAGCAATTGCACTCATATTGGCTTTGATATTTTCAGGAGACACTCCATCAGATCACT 180
DB 121 GGAGCAATTGCACTCATATTGGCTTTGATATTTTCAGGAGACACTCCATCAGATCACT 180
QY 181 ACTGTCGCTCAGCTGGGAACATTGGGAGATGGAATCTGAGCTGCATTTGAACCT 240
DB 181 ACTGTCGCTCAGCTGGGAACATTGGGAGATGGAATCTGAGCTGCATTTGAACCT 240
QY 241 GACATCAAACTTTCGATATGCTGTATCAATGGCTGAAGAGTTTGGCTTGGCT 300
DB 241 GACATCAAACTTTCGATATGCTGTATCAATGGCTGAAGAGTTTGGCTTGGCT 300
QY 301 CATGAGTTCAAAAGAGCAAGATAGCTGTTCGAGCAGATGAATTTTCAGAGCCGG 360
DB 301 CATGAGTTCAAAAGAGCAAGATAGCTGTTCGAGCAGATGAATTTTCAGAGCCGG 360
QY 361 ACAGCAGTGTTCGATCAAGTGAATGATGGCAATGCTCTTGGCGGCTGAAAAAGCTG 420
DB 361 ACAGCAGTGTTCGATCAAGTGAATGATGGCAATGCTCTTGGCGGCTGAAAAAGCTG 420
QY 421 CAATCACAAGATGCTGGCACTTAAGATTTATATCATCACT 462
DB 421 CAATCACAAGATGCTGGCACTTAAGATTTATATCATCACT 462

RESULT 11
US-09-993-604-290
Sequence 290, Application US/09993604
Patent No. US20020137075A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C25
CURRENT APPLICATION NUMBER: US/09/993,604
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326

PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088724
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5,9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGCGAGCGGAGCTCCAGTCACTGAGCCAGTACCGCTGGAGACCTTCCCGAGCC 60
DB 1 GGAGGCGAGCGGAGCTCCAGTCACTGAGCCAGTACCGCTGGAGACCTTCCCGAGCC 60
QY 61 ATGGCTTCCCTGGGCGAGATCCCTCTGGAGCATATAGCATCATCTATTTCTGGCT 120
DB 61 ATGGCTTCCCTGGGCGAGATCCCTCTGGAGCATATAGCATCATCTATTTCTGGCT 120
QY 121 GGAGCAATTCAGCTCATCTATTCGCTTTGGTATTTTCAGGAGACCTTCACAGTCACT 180
DB 121 GGAGCAATTCAGCTCATCTATTCGCTTTGGTATTTTCAGGAGACCTTCACAGTCACT 180
QY 181 ACTGTGCTCAGCTGAGAAACATTTGGGAGAGATGAAATCTGAGCTGCACCTTTGAACCT 240
DB 181 ACTGTGCTCAGCTGAGAAACATTTGGGAGAGATGAAATCTGAGCTGCACCTTTGAACCT 240
QY 241 GACATCAAACTTCTGATATCGATACAAATGGCTGAAGAGGTGTTTAGGCTGGTC 300
DB 241 GACATCAAACTTCTGATATCGATACAAATGGCTGAAGAGGTGTTTAGGCTGGTC 300
QY 301 CATGAGTTCAAGAGAGCAAAAGATGAGCTGCGAGCAGAGATGAAATGTTTCAGAGCCCG 360
DB 301 CATGAGTTCAAGAGAGCAAAAGATGAGCTGCGAGCAGAGATGAAATGTTTCAGAGCCCG 360
QY 361 ACAGCAGTGTGTTGCTGATCAAGTGAATGTTGGCAATGCTCTTTGGCGCTGAAAAACGTG 420
DB 361 ACAGCAGTGTGTTGCTGATCAAGTGAATGTTGGCAATGCTCTTTGGCGCTGAAAAACGTG 420
QY 421 CAAGTCAGAGATGCTGAGCACTTCAAAATGTTATATCACT 462
DB 421 CAAGTCAGAGATGCTGAGCACTTCAAAATGTTATATCACT 462

RESULT 13
US-09-989-721-290
Sequence 290, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auscin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC55
CURRENT APPLICATION NUMBER: US/09/989,721
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12

```

PRIORITY FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/0930863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5.9e-147;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1   GGAGGCGAGCGGCAGCTCCACTCAGCCAGTACCAGATACGCTGGGAACCTTCCCAGCC 60
DB      1   GGAAGGCGAGCGGCAGCTCCACTCAGCCAGTACCAGATACGCTGGGAACCTTCCCAGCC 60

QY      61   ATGGCTTCCTCCGGGGGAGATCCCTTCGAGGCAATAATTAGCATCATCATTTCTGGCT 120
DB      61   ATGGCTTCCTCCGGGGGAGATCCCTTCGAGGCAATAATTAGCATCATCATTTCTGGCT 120

QY     121   GGAGCAATTGCACTCATCATCATTTGCTTTGTATTTCAAGGAGACACTCCATCACAGTCACT 180
DB     121   GGAGCAATTGCACTCATCATCATTTGCTTTGTATTTCAAGGAGACACTCCATCACAGTCACT 180

QY     181   ACTGTGCCCTCAGCTGGGAAACATTTGGGAGAGATGGAATCTTGAGCTGCACCTTTGAACCT 240
DB     181   ACTGTGCCCTCAGCTGGGAAACATTTGGGAGAGATGGAATCTTGAGCTGCACCTTTGAACCT 240

QY     241   GACATCAAACCTTTGTGATTCGTGATTAACAATGCTGAAAGAAGGTGTTTAGGCTGCTC 300
DB     241   GACATCAAACCTTTGTGATTCGTGATTAACAATGCTGAAAGAAGGTGTTTAGGCTGCTC 300

QY     301   CATAGATTCAAAGAAGCAAAAGATGAGCTGTCGAGCAGAGATGAATTTTCAGAGGCCGG 360
DB     301   CATAGATTCAAAGAAGCAAAAGATGAGCTGTCGAGCAGAGATGAATTTTCAGAGGCCGG 360

QY     361   ACAGCAGTGTGTGCTGATCAAGTATGATTTGGCAATGCTCTTTGCGGCTGAAAAAAGCTG 420
DB     361   ACAGCAGTGTGTGCTGATCAAGTATGATTTGGCAATGCTCTTTGCGGCTGAAAAAAGCTG 420

QY     421   CAATCTCACAGATGCTGGCACTTAACAAATGTTATATCATCACT 462
DB     421   CAATCTCACAGATGCTGGCACTTAACAAATGTTATATCATCACT 462

RESULT 14
US-09-992-598-290
Sequence 290, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gettitsen, Mary E.
```

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mackey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655

PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24

	Query Match	100.0%;	Score 462;	DB 9;	Length 1658;
	Best Local Similarity	100.0%;	Pred. No. 5.9e-147;		
	Matches 462;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGAAAGCAGCGGCAAGCTCCACTCAGCCAGTACCCAGATACCGCTGGGAACCTTCCCAACC	60		
Db	1	GGAAAGCAGCGGCAAGCTCCACTCAGCCAGTACCCAGATACCGCTGGGAACCTTCCCAACC	60		
QY	61	ATGGCTTCCCTGGGGGAGATCCTCTTCGGAGCAATATTAGCATCATTTATTCGGCT	120		
Db	61	ATGGCTTCCCTGGGGGAGATCCTCTTCGGAGCAATATTAGCATCATTTATTCGGCT	120		
QY	121	GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAAGCACTCATCAAGTACT	180		
Db	121	GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAAGCACTCATCAAGTACT	180		
QY	181	ACGTGCGCTCAGCTGGGGAACATTGGGGAGATGGAACTCGAGCTGACCTTTGAACCT	240		
Db	181	ACGTGCGCTCAGCTGGGGAACATTGGGGAGATGGAACTCGAGCTGACCTTTGAACCT	240		
QY	241	GACATCAAACTTTCTGATATCGTATACAATAGCGTGAAGGAAGGTTTATAGCTTGGTTC	300		
Db	241	GACATCAAACTTTCTGATATCGTATACAATAGCGTGAAGGAAGGTTTATAGCTTGGTTC	300		
QY	301	CATGATTTCAAAGAGGCAAAAGATGAGCTGTGCGAGCAGATGAAATGTTCAAGAGCCGG	360		
Db	301	CATGATTTCAAAGAGGCAAAAGATGAGCTGTGCGAGCAGATGAAATGTTCAAGAGCCGG	360		
QY	361	ACAGCACTGTTTGGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAAGCTG	420		
Db	361	ACAGCACTGTTTGGCTGATCAAGTATAGTTGGCAATGCTCTTTGGCGCTGAAAAAGCTG	420		

RESULT 15
 US-09-989-293A-290
 : Sequence 290, Application US/09989293A
 : Patent No. US20020177164A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi J.
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan L.
 : APPLICANT: Ferrara, Napoleone
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Geritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Kljavin, Ivar J.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Watanabe, Colin K.
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William I.
 : APPLICANT: Zhang, Zemin
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 : FILE OF INVENTION: Acids Encoding the Same
 : FILE REFERENCE: P2730PIC66
 : CURRENT APPLICATION NUMBER: US/09/989, 293A
 : CURRENT FILING DATE: 2001-11-20
 : PRIOR APPLICATION NUMBER: 60/049787
 : PRIOR FILING DATE: 1997-06-16
 : PRIOR APPLICATION NUMBER: 60/062250
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/065186
 : PRIOR FILING DATE: 1997-11-12
 : PRIOR APPLICATION NUMBER: 60/065311
 : PRIOR FILING DATE: 1997-11-13
 : PRIOR APPLICATION NUMBER: 60/066770
 : PRIOR FILING DATE: 1997-11-24
 : PRIOR APPLICATION NUMBER: 60/075945
 : PRIOR FILING DATE: 1998-02-25
 : PRIOR APPLICATION NUMBER: 60/076910
 : PRIOR FILING DATE: 1998-03-20
 : PRIOR APPLICATION NUMBER: 60/083322
 : PRIOR FILING DATE: 1998-04-28
 : PRIOR APPLICATION NUMBER: 60/084600
 : PRIOR FILING DATE: 1998-05-07
 : PRIOR APPLICATION NUMBER: 60/087106
 : PRIOR FILING DATE: 1998-05-28
 : PRIOR APPLICATION NUMBER: 60/087607
 : PRIOR FILING DATE: 1998-06-02
 : PRIOR APPLICATION NUMBER: 60/087609
 : PRIOR FILING DATE: 1998-06-02
 : PRIOR APPLICATION NUMBER: 60/087759
 : PRIOR FILING DATE: 1998-06-02
 : PRIOR APPLICATION NUMBER: 60/087827
 : PRIOR FILING DATE: 1998-06-03
 : PRIOR APPLICATION NUMBER: 60/088021
 : PRIOR FILING DATE: 1998-06-04
 : PRIOR APPLICATION NUMBER: 60/088025
 : PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246

PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 5.9e-147; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0;

Qy 1 GGAAGCAGCGGACGCTCCAGTACGAGTACCGAGATACGCTGGAGACTTCCCAACC 60
|||||
Db 1 GGAAGCAGCGGACGCTCCAGTACGAGTACCGAGATACGCTGGAGACTTCCCAACC 60
|||||
Qy 61 ATGGCTCCCTGGGAGATCTCTTGGAGCATTAATTAGCATCATTAATTCTGGCT 120

```
Db 61 ATGGCTTCCCTGGGGCAGATCCTCTCTGGAGCATATTAAGCATCATTTATTTCTGGCT 120
QY 121 GGAGCAATTGGCACTCATCATTTGGCTTTGGTAATTTGAGGAGACACTCCATCAGTCACT 180
Db 121 GGAGCAATTGGCACTCATCATTTGGCTTTGGTAATTTGAGGAGACACTCCATCAGTCACT 180
QY 181 ACTGTGCGCTCAGCTGGGAACATTGGGGAGGATGGAAATCCAGAGCTGCACTTTGAAACT 240
Db 181 ACTGTGCGCTCAGCTGGGAACATTGGGGAGGATGGAAATCCAGAGCTGCACTTTGAAACT 240
QY 241 GACATCAAACTTTCTGATATCGTGATACAAATGCGTGAAGAGAGTGTATTTAGGCTTGTC 300
Db 241 GACATCAAACTTTCTGATATCGTGATACAAATGCGTGAAGAGAGTGTATTTAGGCTTGTC 300
QY 301 CATGAGTTCAAAGAGCAAGATGAGCTGTGGAGCAGAGTGAATGTTCAAGAGCCGG 360
Db 301 CATGAGTTCAAAGAGCAAGATGAGCTGTGGAGCAGAGTGAATGTTCAAGAGCCGG 360
QY 361 ACAGCAGTGTGTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGGCGTGAAAAAGTG 420
Db 361 ACAGCAGTGTGTGCTGATCAAGTATAGTTGGCAATGCTCTTTGGGCGTGAAAAAGTG 420
QY 421 CAACTCAGAGTGTGGCACTTCAAAATGTTATATCATCACT 462
Db 421 CAACTCAGAGTGTGGCACTTCAAAATGTTATATCATCACT 462
```

Search completed: May 31, 2005, 10:07:40
Job time : 317.984 secs

THIS PAGE LEFT BLANK

Db 133 GGAGCAATTGCACTCATTCATTTGGCTTTGGTATTTTCAGGGAGACATCCATCAGATCACT 192

QY 181 ACTGTGGCCCTCAGCTGGGAACATTTGGGGAGATGAGATCCCTGAGCTGCACCTTTGAACCT 240

Db 193 ACTGTGGCCCTCAGCTGGGAACATTTGGGGAGATGAGATCCCTGAGCTGCACCTTTGAACCT 252

QY 241 GACATCAAACTTTCTGATATCGTATACATAGCTGAGAGAGATGTTTAAAGCTTGGTC 300

Db 253 GACATCAAACTTTCTGATATCGTATACATAGCTGAGAGAGATGTTTAAAGCTTGGTC 312

QY 301 CATGAGTTCAAAGAGCAAAAGATGAGCTGTGGAGCAGATGAATGTTTCAAGGCCGG 360

Db 313 CATGAGTTCAAAGAGCAAAAGATGAGCTGTGGAGCAGATGAATGTTTCAAGGCCGG 372

QY 361 ACAGCAGTGTTCCTGATCAAGTATGATGAGATGGCAATGCCCTTTGGCGCTGAAAAACGTG 420

Db 373 ACAGCAGTGTTCCTGATCAAGTATGATGAGATGGCAATGCCCTTTGGCGCTGAAAAACGTG 432

QY 421 CAACTCAGAGATGCTGGCACCTTACAAATGTTATATCATCACT 462

Db 433 CAACTCAGAGATGCTGGCACCTTACAAATGTTATATCATCACT 474

RESULT 2
BP255264 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP255264 Sugano cDNA library, kidney epithelial cell Homo sapiens
DEFINITION CDNA clone HRC08664, mRNA sequence.

ACCESSION BP255264
VERSION BP255264.1 GI:52170494
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 583)

AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanebaidai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. 583
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC08664"
/tissue_type="kidney"
/cell_type="epithelial cell"
/clone_lib="Sugano cDNA library, kidney epithelial cell"

ORIGIN
Query Match 100.0%; Score 462; DB 5; Length 583;
Best Local Similarity 100.0%; Pred. No. 8e-130; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCAGCGGAGAGCTCCAGTACAGCCAGTACCAGATACGCTGGAACTTCCCGAGCC 60
Db 13 GGAAGCAGCGGAGAGCTCCAGTACAGCCAGTACCAGATACGCTGGAACTTCCCGAGCC 72
QY 61 ATGGCTTCCTGGGGGAGATCTCTTCTTGAGACATAATTAGATCATATTATTTGGGCT 120
Db 73 ATGGCTTCCTGGGGGAGATCTCTTCTTGAGACATAATTAGATCATATTATTTGGGCT 132
QY 121 GGAAGCAATTCAGTCAATCATTTGGCTTGTGATTTTCAGGGAGACATCCATCAGATCACT 180
Db 133 GGAAGCAATTCAGTCAATCATTTGGCTTGTGATTTTCAGGGAGACATCCATCAGATCACT 192

QY 181 ACTGTGGCCCTCAGCTGGGAACATTTGGGGAGATGAGATCCCTGAGCTGCACCTTTGAACCT 240

Db 193 ACTGTGGCCCTCAGCTGGGAACATTTGGGGAGATGAGATCCCTGAGCTGCACCTTTGAACCT 252

QY 241 GACATCAAACTTTCTGATATCGTATACATAGCTGAGAGAGATGTTTAAAGCTTGGTC 300

Db 253 GACATCAAACTTTCTGATATCGTATACATAGCTGAGAGAGATGTTTAAAGCTTGGTC 312

QY 301 CATGAGTTCAAAGAGCAAAAGATGAGCTGTGGAGCAGATGAATGTTTCAAGGCCGG 360

Db 313 CATGAGTTCAAAGAGCAAAAGATGAGCTGTGGAGCAGATGAATGTTTCAAGGCCGG 372

QY 361 ACAGCAGTGTTCCTGATCAAGTATGATGAGATGGCAATGCCCTTTGGCGCTGAAAAACGTG 420

Db 373 ACAGCAGTGTTCCTGATCAAGTATGATGAGATGGCAATGCCCTTTGGCGCTGAAAAACGTG 432

QY 421 CAACTCAGAGATGCTGGCACCTTACAAATGTTATATCATCACT 462

Db 433 CAACTCAGAGATGCTGGCACCTTACAAATGTTATATCATCACT 474

RESULT 3
BX499180 604 bp mRNA linear EST 04-SEP-2003
LOCUS BX499180
DEFINITION DKFZp779B1644_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
ACCESSION BX499180
VERSION BX499180.1 GI:32017386
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 604)
AUTHORS Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Oeanger,A., Podo,G., Han,M., and Wiemann,S.
TITLE EST (Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS

FEATURES
source
1. 604
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp779B1644"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiI"

ORIGIN
Query Match 100.0%; Score 462; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 8.1e-130; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCAGCGGAGAGCTCCAGTACAGCCAGTACCAGATACGCTGGAACTTCCCGAGCC 60
Db 12 GGAAGCAGCGGAGAGCTCCAGTACAGCCAGTACCAGATACGCTGGAACTTCCCGAGCC 71
QY 61 ATGGCTTCCTGGGGGAGATCTCTTCTTGAGACATAATTAGATCATATTATTTGGGCT 120

Db 72 ATGGCTTCCCTGGGGAGATCTCTTCTGGAGCATTAATAGCATCATCATTTATCTGGCT 131
|||
Qy 121 GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAGTCACT 180
|||
Db 132 GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAGTCACT 191
|||
Qy 181 ACTGTGCTCAGCTGGGAAACATTGGGGAGATGGAAATCCGAGCTGCACTTTTGAACCT 240
|||
Db 192 ACTGTGCTCAGCTGGGAAACATTGGGGAGATGGAAATCCGAGCTGCACTTTTGAACCT 251
|||
Qy 241 GACATCAAACTTTCTGATATCGTATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 300
|||
Db 252 GACATCAAACTTTCTGATATCGTATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 311
|||
Qy 301 CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAATGTTTCAAGGCCGG 360
|||
Db 312 CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAATGTTTCAAGGCCGG 371
|||
Qy 361 ACAGCAGTGTTCCTGATCAAGTATGTTGGCAATGCTCTTGGCGGCTGAAGAACGTG 420
|||
Db 372 ACAGCAGTGTTCCTGATCAAGTATGTTGGCAATGCTCTTGGCGGCTGAAGAACGTG 431
|||
Qy 421 CAACTCAGAGTCTGGCAGCTTACAAATGTTATATCATCT 462
|||
Db 432 CAACTCAGAGTCTGGCAGCTTACAAATGTTATATCATCT 473
|||

RESULT 4
BP255229 584 bp mRNA linear EST 16-SEP-2004
LOCUS BP255229 Sugano cDNA library kidney epithelial cell Homo sapiens
DEFINITION cDNA clone HRC08590, mRNA sequence.
ACCESSION BP255229
VERSION BP255229.1 GI:52170459
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 584)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison in the promoter regions
block structure in the promoter reveals a homologous

AUTHORS

Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

JOURNAL

Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

1..584
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC08590"
/tissue_type="kidney"
/cell_type="epithelial cell"
/clone_lib="Sugano cDNA library, kidney epithelial cell"

ORIGIN

Query Match 99.7%; Score 460.4; DB 5; Length 584;
Best Local Similarity 99.8%; Pred. No. 2.5e-129;
Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGGAGGCGGAGCTCCAGTCCAGGAGTACCCAGATACGCTGGAACTTCCCGAGCC 60
|||
Db 11 GGAAGGAGGCGGAGCTCCAGTCCAGGAGTACCCAGATACGCTGGAACTTCCCGAGCC 70
|||
Qy 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGAGCATTAATAGCATCATCATTTATCTGGCT 120
|||
Db 71 ATGGCTTCCCTGGGGGAGATCTCTTCTGAGCATTAATAGCATCATCATTTATCTGGCT 130
|||

Qy 121 GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAGTCACT 180
|||
Db 131 GGAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAGTCACT 190
|||
Qy 181 ACTGTGCTCAGCTGGGAAACATTGGGGAGATGGAAATCCGAGCTGCACTTTTGAACCT 240
|||
Db 191 ACTGTGCTCAGCTGGGAAACATTGGGGAGATGGAAATCCGAGCTGCACTTTTGAACCT 250
|||
Qy 241 GACATCAAACTTTCTGATATCGTATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 300
|||
Db 251 GACATCAAACTTTCTGATATCGTATCAATGCTGAAAGGATGTTTAAAGCTTGGTC 310
|||
Qy 301 CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAATGTTTCAAGGCCGG 360
|||
Db 311 CATGAGTTCAAGAAGGCAAGATGAGCTGCGAGCAGATGAATGTTTCAAGGCCGG 370
|||
Qy 361 ACAGCAGTGTTCCTGATCAAGTATGTTGGCAATGCTCTTGGCGGCTGAAGAACGTG 420
|||
Db 371 ACAGCAGTGTTCCTGATCAAGTATGTTGGCAATGCTCTTGGCGGCTGAAGAACGTG 430
|||
Qy 421 CAACTCAGAGTCTGGCAGCTTACAAATGTTATATCATCT 462
|||
Db 431 CAACTCAGAGTCTGGCAGCTTACAAATGTTATATCATCT 472
|||

RESULT 5
CD686218 578 bp mRNA linear EST 25-JUN-2003
LOCUS CD686218
DEFINITION EST2739 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD686218
VERSION CD686218.1 GI:32202914
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 578)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

AUTHORS

1 (bases 1 to 578)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

JOURNAL

Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

FEATURES

1..578
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 99.3%; Score 458.8; DB 6; Length 578;
Best Local Similarity 99.6%; Pred. No. 7.6e-129;
Matches 460; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAAGGAGGCGGAGCTCCAGTCCAGGAGTACCCAGATACGCTGGAACTTCCCGAGCC 60
|||
Db 51 GGAAGGAGGCGGAGCTCCAGTCCAGGAGTACCCAGATACGCTGGAACTTCCCGAGCC 110
|||
Qy 61 ATGGCTTCCCTGGGGGAGATCTCTTCTGAGCATTAATAGCATCATCATTTATCTGGCT 120
|||
Db 111 ATGGCTTCCCTGGGGGAGATCTCTTCTGAGCATTAATAGCATCATCATTTATCTGGCT 170
|||
Qy 121 GGAAGCAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGAGACACTCCATCAGTCACT 180
|||

```

Db      171 GGAGCAATTGCACTCATTCATTGGCTTCGGATTTTCAGGGAGACATCCATCAAGTCACT 230
Qy      181 ACTGTCGCTCAGCTGAGGAACATTTGGGGAGATGGAATCTTGAGCTGCACCTTTGAACCT 240
Db      231 ACTGTCGCTCAGCTGAGGAACATTTGGGGAGATGGAATCTTGAGCTGCACCTTTGAACCT 290
Qy      241 GACATCAAACTTTCTGATATCGTATACAAATGGCTGAAGAAAGTGTCTTTAGGCTTGTC 300
Db      291 GACATCAAACTTTCTGATATCGTATACAAATGGCTGAAGAAAGTGTCTTTAGGCTTGTC 350
Qy      301 CATGACTTCAAAAGAGCAAGATGAGCTGTGCGAGCAGATGAAATGTTTCAGAGCCGG 360
Db      351 CATGACTTCAAAAGAGCAAGATGAGCTGTGCGAGCAGATGAAATGTTTCAGAGCCGG 410
Qy      361 ACAGCAGTGTTCGTGATCAAGTGAATGTTGGCAATGCTCTTTGGGGCTGAAAAACGTG 420
Db      411 ACAGCAGTGTTCGTGATCAAGTGAATGTTGGCAATGCTCTTTGGGGCTGAAAAACGTG 470
Qy      421 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 462
Db      471 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 512

```

```

RESULT 6
BP275659 580 bp mRNA linear EST 16-SEP-2004
LOCUS BP275659 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION
BP275659 Sugano cDNA library, kidney Homo sapiens cDNA clone
ACCESSION
BP275659
VERSION
BP275659.1 GI:52189391
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE
1 (bases 1 to 580)
Suzuki.Y., Yamashita.R., Shirota.M., Sakakibara.Y., Chiba.J.,
Mizushima-Sugano.J., Nakai.K. and Sugano.S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

```

```

FEATURES
source
1..580
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KDN04132"
/issue_type="kidney"
/clone_lib="Sugano cDNA library, kidney"

```

```

ORIGIN
Query Match 95.2%; Score 440; DB 5; Length 580;
Best Local Similarity 98.3%; Pred. No. 4.3e-123;
Matches 454; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```

```

Qy      1 GGAAGCAGCAGCAGCTCCAGCTCAGCAGATACCCAGATACGCTGGAACTTCCAGCC 60
Db      13 GGAAGCAGCAGCAGCTCCAGCTCAGCAGATACCCAGATACGCTGGAACTTCCAGCC 72
Qy      61 ATGCGCTTCCTGGGAGATCTCTTCTGAGCATAATTAATGATCAATTAATTCGCT 120
Db      73 ATGCGCTTCCTGGGAGATCTCTTCTGAGCATAATTAATGATCAATTAATTCGCT 132
Qy      121 GGAGCAATTCGACTCATTCATTTGGCTTTGGATTTTCAGGAGACATCCATCAAGTCACT 180
Db      133 GGAGCAATTCGACTCATTCATTTGGCTTTGGATTTTCAGGAGACATCCATCAAGTCACT 192

```

```

Qy      181 ACTGTCGCTCAGCTGAGGAACATTTGGGGAGATGGAATCTTGAGCTGCACCTTTGAACCT 240
Db      193 ACTGTCGCTCAGCTGAGGAACATTTGGGGAGATGGAATCTTGAGCTGCACCTTTGAACCT 252
Qy      241 GACATCAAACTTTCTGATATCGTATACAAATGGCTGAAGAAAGTGTCTTTAGGCTTGTC 300
Db      253 GACATCAAACTTTCTGATATCGTATACAAATGGCTGAAGAAAGTGTCTTTAGGCTTGTC 312
Qy      301 CATGACTTCAAAAGAGCAAGATGAGCTGTGCGAGCAGATGAAATGTTTCAGAGCCGG 360
Db      313 CATGACTTCAAAAGAGCAAGATGAGCTGTGCGAGCAGATGAAATGTTTCAGAGCCGG 372
Qy      361 ACAGCAGTGTTCGTGATCAAGTGAATGTTGGCAATGCTCTTTGGGGCTGAAAAACGTG 420
Db      373 ACAGCAGTGTTCGTGATCAAGTGAATGTTGGCAATGCTCTTTGGGGCTGAAAAACGTG 432
Qy      421 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 462
Db      433 CAACTCAGAGATGCTGGACCTTACAAATGTTATATCATCACT 473

```

```

RESULT 7
BX358434 767 bp mRNA linear EST 08-APR-2004
LOCUS BX358434 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION
clone CSODI039YG21 5-PRIME, mRNA sequence.
ACCESSION
BX358434
VERSION
BX358434.2 GI:46285747
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE
1 (bases 1 to 767)
Li.W.B., Gruber.C., Jeesee.J. and Polayes.D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30366215.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, web : www.genoscope.cns.fr

```

```

JOURNAL
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
742.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CSODI039AD11QP1&c=742.r.

```

```

FEATURES
source
1..767
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI039YG21"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/issue_type="PLACENTA COT 25-NORMALIZED"

```

```

ORIGIN
Query Match 90.6%; Score 418.6; DB 5; Length 767;
Best Local Similarity 98.9%; Pred. No. 1.7e-116;
Matches 432; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

```

Qy      26 CCAATACCAATGAGTGTGGGAACCTTCCCGCAGCATGGCTTCTGGGGCAGATCTCT 85
Db      1 CCGGATTCAGATACGCTGGGA-CTTCCCGCAGCATGGCTTCTGGGGCAGATCTCT 59
Qy      86 TCTGGAGCAATTAATGATCATCATTAATTTGGCTGAGCAATTCAGTCAATTTGCT 145

```

Db 60 TCTGAGCATATTAGCATCATATTATTGGGAGCAATGCACTCATATTGGCT 119
Qy 146 TTGGTATTTCAGGAGACATCTCATACAGTCACTACTGTGGCTCAGCTGGAAATG 205
Db 120 TTGGTATTTCAGGAGACATCTCATACAGTCACTACTGTGGCTCAGCTGGAAATG 179
Qy 206 GGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAATCTTGATATCGTA 265
Db 180 GGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAATCTTGATATCGTA 239
Qy 266 TACATGCTGAGAGAGAGTGTGTTAGGCTTGTCATGATTCGAAAGAGCAAGATG 325
Db 240 TACATGCTGAGAGAGAGTGTGTTAGGCTTGTCATGATTCGAAAGAGCAAGATG 299
Qy 326 AGCTGTCGAGACAGATGAATGTTGAGAGCCGAGACAGAGTGTGTCATCAAGTGA 385
Db 300 AGCTGTCGAGACAGATGAATGTTGAGAGCCGAGACAGAGTGTGTCATCAAGTGA 359
Qy 386 TAGTTGGCAATGCTCTTGGGCTGAAAAAGTGCACATCAAGATGCTGGCACTTCA 445
Db 360 TAGTTGGCAATGCTCTTGGGCTGAAAAAGTGCACATCAAGATGCTGGCACTTCA 419
Qy 446 AATGTTATATCATCACT 462
Db 420 AATGTTATATCACTCACT 436

RESULT 8
CN259813 714 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600041697 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN259813
ACCESSION CN259813.1 GI:47276227
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 714)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.

TITLE
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL
Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 714 Std Error: 0.00.

FEATURES
source
Location/Qualifiers
1..714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Query Match 89.6%; Score 414; DB 7; Length 714;
Best Local Similarity 100.0%; Pred. No. 4.2e-115;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
49 CCTTCCAGCAGATGGCTTCCCTGGGAGATCTCTTGGAGCATATATAGCATATC 108
|||||

Db 1 CCTTCCAGCAGATGGCTTCCCTGGGAGATCTCTTGGAGCATATATAGCATATC 60
Qy 109 ATTATTTGCTGGAGCAATTGCACTATATTGGCTTTGGTATTTCAGGAGACATCTCC 168
Db 61 ATTATTTGCTGGAGCAATTGCACTATATTGGCTTTGGTATTTCAGGAGACATCTCC 120
Qy 169 ATCAGAGCTACTATGTCGCTGAGCTGGGAGCAATGGGAGGATGGAAATCTGAGCTGC 228
Db 121 ATCAGAGCTACTATGTCGCTGAGCTGGGAGCAATGGGAGGATGGAAATCTGAGCTGC 180
Qy 229 ACTTTGACCTGACATCAACTTTCTGATATCTGTATACATGCTGAAAGAGTGT 288
Db 181 ACTTTGACCTGACATCAACTTTCTGATATCTGTATACATGCTGAAAGAGTGT 240
Qy 289 TTAGGCTTGGTCCATGAGTTCAAAAGAGCAAGATGAGTGTGAGCAGAGATGAATG 348
Db 241 TTAGGCTTGGTCCATGAGTTCAAAAGAGCAAGATGAGTGTGAGCAGAGATGAATG 300
Qy 349 TTGAGAGCCGAGACAGAGTGTGTCATCAAGTATAGTGGCAATGCTCTTGGCGG 408
Db 301 TTGAGAGCCGAGACAGAGTGTGTCATCAAGTATAGTGGCAATGCTCTTGGCGG 360
Qy 409 CTGAAAAAGCTGCACTCAGATGCTGGACCTTCAATGTTATATCATCACT 462
Db 361 CTGAAAAAGCTGCACTCAGATGCTGGACCTTCAATGTTATATCATCACT 414

RESULT 9
BF680206 845 bp mRNA linear EST 21-DEC-2000
LOCUS 602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5',
DEFINITION BF680206
ACCESSION BF680206.1 GI:11954101
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 845)
NIH-MGC http://mgc.ncl.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strauberg, Ph.D.
Email: c9abds-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM147 row: d column: 16
High quality sequence stop: 657.

FEATURES
source
Location/Qualifiers
1..845
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4295775"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: Prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgcgtcggcc); Site 2: SfiI
(ggcctatcgcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGACC-3'
and 3' adaptor sequence:
5'-ATCTAGAGCCAGGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN

Query Match 77.6%; Score 358.6; DB 2; Length 845;
Best Local Similarity 83.4%; Pred. No. 3.9e-98;
Matches 458; Conservative 0; Mismatches 4; Indels 87; Gaps 1;

```
QY 1 GGAAGCAGCGGAGCTCCACTGAGCAGTACCAGATAGCTGGGAACTTCCCGAGCC 60
  |||||
DB 14 GGAAGCAGCGGAGCTCCACTGAGCAGTACCAGATAGCTGGGAACTTCCCGAGCC 73
  |||||
QY 61 ATGGCTTCCCTGGGCGAGATCTCTTCTGGAGATTAATGATCATCATTTCTGGCT 120
  |||||
DB 74 ATGGCTTCCCTGGGCGAGATCTCTTCTGGAGATTAATGATCATCATTTCTGGCT 133
  |||||
QY 121 GGAGCAATGCACTCATCTGCTTGGCTTGG----- 148
  |||||
DB 134 GGAGCAATGCACTCATCTGCTTGGCTTGGTAATTTCAGAACTCTCTGCTTGGCAAA 193
  |||||
QY 149 -----GTAAT 153
  |||||
DB 194 TGAAGGTTGGTGAAGTTCAGAGCTTCCCTTAGCATGATCTTGGCTTCTGAACT 253
  |||||
QY 154 TCAGGAGACATCTCCATCAGTCACTACTGTGCTCAGCTGGAACTTGGGAGAT 213
  |||||
DB 254 GCAAGGAGACATCTCCATCAGTCACTACTGTGCTCAGCTGGAACTTGGGAGAT 313
  |||||
QY 214 GGAATCCTGAGCTGCACTTTTGAACCTGATCAAACTTCTGATATCGTATACATGG 273
  |||||
DB 314 GGAATCCTGAGCTGCACTTTTGAACCTGATCAAACTTCTGATATCGTATACATGG 373
  |||||
QY 274 CTGAAGAGAGTGTGTTAGGCTTGTGTCATGATTCAGAAAGCAAAAGATGAGCTGC 333
  |||||
DB 374 CTGAAGAGAGTGTGTTAGGCTTGTGTCATGATTCAGAAAGCAAAAGATGAGCTGC 433
  |||||
QY 334 GAGCAGATGAATGTTCAAGGCGGACGACAGTGTCTGATCAAGTATGTTGGC 393
  |||||
DB 434 GAGCAGATGAATGTTCAAGGCGGACGACAGTGTCTGATCAAGTATGTTGGC 493
  |||||
QY 394 AATGCCCTTGGGCGTGAAGAAAGTGAACCTCAAGATGCTGGCACTTCAAAATGTTAT 453
  |||||
DB 494 AATGCCCTTGGGCGTGAAGAAAGTGAACCTCAAGATGCTGGCACTTCAAAATGTTAT 553
  |||||
QY 454 ATCATCACT 462
  |||||
DB 554 ATCATCACT 562
  |||||
```

RESULT 10
CR603772 2431 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1039YG21 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR603772
VERSION CR603772.1 GI:50484579
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Fairway Avenue
Genoscope.
2 (bases 1 to 2431)
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a Noci-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source

1..2431
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1039YG21"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 68.3%; Score 315.4; DB 3; Length 2431;
Best Local Similarity 96.7%; Pred. No. 9.3e-85;
Matches 322; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
QY 130 GCATCATCATTTGGCTTGGTATTTTCAGGAGACACTCCATCAGTCACTGCTGCC 189
  |||||
DB 1 GCATCATCATTTGGCTTGGTATTTTCAGGAGACACTCCATCAGTCACTGCTGCC 60
  |||||
QY 190 TCAGCTGGGAAATGCGGAGAGATGAATCCAGCTGCACTTTGAACCTGATCAAA 249
  |||||
DB 61 TCAGCTGGGAAATGCGGAGAGATGAATCCAGCTGCACTTTGAACCTGATCAAA 120
  |||||
QY 250 CTTTCTGATATGCTGATATCAATGCTGGAAGAGTGTGTTAGGCTTGGTCCATGTTTC 309
  |||||
DB 121 CTTTCTGATATGCTGATATCAATGCTGGAAGAGTGTGTTAGGCTTGGTCCATGTTTC 180
  |||||
QY 310 AAAGAGGCAAAAGATGAGCTGTGCGAGCAGATGAATGTTTGAAGGCCGAGACAGCTG 369
  |||||
DB 181 AAAGAGGCAAAAGATGAGCTGTGCGAGCAGATGAATGTTTGAAGGCCGAGACAGCTG 240
  |||||
QY 370 TTTTCTGATCACTGATATTTTGGCAATGCTCTTTGGCGCTGAAGAAAGTGAACCTCACA 429
  |||||
DB 241 TTTTCTGATCACTGATATTTTGGCAATGCTCTTTGGCGCTGAAGAAAGTGAACCTCACA 300
  |||||
QY 430 GATGCTGCACCTACCAATGTTATATCATCACT 462
  |||||
DB 301 GATGCTGCACCTACCAATGTTATATCATCACT 333
  |||||
```

RESULT 11
BB666051 670 bp mRNA linear EST 26-OCT-2001
LOCUS BB666051
DEFINITION BB666051 RIKEN full-length enriched, 2 days pregnant adult female
cviduct Mus musculus cDNA clone B230029B13 5', mRNA sequence.
ACCESSION BB666051
VERSION BB666051.1 GI:16499684
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ono, M., Okazaki, T., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
JOURNAL Unpublished (2001)
REMARK Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

Wagti, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wachihi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.,

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.,

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamataka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.,

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome*, 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

```

Location/Qualifiers
1. 670
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="E230029B13"
/sex="female"
/tissue_type="oviduct"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/clone_id="Riken full-length enriched, 2 days pregnant adult female oviduct"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15',
GAGGAGAGAGCGGCCGCCACATCTGACATTTTITTTTTTTTTTNN 3'), cDNA was prepared by using triethanol thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trisep. Second strand cDNA was prepared with the primer adapter of sequence 15',
GAGGAGAGGATTCCTCCAGTAAATTAATTAATTAATCCCCCCCCCCC 3'). cDNA was cleaved with BamHI and XhoI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda PUC I."

```

ORIGIN

Query Match	65.5%	Score 302.8;	DB 2;	Length 670;
Best Local Similarity	83.7%	Pred. No. 4.3e-81;		
Matches 343; Conservative	0;	Mismatches 67;	Indels 0;	Gaps 0

[illegible]

QY	292	GGCTTGGTCATGAGTTCAAAAGAGGCCAAATATAGCTGTGCGAGCAGATGAAAGTTC	351
Db	333	GGTTTGGTCAAGAGTTCAAGAAAGCCAAACGACTCTCAGCAGCAGATGAGAGTTC	392
QY	352	AGAGGCCGCGACAGAGTTTGTGTCGATCAATGATGATGGCAATGCTCTTTGGCGCTG	411
Db	393	AGAGGCCGCGACAGAGTTTGTGTCGATCAAGTGTGATGTGCATATGCTTCTCTGAGACTG	452
QY	412	AAAAAGTGCACACTCAGAGATGCTGGCAGCTCAAAATGTTATATATCATCAC	461
Db	453	AAAAAGTGCACACTCAGAGATGCTGGCAGCTCAACATGTATCATCTCGCAC	502

RESULT 12

LOCUS	BY736335	702 bp	mRNA	linear	EST 17-DEC-2002
DEFINITION	BY736335 RIKEN full-length enriched, cDNA clone 11c0027j19 5', mRNA sequence.				
ACCESSION	BY736335				
VERSION	BY736335.1	GI:27149462			
KEYWORDS	EST.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Mus musculus				

Takeda, Y., Takaki, K., Watabiki, A., Muramatsu, M. and Haysliaki, Y. Direct Submission. Computational Analysis of Full-length cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 672-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

```
FEATURES
    source
        Location/Qualifiers
            1..702
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="T1C0027019"
                /dev_stage="blastocyst"
                /clone_lib="RIKEN full-length enriched, blastocyst"
```

Query Match	65.5%;	Score 302.8;	DB 6;	Length 702;
Best Local Similarity	83.7%;	Pred. No. 4.4e-81;		
Matches 343; Conservative	0;	Mismatches 67;	Indels 0;	Gaps 0

QY	52	TTCCGAGCCATGGCTCCCTGGGGGAGATCCCTCTGAGACATTAATGATCATCATTT	111
Db	92	TCCCTCTCATGGCTTCTCTTGGGGGAGATCATCTTTTGAAGTATTTATTAACATCATATC	151
QY	112	ATTCTGGCTGAGACATTTGCACTCATATCTGGCTTTGGTATTTTCAGGAGAGACATCCATC	171
Db	152	ATCTGGCTGGGGGCCATGCGACATCATATGGCTTTGGCATTTTCAGGAGAGACATTCATC	211
QY	172	ACAGTCACTACTGTCCCTCAGCTGGGAACATTTGGGGAGATGGAATCTGAGCTGCATC	231
Db	212	ACGGTACACACTTTCACCTCAGCTGGAAACATTTGAGAGGAGCGGAGCCCTGAGCTGCATC	271
QY	232	TTTGAACCTGACATCAAACTTTCTGATATCGTATACATATGGCTGAGAGAGAGGTGTTTA	291
Db	272	TTTGAACCTGACATCAAACTTCAACGGCATCGTCACTCCAGTGGCTGGAAGAGGSCATAAA	331
QY	292	GGCTTGCTCATATGTTTCAAAGAGGCAAAAGATGAGCTGTGGAGACGAGATGAATGTTTC	351
Db	332	GGTTTGCTCAAGATTTCAAGAGAGGCAAAAGACGACCTCTACAGCAGCATGAGATGTTTC	391
QY	352	AGAGGCCGAGACAGCACTGTTTGCTGATCAAGTATGATGTTGGCAATGCTCTTTGCGGCTG	411
Db	392	AGAGGCCGAGACAGCACTGTTTGCTGATCAGGCTGATGTTGGCAATGCTCTCCCTGAGACTG	451
QY	412	AAAAAGTGCACACTCAGATCTGTGGCACTTACAAATTTATATATATATTTT	461
Db	452	AAAAAGTGCACACTCAGATCTGTGGCACTTACCAATGTTATATCTCGAC	501

RESULT 13					
B1454643					
LOCUS					
DEFINITION	B1454643	757 bp	mRNA	linear	EST 21-AUG-2000
ACCSSION	603170558F1	NCI_GCAP	Mam5 Mus musculus	cDNA clone IMAGE:5250177	5'
VERSION	B1454643				
KEYWORDS	B1454643.1	GI:15245299			
SOURCE	EST.				
	Mus musculus (house mouse)				

ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT
Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 757)	
NIH-MGC http://mgc.nci.nih.gov/	
National Institutes of Health, Mammalian Gene Collection (MGC)	
Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: cgsab@nci.nih.gov	
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be	
found through the I.M.A.G.E. Consortium/LNL at:	
http://image.llnl.gov	
plate: LHAM1631 row: k column: 10	
High quality sequence stop: 742.	
Location/Qualifiers	
source	
1..757	

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5250177"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_idb="NCI CGAP Mam5"
/notes="Organ: mammary; Vector: PMV-SPORT6; Site: 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by life technologies. Investigators providing samples: Lochar Hennighausen/Robin Humphreys, NIH"

```

Query Match	65.5%	Score 302.8	DB 4	Length 757
Best Local Similarity	83.7%	Prod. No. 4,5e-81		
Matches 343	Conservative 0	Mismatches 67	Indels 0	Gaps 0
QY	52	TCGCCAGCCATGCGCTTCCCTGGGGGAGATCCTCTTCTGGAGCATTAATTAGCATCATCATTT	111	
Db	63	TCCTCTCCATGCGCTTCTGGGGGAGATCATCTTTTGGAGTATTAATTAATCATCATCATC	122	
QY	112	ATTCTGGCTGGAGCAATTGCACTCATCATATTGGCTTTGGTATTTACAGGAGACACTCCATC	171	
Db	123	ATCTGGCTGGGGGCATTCGCACTCATCATATTGGCTTTGGCATTTTCAGGCAAGCACTTCATC	182	
QY	172	ACAAGTCACTACTGTGCGCTCAGCTGGGACATTGGGGAGAGATGGAATCTCTGAGCTGACT	231	
Db	183	ACGCTACAGCACTTTCACCTCAGCTGGGAAATTGGAGAGAGACGGGACCTCTGAGCTGACT	242	
QY	232	TTTGAACCTGACATCCAAACTCTTCTGATATCGTATACATATGAGTGGTGAAGGAGGTGTTTA	291	
Db	243	TTTGAACCTGACATCCAAACTCAAGGAGATCGTATACATGAGTGGTGAAGGAGGATCAAA	302	
QY	292	GGCTTGGTCCATGATGTTCAAGAAGGCAAAAGATGAGCTGTCCGAGCAGGATGAAATGTTTC	351	
Db	303	GGTTTGGTCCACAGTTCAAAGGAGGAAAGGACGACCTTCACAGCAGCATGAGATGTTTC	362	
QY	352	AGAGGCGGAGACAGAGTGTGGCTGATCAAGTATAGTTGGCAATGCCCTTTGGCGGCTG	411	
Db	363	AGAGGCGGAGACAGAGTGTGGCTGATCAAGTATAGTTGGCAATGCTTCCCTGAGACTG	422	
QY	412	AAAAAGCTGCACTCACAGATGCTGGGACCTTACAAATGTTATATCATCAC	461	
Db	423	AAAAAGCTGAGCTCACAGATGCTGGGACCTTACAAATGTTATATCTCGCAC	472	

RESULT	14
CV079354	
LOCUS	
DEFINITION	
AGENCOCURT_31473506	827 bp mRNA linear EST 25-AUG-2004
NIH_MGC_251	Rattus norvegicus cDNA clone

Search completed: May 31, 2005, 00:10:57
Job time : 1798.88 secs

```
FEATURES
source
location/Qualifiers
1..2627
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
```

ORIGIN

Query Match 90.6%; Score 806.4; DB 6; Length 2627;
Best Local Similarity 91.9%; Pred. No. 8.8e-239;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTTCATCTCTGCGTGAACAGCTTAAGACTTCAATTA 60
DB 1721 CAAGCTGAGGCTTCTCTTTCATCTCTGCGTGAACAGCTTAAGACTTCAATTA 1780
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGTGATTTCCGCCCATCTCCGGGGAAATGTC 120
DB 1781 GCATCTAGAGCAGTGGGACTCAGCTGGGTGATTTCCGCCCATCTCCGGGGAAATGTC 1840
QY 121 TGAAGACAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB 1841 TGAAGACAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTGTCTACCAAC 1900
QY 181 NNNCAT 240
DB 1901 TAGTGATTAAGGCCAGGGATGCTGTCAACTCTACCATGTACAGAGCGTCTCCCAT 1960
QY 241 TACAATCACTCCCAATCCGAAGTGTCACTGTCTAGAGCTTAAGAAACCTGTGTTTGAATA 300
DB 1961 TACAATCACTCCCAATCCGAAGTGTCACTGTCTAGAGCTTAAGAAACCTGTGTTTGAATA 2020
QY 301 GAAAAGGCGCTGGGAAAGAGGGAGCAACAATCTGTCTGCTCTCAATTAATGTCATT 360
DB 2021 GAAAAGGCGCT-GGAAAAGGGAGGAGCCAAATCTGTCTGCTCTCAATTAATGTCATT 2079
QY 361 GGGAAATAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 2080 GGGAAATAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
QY 421 GGGCAACAGGATTAACATCTCTCACTGAAACAGAGTTGACAAAGGCTTAAGGAAATGCCCTGA 480
DB 2140 GGGCAACAGGATTAACATCTCTCACTGAAACAGAGTTGACAAAGGCTTAAGGAAATGCCCTGA 2199
QY 481 TGGGATTAATCTTCAGCTTGTGAGCTTCTTAAGTTCTTCCCTCAATTCACCTGCAAG 540
DB 2200 TGGGATTAATCTTCAGCTTGTGAGCTTCTTAAGTTCTTCCCTCAATTCACCTGCAAG 2259
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTAATTTAGA 600
DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTAATTTAGA 2319
QY 601 TCTCCAGACCTGCTGGCCCAATTCAAATTAAGGCAACAAATATACCTTCATGAA 660
DB 2320 TCTCCAGACCTTCTGGCCCAATTCAAATTAAGGCAACAAATATACCTTCATGAA 2379
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTGAAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTGAAGAAATG 2439
QY 721 AAGCTTTGAAGAAAAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 780
DB 2440 AAGCTTTGAAGAAAAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 2499
QY 781 ACCACTGCTTCTGAGACTTGGAGCCAGGCTGACTGTATTAATGTTTGAAGAAAC 840
DB 2500 ACCACTGCTTCTGAGACTTGGAGCCAGGCTGACTGTATTAATGTTTGAAGAAAC 2559
QY 841 TGAATTTAGAGTTCTGATGCTCAAGAGAAATGATTAATATACATTTCT 890
DB 2560 TGAATTTAGAGTTCTGATGCTCAAGAGAAATGATTAATATACATTTCT 2609

RESULT 2
AR238405 2627 bp DNA linear PAT 20-DEC-2002
LOCUS AR238405
DEFINITION Sequence 391 from patent US 6468546.
ACCESSION AR238405
VERSION AR238405.1 GI:27283369

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2627)
AUTHORS Mitcham, J.L., King, G.E. and Algate, P.A.
TITLE Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6468546-A 391 22-OCT-2002;
FEATURES
source location/Qualifiers
1..2627
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 90.6%; Score 806.4; DB 6; Length 2627;
Best Local Similarity 91.9%; Pred. No. 8.8e-239;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTGAGGCTTCTCTTTCATCTCTGCGTGAACAGCTTAAGACTTCAATTA 60
DB 1721 CAAGCTGAGGCTTCTCTTTCATCTCTGCGTGAACAGCTTAAGACTTCAATTA 1780
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGTGATTTCCGCCCATCTCCGGGGAAATGTC 120
DB 1781 GCATCTAGAGCAGTGGGACTCAGCTGGGTGATTTCCGCCCATCTCCGGGGAAATGTC 1840
QY 121 TGAAGACAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB 1841 TGAAGACAATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGTGTCTACCAAC 1900
QY 181 NNNCAT 240
DB 1901 TAGTGATTAAGGCCAGGGATGCTGTCAACTCTACCATGTACAGAGCGTCTCCCAT 1960
QY 241 TACAATCACTCCCAATCCGAAGTGTCACTGTCTAGAGCTTAAGAAACCTGTGTTTGAATA 300
DB 1961 TACAATCACTCCCAATCCGAAGTGTCACTGTCTAGAGCTTAAGAAACCTGTGTTTGAATA 2020
QY 301 GAAAAGGCGCTGGGAAAGAGGGAGCCAAATCTGTCTGCTCTCAATTAATGTCATT 360
DB 2021 GAAAAGGCGCT-GGAAAAGGGAGGAGCCAAATCTGTCTGCTCTCAATTAATGTCATT 2079
QY 361 GGGAAATAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 2080 GGGAAATAAGCAATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2139
QY 421 GGGCAACAGGATTAACATCTCTCACTGAAACAGAGTTGACAAAGGCTTAAGGAAATGCCCTGA 480
DB 1961 TACAATCACTCCCAATCCGAAGTGTCACTGTCTAGAGCTTAAGAAACCTGTGTTTGAATA 2020
QY 481 TGGGATTAATCTTCAGCTTGTGAGCTTCTTAAGTTCTTCCCTCAATTCACCTGCAAG 540
DB 2200 TGGGATTAATCTTCAGCTTGTGAGCTTCTTAAGTTCTTCCCTCAATTCACCTGCAAG 2259
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTAATTTAGA 600
DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTAATCTGTAATTTAGA 2319
QY 601 TCTCCAGACCTGCTGGCCCAATTCAAATTAAGGCAACAAATATACCTTCATGAA 660
DB 2320 TCTCCAGACCTTCTGGCCCAATTCAAATTAAGGCAACAAATATACCTTCATGAA 2379
QY 661 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTGAAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGCAAGCAATGACTGCTTGAATGAGGCTTGAAGAAATG 2439
QY 721 AAGCTTTGAAGAAAAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 780
DB 2440 AAGCTTTGAAGAAAAAATACTTTGTTTCCAGCCCCCTTCCACACTCTTCATGTGTTA 2499
QY 781 ACCACTGCTTCTGAGACTTGGAGCCAGGCTGACTGTATTAATGTTTGAAGAAAC 840

Db	2500	ACCAATGCGCTTCTCTGGACCTTGGACCCACCGGAGCTGATTACATGTTGTTATAGAAAC	2553
Qy	841	TGATTTAGAGTCTTGATGCTTCAAGAGAATGATTAATATACATTTTCT	890
Db	2560	TGATTTTAGAGTCTTGATGCTTCAAGAGAATGATTAATATACATTTTCT	2609
RESULT 3			
LOCUS	AR478744	2627 bp	DNA
DEFINITION	Sequence 391 from patent US 6699664.		linear
ACCESSION	AR478744		
VERSION	AR478744.1	GI:47237396	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2627)		
TITLE	Mitcham,J.L., King,G.E., Algate,P.A., Pling,S.P., Reter,M.W., Fanger,G.R., Reed,S.G., Vedvik,T.S. and Carter,D. Comparisons and methods for the therapy and diagnosis of ovarian cancer		
JOURNAL	Patent: US 6699664-A 391 02-MAR-2004;		
FEATURES	Location/Qualifiers		
source	1..2627 /organism="unknown" /mol_type="genomic DNA"		
ORIGIN			
Query Match	90.6%; Score 806.4; DB 6; Length 2627;		
Best Local Similarity	91.9%; Pred. No. 8.8e-239;		
Matches	818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;		
Qy	1	CAAGCTTGAGGCTTCTCTTCCATCTCTGCGTGACAGCTAAGACCTCAGTTTCAATA	60
Db	1721	CAAGCTTGAGGCTTCTCTTCCATCTCTGCGTGAGACGTAAGACCTCAGTTTCAATA	1780
Qy	61	GCATCTAAGAGAGTGGGACCTCAGCTGGGGGTATTTGGCCCCCATCTCCGGGGGAATGTC	120
Db	1781	GCATCTAAGAGAGTGGGACCTCAGCTGGGGGTATTTGGCCCCCATCTCCGGGGGAATGTC	1840
Qy	121	TGAAGACATTTTGGTTACTCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNNNN	180
Db	1841	TGAAGACATTTTGGTTACTCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC	1900
Qy	181	NN	240
Db	1901	TAGTGGATTAAGGCGCAGGATGCTGCTCAACCTCTACATGTAACAGAGCTCTCCCAT	1960
Qy	241	TACAACCTCAATCCGAAGTGTCAACGTGTGACAGGACTAGAAACCTGGTTTGAATA	300
Db	1961	TACAACCTCAATCCGAAGTGTCAACGTGTGACAGGACTAGAAACCTGGTTTGAATA	2020
Qy	301	GAAGAGGCGCTGGGAAAGAGGGGAGCCAAACAATCTGTCTGCTTCTTCAATTAAGTATT	360
Db	2021	GAAGAGGCGCT- GGAAGAGGGGAGCCAAACAATCTGTCTGCTTCTTCAATTAAGTATT	2079
Qy	361	GGCAATTAAGCATTTCTGTCTTTTGGCTGTGCTCAGACAGAGAGCCAGAACTATAC	420
Db	2080	GGCAATTAAGCATTTCTGTCTTTTGGCTGTGCTCAGACAGAGAGCCAGAACTATATC	2139
Qy	421	GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAGGCGCTATGGGAAATGGCTGA	480
Db	2140	GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAGGCGCTATGGGAAATGGCTGA	2199
Qy	481	TGGATTAATCTTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATCTACCTGCAAG	540
Db	2200	TGGATTAATCTTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCAATCTACCTGCAAG	2259
Qy	541	CCAAGTCTCTGAAGAGAAATGCTGAGTTCACGCTCAGGTTTTCTTACTGAAATTTAGA	600
Db	2260	CCAAGTCTCTGAAGAGAAATGCTGAGTTCACGCTCAGGTTTTCTTACTGAAATTTAGA	2319

[illegible]

RESULT 5				
AX366624	LOCUS	2627 bp	DNA	linear
	DEFINITION	Sequence 391 from Patent WO0206317.		
	ACCESSION	AX366624		
	VERSION	AX366624.1		
	KEYWORDS	GI:18698046		
	SOURCE			
	ORGANISM	Homo sapiens (human)		
		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE				
AUTHORS				
		Mitcham, J. L., King, G. E., Algate, P. A., Flinn, S. P., Retter, M. W.,		
		Fanger, G. R., Reed, S. G., Vedvick, T. S., Carter, D., Hill, P. and		
		Albone, E.		
TITLE				
		Compositions and methods for the therapy and diagnosis of ovarian		

[illegible]

RESULT 6	AL391476/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
	AL391476	171595 bp	Human DNA sequence from clone RP11-229A19 on chromosome 1, complete sequence.	AL391476	AL391476.20	GI:15131484	HRC.	Homo sapiens (human)				
								Homo sapiens				
								Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
								1 (bases 1 to 171595)				
								Wallis J				
								Direct Submission				
								Submitted (03-AUG-2001)	Sanger Centre, Hinxton, Cambridgeshire,			
								CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk				
								requests: clonerequest@sanger.ac.uk				

COMMENT

On Aug 9, 2001 this sequence version replaced gi:14970375. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP11-229A19 is from the library RP11-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6

This sequence is the entire insert of clone RP11-229A19 The true left end of clone RP11-287H7 is at 67254 in this sequence. The true right end of clone RP4-570D9 is at 57439 in this sequence.

FEATURES

source

```
1..171595
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-229A19"
/clone_1fb="RP11-11.1"
324..685
repeat_region
/note="LIM3 repeat: matches 5769..6141 of consensus"
745..1182
repeat_region
/note="LIMD2 repeat: matches 5890..6341 of consensus"
1261..1466
repeat_region
/note="AluX repeat: matches 1..183 of consensus"
1471..1567
repeat_region
/note="L1 repeat: matches 5042..5132 of consensus"
1568..1880
repeat_region
/note="AluX repeat: matches 1..312 of consensus"
1881..2391
repeat_region
/note="L1 repeat: matches 4471..5042 of consensus"
2392..2668
repeat_region
/note="AluY repeat: matches 1..291 of consensus"
2669..2813
repeat_region
/note="L1 repeat: matches 4336..4471 of consensus"
3066..3198
repeat_region
/note="FLAM_C repeat: matches 1..133 of consensus"
3264..3367
repeat_region
/note="MIR repeat: matches 32..134 of consensus"
3758..4064
repeat_region
/note="AluX repeat: matches 1..305 of consensus"
4312..4610
repeat_region
/note="AluX repeat: matches 1..306 of consensus"
5330..5607
repeat_region
/note="LIP45 repeat: matches 5866..6143 of consensus"
6639..6803
repeat_region
/note="MIR repeat: matches 27..189 of consensus"
7176..7218
repeat_region
/note="L2 repeat: matches 2654..2698 of consensus"
7287..7593
repeat_region
/note="MER7A repeat: matches 1..346 of consensus"
8914..8963
repeat_region
/note="MADE1 repeat: matches 31..80 of consensus"
9335..9484
repeat_region
/note="LIMC5 repeat: matches 7699..7849 of consensus"
9485..9784
repeat_region
/note="AluX repeat: matches 1..300 of consensus"
9785..9811
repeat_region
/note="LIMC5 repeat: matches 7673..7699 of consensus"
9812..9975
repeat_region
/note="FAM repeat: matches 1..170 of consensus"
9976..10469
repeat_region
/note="LIMC5 repeat: matches 7185..7673 of consensus"
11613..11858
repeat_region
/note="LIP16 repeat: matches 5857..6157 of consensus"
13950..14280
repeat_region
/note="MER44A repeat: matches 1..333 of consensus"
14390..14493
repeat_region
/note="L2 repeat: matches 2601..2705 of consensus"
16020..16325
repeat_region
/note="AluX repeat: matches 1..308 of consensus"
16726..16892
repeat_region
/note="MIR repeat: matches 79..261 of consensus"
17071..17373
repeat_region
/note="AluX repeat: matches 1..301 of consensus"
17708..18140
repeat_region
/note="MER68A repeat: matches 1..435 of consensus"
19282..19574
repeat_region
/note="AluY repeat: matches 1..294 of consensus"
19774..19904
repeat_region
/note="FLAM_A repeat: matches 1..133 of consensus"
20023..20325
repeat_region
/note="AluY repeat: matches 1..303 of consensus"
20904..21029
repeat_region
/note="AluY repeat: matches 10..136 of consensus"
22334..22596
repeat_region
/note="AluX repeat: matches 1..264 of consensus"
23089..23144
repeat_region
/note="2 copies 28 mer 98% conserved"
23310..23345
repeat_region
/note="9 copies 4 mer tgcg 94% conserved"
24358..24654
repeat_region
/note="AluX repeat: matches 1..297 of consensus"
25318..25615
repeat_region
/note="AluY repeat: matches 1..297 of consensus"
26469..26775
repeat_region
/note="AluY repeat: matches 1..304 of consensus"
31909..32321
repeat_region
/note="L2 repeat: matches 2035..2515 of consensus"
33438..33739
repeat_region
/note="AluX repeat: matches 1..302 of consensus"
35428..35499
repeat_region
/note="MIR repeat: matches 78..145 of consensus"
35687..35883
repeat_region
/note="MER58C repeat: matches 9..45 of consensus"
36245..36311
repeat_region
/note="LIMD3 repeat: matches 7674..7739 of consensus"
36338..36699
repeat_region
/note="LIMC4 repeat: matches 7558..7643 of consensus"
36702..36938
repeat_region
/note="L2 repeat: matches 1141..1372 of consensus"
37430..37621
repeat_region
/note="L2 repeat: matches 2088..2281 of consensus"
37655..38005
repeat_region
/note="L2 repeat: matches 2335..2710 of consensus"
38922..39220
repeat_region
/note="AluY repeat: matches 1..299 of consensus"
39802..39885
repeat_region
/note="3 copies 28 mer 96% conserved"
39931..40073
repeat_region
/note="MIR repeat: matches 11..157 of consensus"
40191..40247
repeat_region
/note="Charlie4 repeat: matches 1906..1961 of consensus"
40286..40363
repeat_region
/note="MIR repeat: matches 288..372 of consensus"
40657..40734
repeat_region
/note="MIR repeat: matches 28..99 of consensus"
```

Db	81543	CAACCTCGAGGGCTTCTCTTCCATCTGCGTGAAGAGCTACAGCTCAGTTTCAATA	60
Oy		GCATCTAGAGCAGTGGGACTCAGTGGGGTGATTTGCCCCCATCTCGGGGGGAATGTC	120
Db	81483	GCATCTAGAGCAGTGGGACTCAGTGGGGTGATTTGCCCCCATCTCGGGGGGAATGTC	81424
Oy	121	TGAAGACAAATTTTGTTTACCTCAATGAGGGAGTGGAGAGATACAGNNNNNNNNNNNN	180
Db	81423	TGAAGACAAATTTTGTTTACCTCAATGAGGGAGTGGAGAGATACAGTGTACTACCAAC	81364
Oy	181	NNCAT	240
Db	81363	TATGTGATAGAGCCAGGGATGCTGTCACCTTCACATGTACAGAGCGTCTCCCCAT	81304
Oy	241	TACAACCTACCCAATCCGAAGTGTCAACTGTGTGACAGCTAAGAAACCTGGTTTTGAGTA	300
Db	81303	TACAACCTACCCAATCCGAAGTGTCAACTGTGTGACAGGCTAAGAAACCTGGTTTTGAGTA	81244
Oy	301	GAAAAGGCGCTGGGAAAGAGGGGAGCCAAACAAATCTGTCTGTTCTTCACATTAGTCATT	360
Db	81243	GAAAAGGCGCT-GGAAAGAGGGGAGCCAAACAAATCTGTCTGTTCTTCACATTAGTCATT	81185
Oy	361	GGCAAAATAGCATTCTGTCTTTTGAGTGTGCTGCCTCAGACAAGAGAGCCGAATCTATATC	420
Db	81184	GGCAAAATAGCATTCTGTCTTTTGAGTGTGCTGCCTCAGACAAGAGAGCCGAATCTATATC	81125
Oy	421	GGGCAACCAAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCGCTATGGGAAATGCGCTGA	480

RESULT 7				
AX403048				
LOCUS	AX403048	2603 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO202624.			
ACCESSION	AX403048			
VERSION	AX403048.1	GI:21388028		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 Fox,G., Sullivan,J.K. and Fang,M.			
AUTHORS	B7-like molecules and uses thereof			
TITLE	Patent: WO 0205624-A 1 10-JUN-2002;			
JOURNAL	Amgen, Inc. (US)			

Query	March	Similarity	90.6%	Score	806	DB	6	Length	2603
Best	Local	Similarity	91.8%	Pred.	No.1.2e-38				
Matches	817	Conservative	1	Mismatches	71	Indels	1	Gaps	1

Qy	1	CAAGCTGAGGCTTCCTTCCTTCACATCCGCGGAGACACATAAGACTCAGTTTCATA	60
Db	1691	CAACCTGTGAGGCTTCCTTCCTTCACATCCGCGGAGACACATAAGACTCAGTTTCATA	1750

LOCUS	DEFINITION	SEQUENCE	7 FROM PATENT	WO0194641	2626 bp	DNA	linear	PAT	01-MAR-2002
AX375860	AX375860	AX375860	AX375860	1	GI:19170332				
VERSION	KEYWORDS								
SOURCE	ORGANISM								
REFERENCE	AUTHORS								
TITLE									
JOURNAL									

Gene targets and ligands that bind thereto for treatment and diagnosis of ovarian carcinomas
Patent: WO 0194641-A 7 13-DEC-2001;

FEATURES	source	Idesc Pharmaceuticals Corporation (US)	Location/Qualifiers
		1..2626	/organism="Homo sapiens"
			/mol_type="unassigned DNA"
			/db_xref="taxon:9606"
ORIGIN			
Query Match	90.4%;	Score 804.8;	DB 6; Length 2626;
Best Local Similarity	91.8%;	Pred. No. 2.8e-218;	
Matches 817;	Conservative 0;	Mismatches 72;	Indels 1; Gaps 1;
QY	1	CAAGCTGAGGCTTCTCTTCCATCTCTGCTGGAACAAGCTCACTGTTTCATA	60
DB	1699	CAAGCTGAGGCTTCTCTTCCATCTCTGCTGGAACAAGCTCACTGTTTCATA	1758
QY	61	GCATCTGAGAGTGGGAGCTCAGCTGGGGGATTGGCCCCCATCTCGGGGGAATGTC	120
DB	1759	GCATCTGAGAGTGGGAGCTCAGCTGGGGGATTGGCCCCCATCTCGGGGGAATGTC	1818
QY	121	TGAAGACAATTTGGTTACTCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNN	180
DB	1819	TGAAGACAATTTGGTTACTCTCAATGAGGAGTGGAGAGATACAGTGTACTACCAAC	1878
QY	181	NN	240
DB	1879	TAGTGATTAAGGCGCAGGAGTGTCTCAACTCTCTCACTGTAAGAGAGTCTCCCA	1938
QY	241	TACAACTAACCAATCCGAATGTCACTGTGTCAGACTAAGAAACCTGTGTTTGTA	300
DB	1939	TACAACTAACCAATCCGAATGTCACTGTGTCAGACTAAGAAACCTGTGTTTGTA	1998
QY	301	GAAAGGGGCTGGGAAAGAGGGAGCAAAATCTGTCTGCTTCTCATTAATGATTT	360
DB	1999	GAAAGGGGCT -GAAAGAGGGAGCCAAATCTGTCTGCTTCTCATTAATGATTT	2057
QY	361	GGCAATTAAGCATTCTGTCTTCTTGGCTGTGCTCTGACGACAGAGGCGAACTATTC	420
DB	2058	GGCAATTAAGCATTCTGTCTTCTTGGCTGTGCTCTGACGACAGAGGCGAACTATTC	2117
QY	421	GGGACCAAGATTAACATCTCTCACTGAACAGATTTGACAGGCTATGGGAAATGCTGA	480
DB	2118	GGGACCAAGATTAACATCTCTCACTGAACAGATTTGACAGGCTATGGGAAATGCTGA	2177
QY	481	TGGATATATCTTCACTGTTTGAGCTCTTAAGTTTCTTCCCTTCATTTACCTCGAAG	540
DB	2178	TGGATATATCTTCACTGTTTGAGCTCTTAAAGTTTCTTCCCTTCATTTACCTCGAAG	2237
QY	541	CCAAATCTGTAGAGAAATGCTGAGTTTCTAGCTCAGTTTCTTACTGTGAATTTAGA	600
DB	2238	CCAAATCTGTAGAGAAATGCTGAGTTTCTAGCTCAGTTTCTTACTGTGAATTTAGA	2297
QY	601	TCTCCAGACCTGCTGCTGGCCCAATTTAAATTTAAGGCAACAACTATACCTTCATGAA	660
DB	2298	TCTCCAGACCTGCTGCTGGCCCAATTTAAATTTAAGGCAACAACTATACCTTCATGAA	2357
QY	661	GCAACACAGACTTTTAAAGCAAGACATTTGACTGTTGAATTTGAGGCTTGAAGAAATG	720
DB	2358	GCAACACAGACTTTTAAAGCAAGACATTTGACTGTTGAATTTGAGGCTTGAAGAAATG	2417
QY	721	AAGCTTTGAAGAAAGAAATACATTTGTTTTCAGACCCCTTCCCACTCTTCAATGTGTTA	780
DB	2418	AAGCTTTGAAGAAAGAAATACATTTGTTTTCAGACCCCTTCCCACTCTTCAATGTGTTA	2477
QY	781	ACCACTGCTTCTTCTGGAACCTTGAAGCCAGGTGACTGTATTAATGTTGTTAAGAAAC	840
DB	2478	ACCACTGCTTCTTCTGGAACCTTGAAGCCAGGTGACTGTATTAATGTTGTTAAGAAAC	2537
QY	841	TGATTTTGAAGTTCTGATGCTTCAAGAAATGATTTAAATTAATTTCTTCCCT	890
DB	2538	TGATTTTGAAGTTCTGATGCTTCAAGAAATGATTTAAATTAATTTCTTCCCT	2587

```
RESULT 9
LOCUS HSM808167 2671 bp mRNA linear PRI 30-AUG-2003
DEFINITION Homo sapiens mRNA; cDNA DKFZp779B1717 (from clone DKFZp779B1717).
ACCESSION BX648021
VERSION BX648021.1 GI:34367180
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 2671)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Oesanger,A., Fobo,G., Han,M. and
Wiemann,S.
CONSTRM The German Human cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp779B1717) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
source
1..2671
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cclone="DKFZp779B1717"
/rclone="DKFZp779B1717"
/rclone_type="liver"
/dh10b; sites SfiI + SfiIb"
/dev stage="fetal"
2599..2604
polyA_signal
2616
ORIGIN
Query Match 90.4%; Score 804.8; DB 9; Length 2671;
Best Local Similarity 91.8%; Pred. No. 2.8e-238;
Matches 817; Conservative 0; Mismatches 72; Indels 1; Gaps 1;
1 CAAGCTCGAGGCTTCTCTTCTTCATCTCGCTGACAGCTTAAGCTTTCATTA 60
1728 CAAGCTCGAGGCTTCTCTTCTTCATCTCGCTGACAGCTTAAGCTTTCATTA 1787
61 GCATCTAGAGCAGTGGAGCTGAGCTGGGGTGATTTGCGCCCCCATCTCGGGGAATGTC 120
1788 GCATCTAGAGCAGTGGAGCTGAGCTGGGGTGATTTGCGCCCCCATCTCGGGGAATGTC 1847
121 TGAAGACAAATTTGGTTACTTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
1848 TGAAGACAAATTTGGTTACTTCAATGAGGAGTGAAGAGATACAGGCCACTACCAAC 1907
181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
1908 TAGTGATTAAGAGCCAGGAGATCTGCTCAACCTCTACCATGTACAGACGTCTCCCAT 1967
241 TACAACCTACCCCAATCCGAAGTGTCAAGTGTCAAGACCTAAGAAACCTGGTTTGAAGA 300
1968 TACAACCTACCCCAATCCGAAGTGTCAAGTGTCAAGACCTGGTTTGAAGA 2027
301 GAAAAGGCGCTGGGAAAGAGGAGGAGCAAAATCTGTCTGCTTCTCACTAGTCAAT 360
2028 GAAAAGGCGCTGGGAAAGAGGAGGAGCAAAATCTGTCTGCTTCTCACTAGTCAAT 2086
361 GCGAATAAGCAATCTGTCTGCTTCTGCTGCTGCTCAAGACAGAGAGCCAGAACTCTATC 420
```

```
Db 2087 GCGAATAAGCAATCTGTCTGCTTCTGCTGCTGCTCAAGACAGAGAGCCAGAACTCTATC 2146
Qy 421 GGGGACACGAGATTAATCATCTCTCACTGAGACAGAGTTGACAGAGCCATAGGAAATGCTGTA 480
Db 2147 GGGGACACGAGATTAATCATCTCTCACTGAGACAGAGTTGACAGAGCCATAGGAAATGCTGTA 2206
Qy 481 TGGGATTAATCTTCACTGCTGTTGAGCTTCTTAAGTTTCTTCCCTTCATTTACCTGCAAG 540
Db 2207 TGGGATTAATCTTCACTGCTGTTGAGCTTCTTAAGTTTCTTCCCTTCATTTACCTGCAAG 2266
Qy 541 CCAAGTTCTGTAAGGAAGATGCTGAGTTCTAGCTCAGGTTTCTTCTCACTGTAATTTAGA 600
Db 2267 CCAAGTTCTGTAAGGAAGATGCTGAGTTCTAGCTCAGGTTTCTTCTCACTGTAATTTAGA 2326
Qy 601 TCTCCAGACCTGCTGCGCCCAATTAATTAAGCAACAATTAATTAATTAATTAATTAATTAAT 660
Db 2327 TCTCCAGACCTGCTGCGCCCAATTAATTAAGCAACAATTAATTAATTAATTAATTAATTAAT 2386
Qy 661 GCACACACAGCTTTTGAAGCAAGACATGATGCTTGAATTTAGAGCCCTTGAAGATG 720
Db 2387 GCACACACAGCTTTTGAAGCAAGACATGATGCTTGAATTTAGAGCCCTTGAAGATG 2446
Qy 721 AAGCTTGAAGGAAGAAATCTTGTTCAGGCCCCCTTCCACACTCTTCATGTGTTA 780
Db 2447 AAGCTTGAAGGAAGAAATCTTGTTCAGGCCCCCTTCCACACTCTTCATGTGTTA 2506
Qy 781 ACCACTGCTCTCTGACCTTGAAGCAGCGTGAATTAATTAATTAATTAATTAATTAATTAAT 840
Db 2507 ACCACTGCTCTCTGACCTTGAAGCAGCGTGAATTAATTAATTAATTAATTAATTAATTAAT 2566
Qy 841 TGAATTTAGCTTCTGATCGTTCAAGAGATGATTAATTAATTAATTAATTTCT 890
Db 2567 TGAATTTAGCTTCTGATCGTTCAAGAGATGATTAATTAATTAATTAATTTCT 2616
RESULT 10
LOCUS BD235840 890 bp DNA linear PAT 17-JUL-2003
DEFINITION A novel method of diagnosing, monitoring, staging and
treating various cancers.
ACCESSION BD235840
VERSION BD235840.1 GI:33045610
KEYWORDS JP 2002523760-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 890)
Salceda,S., Sun,Y., Recipon,H. and Cafferykey,R.
A novel method of diagnosing, monitoring, staging, imaging and
treating various cancers
Patent: JP 2002523760-A 11 30-JUL-2002;
DIADEXUS INC
COMMENT OS Homo sapiens (human)
PN JP 2002523760-A/11
PD 30-JUL-2002
PR 01-SEP-1999 JP 2000567741
PF 02-SEP-1998 US 60/098880
PI SUSANA SALCEDA, YONGMING SUN, HERVE RECIPON, ROBERT CAFFERKEY PC
GOIN33/574, A61K39/395, A61K39/395, A61K39/395, A61K39/395 PC
,A61K49/00,A61K49/00,
PC A61K51/00,C07K16/32,C12N15/09,C12Q1/68,C12N15/00,A61K49/02 CC
A novel method of diagnosing, monitoring,
staging, imaging and
treating
CC various cancers
CC key
FH source 1..890
FT location/Qualifiers
location/Qualifiers
1..890
/organism="Homo sapiens (human)".
/organism="Homo sapiens"
/mol_type="genomic DNA"
```


Db 1097 GGGGACCAAGATATCATCTCTCAAGTGAACAGAGTTGACAGAGCCCTAATGGGAAATGCTTGA 1156
Qy 481 TGGATTATCTTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTAACCTGCAAG 540
Db 1157 TGGATTATCTTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTAACCTGCAAG 1216
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 1276
Qy 601 TCTCAGAGCCCTGCGGCAATTCGAATTAAGCAACAAACATATACCTTCATGA 660
Db 1277 TCTCAGAGCCCTGCGGCAATTCGAATTAAGCAACAAACATATACCTTCATGA 1336
Qy 661 GCACACAGACTTTTGAAGCAAGACATGCTGTGAATTAAGGCTTGAAGAAATG 720
Db 1337 GCACACAGACTTTTGAAGCAAGACATGCTGTGAATTAAGGCTTGAAGAAATG 1396
Qy 721 AAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCCCACTCTTCATGTGTTA 780
Db 1397 AAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCCCACTCTTCATGTGTTA 1456
Qy 781 ACCACTGCTTCTGAGACCTTGAGGCAAGGTAAGTATTACATGTTGTTATAGAAAC 840
Db 1457 ACCACTGCTTCTGAGACCTTGAGGCAAGGTAAGTATTACATGTTGTTATAGAAAC 1516
Qy 841 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 890
Db 1517 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 1566

RESULT 12
LOCUS AR238092 1567 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 74 from patent US 6468546.
ACCESSION AR238092
VERSION AR238092.1 GI:27283056
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., King,G.E. and Algate,P.A.
TITLE Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6468546-A 74 22-OCT-2002;
FEATURES
source location/qualifiers
1..1567
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 89.3%; Score 794.4; DB 6; Length 1567;
Best Local Similarity 91.8%; Pred. No. 4.5e-235;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;
Qy 1 CAAGCTTGAGGCTTCTCTTCATCTCGCTGACAGCTAAGACTTCAGTTTCAATA 60
Db 679 CAAGCTTGAGGCTTCTCTTCATCTCGCTGACAGCTAAGACTTCAGTTTCAATA 738
Qy 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTATTTCCGCCCACTCCGGGGGAATGTC 120
Db 739 GCATCTAGAGCAGTGGGACTCAGCTGGGGTATTTCCGCCCACTCCGGGGGAATGTC 798
Qy 121 TGAAGACATTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 799 TGAAGACATTTT -GTTACTTAATGAGGAGTGAAGAGATACAGTGTACTACCAAC 857
Qy 181 NNN 240
Db 858 TAGGTGATTAAGGCGAGGGATGCTGCTCAACTCTCAACATGTACAGAGCGTCCCAT 917
Qy 241 TACAACCTACCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTCGGTTTGAGTA 300

Db 918 TACAACCTACCAATCCGAAGTGTCAACTGTGTCAAGACTAAGAAACCTCGGTTTGAGTA 977
Qy 301 GAAAGGGCTGAGGAAAGGGAGCCAAACAATCTGTGCTCTCTCACATTAATGATCT 360
Db 978 GAAAGGGCTT -GGAAGAGGGAGCCAAACAATCTGTGCTCTCTCACATTAATGATCT 1036
Qy 361 GCAAAATTAAGGATTTCTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 420
Db 1037 GCAAAATTAAGGATTTCTGCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 1096
Qy 421 GGGACCAAGATTAATCTCTCAATGAAACAGATTTGAACAGGCTTAAGGAAAGCTTGA 480
Db 1097 GGGACCAAGATTAATCTCTCAATGAAACAGATTTGAACAGGCTTAAGGAAAGCTTGA 1156
Qy 481 TGGATTATCTTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTAACCTGCAAG 540
Db 1157 TGGATTATCTTCAGCTTGTGAGCTTCTAAGTTTCTTCCCTTCATTCTAACCTGCAAG 1216
Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 1276
Qy 601 TCTCAGAGCCCTGCTGCGGCAATTCGAATTAAGGCAACAAATACCTTCATGA 660
Db 1277 TCTCAGAGCCCTGCTGCGGCAATTCGAATTAAGGCAACAAATACCTTCATGA 1336
Qy 661 GCACACAGACTTTTGAAGCAAGCAATGCTGTGAATTAAGGCTTGAAGAAATG 720
Db 1337 GCACACAGACTTTTGAAGCAAGCAATGCTGTGAATTAAGGCTTGAAGAAATG 1396
Qy 721 AAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCCCACTCTTCATGTGTTA 780
Db 1397 AAGCTTTGAAGAAAGAAATCTTTGTTCCAGCCCTTCCCACTCTTCATGTGTTA 1456
Qy 781 ACCACTGCTTCTGAGACCTTGAGGCAAGGTAAGTATTACATGTTGTTATAGAAAC 840
Db 1457 ACCACTGCTTCTGAGACCTTGAGGCAAGGTAAGTATTACATGTTGTTATAGAAAC 1516
Qy 841 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 890
Db 1517 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 1566

RESULT 13
LOCUS AR257633 1567 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 74 from patent US 6488931.
ACCESSION AR257633
VERSION AR257633.1 GI:27307708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLE Compositions and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6488931-A 74 03-DEC-2002;
FEATURES
source location/qualifiers
1..1567
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 89.3%; Score 794.4; DB 6; Length 1567;
Best Local Similarity 91.8%; Pred. No. 4.5e-235;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;
Qy 1 CAAGCTTGAGGCTTCTCTTCATCTCGCTGAGACAGCTAAGACTTCAGTTTCAATA 60
Db 679 CAAGCTTGAGGCTTCTCTTCATCTCGCTGAGACAGCTAAGACTTCAGTTTCAATA 738

QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGAGTATTTGCCCCCATCTCCGGGGAATGTC 120
| | | | |
DB 739 GCATCTAGAGCAGTGGGACTCAGCTGGGAGTATTTGCCCCCATCTCCGGGGAATGTC 798
| | | | |
QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACGNNNNNNNNNNNN 180
| | | | |
DB 799 TGAAGCAATTTT-GTTACTCTCAATGAGGAGTGAAGAGATACAGTGTACTACCAAC 857
| | | | |
QY 181 NNNCAT 240
| | | | |
DB 858 TAGTGATTAAGGCCAGGAGTGTCTCTCAACCTCTACATGTACAGAGCTCTCCCAT 917
| | | | |
QY 241 TACAATCAATCCCAATCCGAAGTGTCAACTGTGAGAGCTTAAGAAACCTGTGTTAGTA 300
| | | | |
DB 918 TACAATCAATCCCAATCCGAAGTGTCAACTGTGAGAGCTTAAGAAACCTGTGTTAGTA 977
| | | | |
QY 301 GAAAAGGCTCTGGGAAAAGAGGAGCCAACTGTCTGTCTCTCTCAATTAGTATT 360
| | | | |
DB 978 GAAAAGGCTCT-GGAAAAGAGGAGCCAACTGTCTGTCTCTCTCAATTAGTATT 1036
| | | | |
QY 361 GCGAATTAAGCATTTCTCTCTTTGGCTGTGCTCTCAGCAGAGAGCCAGAACTTATC 420
| | | | |
DB 1037 GCGAATTAAGCATTTCTCTCTTTGGCTGTGCTCTCAGCAGAGAGCCAGAACTTATC 1096
| | | | |
QY 421 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTAAGGAAATGCTGA 480
| | | | |
DB 1097 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTAAGGAAATGCTGA 1156
| | | | |
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATTCACCTGCAAG 540
| | | | |
DB 1157 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATTCACCTGCAAG 1216
| | | | |
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTTCTACTCAGGTTTCTTACTCTGAATTTAGA 600
| | | | |
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTTCTACTCAGGTTTCTTACTCTGAATTTAGA 1276
| | | | |
QY 601 TCTCCAGACCCCTCTGCGCACAATTCAAATTAAAGCAACAACTATACCTTCATGAA 660
| | | | |
DB 1277 TCTCCAGACCCCTCTGCGCACAATTCAAATTAAAGCAACAACTATACCTTCATGAA 1336
| | | | |
QY 661 GCAACACAGACTTTTGAAGCAAGACAATGACTCTTGAATGAGGCTTGAGGAATG 720
| | | | |
DB 1337 GCAACACAGACTTTTGAAGCAAGACAATGACTCTTGAATGAGGCTTGAGGAATG 1396
| | | | |
QY 721 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTGA 780
| | | | |
DB 1397 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTGA 1456
| | | | |
QY 781 ACCACTGCTCTCTGAGACCTTGAGGCAAGGTAAGTATTAATGTTTATAGAAAAC 840
| | | | |
DB 1457 ACCACTGCTCTCTGAGACCTTGAGGCAAGGTAAGTATTAATGTTTATAGAAAAC 1516
| | | | |
QY 841 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCT 890
| | | | |
DB 1517 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCT 1566
| | | | |
RESULT 14
AR283679 1567 bp DNA linear PAT 10-APR-2003
LOCUS AR283679
DEFINITION Sequence 74 from patent US 6528253.
ACCESSION AR283679
VERSION AR283679.1 GI:29720576
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLES Compositions and methods for diagnosis of ovarian cancer
JOURNAL Patent: US 6528253-A 74 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..1567

ORIGIN /organism="unknown"
/mol_type="genomic DNA"
Query Match 89.3%; Score 794.4; DB 6; Length 1567;
Best Local Similarity 91.8%; Pred. No. 4,5e-235;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;
QY 1 CAAAGCTCTAGAGCTTCTCTTCCATCTCTGCTGAGCAGCTTAAGACCTCAGTTTCAATA 60
| | | | |
DB 679 CAAAGCTCTAGAGCTTCTCTTTCATCTCTGCTGAGCAGCTTAAGACCTCAGTTTCAATA 738
| | | | |
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGAGTATTTGCCCCCATCTCCGGGGAATGTC 120
| | | | |
DB 739 GCATCTAGAGCAGTGGGACTCAGCTGGGAGTATTTGCCCCCATCTCCGGGGAATGTC 798
| | | | |
QY 121 TGAAGCAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACGNNNNNNNNNNNN 180
| | | | |
DB 799 TGAAGCAATTTT-GTTACTCTCAATGAGGAGTGAAGAGATACAGTGTACTACCAAC 857
| | | | |
QY 181 NNNCAT 240
| | | | |
DB 858 TAGTGATTAAGGCCAGGAGTGTCTCTCAACCTCTACATGTACAGAGCTCTCCCAT 917
| | | | |
QY 241 TACAATCAATCCCAATCCGAAGTGTCAACTGTGAGAGCTTAAGAAACCTGTGTTAGTA 300
| | | | |
DB 918 TACAATCAATCCCAATCCGAAGTGTCAACTGTGAGAGCTTAAGAAACCTGTGTTAGTA 977
| | | | |
QY 301 GAAAAGGCTCTGGGAAAAGAGGAGCCAACTGTCTGTCTCTCTCAATTAGTATT 360
| | | | |
DB 978 GAAAAGGCTCT-GGAAAAGAGGAGCCAACTGTCTGTCTCTCTCAATTAGTATT 1036
| | | | |
QY 361 GCGAATTAAGCATTTCTCTCTTTGGCTGTGCTCTCAGCAGAGAGCCAGAACTTATC 420
| | | | |
DB 1037 GCGAATTAAGCATTTCTCTCTTTGGCTGTGCTCTCAGCAGAGAGCCAGAACTTATC 1096
| | | | |
QY 421 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTAAGGAAATGCTGA 480
| | | | |
DB 1097 GGGACACAGGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTTAAGGAAATGCTGA 1156
| | | | |
QY 481 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATTCACCTGCAAG 540
| | | | |
DB 1157 TGGGATTAATCTTCAAGCTTGTGAGCTTCTAAGTTTCTTCCCTCAATTCACCTGCAAG 1216
| | | | |
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTTCTACTCAGGTTTCTTACTCTGAATTTAGA 600
| | | | |
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTTCTACTCAGGTTTCTTACTCTGAATTTAGA 1276
| | | | |
QY 601 TCTCCAGACCCCTCTGCGCACAATTCAAATTAAAGCAACAACTATACCTTCATGAA 660
| | | | |
DB 1277 TCTCCAGACCCCTCTGCGCACAATTCAAATTAAAGCAACAACTATACCTTCATGAA 1336
| | | | |
QY 661 GCAACACAGACTTTTGAAGCAAGACAATGACTCTTGAATGAGGCTTGAGGAATG 720
| | | | |
DB 1337 GCAACACAGACTTTTGAAGCAAGACAATGACTCTTGAATGAGGCTTGAGGAATG 1396
| | | | |
QY 721 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTGA 780
| | | | |
DB 1397 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTGA 1456
| | | | |
QY 781 ACCACTGCTCTCTGAGACCTTGAGGCAAGGTAAGTATTAATGTTTATAGAAAAC 840
| | | | |
DB 1457 ACCACTGCTCTCTGAGACCTTGAGGCAAGGTAAGTATTAATGTTTATAGAAAAC 1516
| | | | |
QY 841 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCT 890
| | | | |
DB 1517 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATATACATTTCT 1566
| | | | |
RESULT 15
AR443353 1567 bp DNA linear PAT 20-FEB-2004
LOCUS AR443353
DEFINITION Sequence 74 from patent US 6670463.

ACCESSION AR443353
VERSION AR443353.1 GI:42671132
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1567)
AUTHORS Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLE Compositions and methods for therapy of ovarian cancer
JOURNAL Patent: US 6670463-A 74 30-DEC-2003;
FEATURES location/Qualifiers
1..1567
source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 89.3%; Score 794.4; DB 6; Length 1567;
Best Local Similarity 91.8%; Pred.No. 4.5e-235;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

```
QY 1 CAAGCTGAGGCTCTCTCTTCATCCCTGCGAGACAGCTAAGACTCAGTTTCAATA 60
DB 679 CAAGCTGAGGCTCTCTCTTCATCCCTGCGAGACAGCTAAGACTCAGTTTCAATA 738
QY 61 GCATCTAAGAGAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAATGTC 120
DB 739 GCATCTAAGAGAGTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAATGTC 798
QY 121 TGAAGACAATTTGGTTACCTCAATAGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB 799 TGAAGACAATTTT-GTACCTCAATAGAGGAGTGAAGATACAGTGTACTACCAAC 857
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
DB 858 TAGTGATATAAGGCCAGGAGTGTCTCAACTCTACATATACAGAGAGCTCTCCCAT 917
QY 241 TACAACCTACCCATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGGTTTGAATA 300
DB 918 TACAACCTACCCATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGGTTTGAATA 977
QY 301 GAAAAGGCTCTGGGAAAGAGGGAGCCAAACAATCTGTCTGCTCTCAATATAGCATT 360
DB 978 GAAAAGGCTCT-GGAAAGGGAGCCAAACAATCTGTCTGCTCTCAATATAGCATT 1036
QY 361 GGCAATAAGCATCTGTCTCTTTGGCTGTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 1037 GGCAATAAGCATCTGTCTCTTTGGCTGTGCTCAGACAGAGAGCCAGAACTCTATC 1096
QY 421 GGGCACCAAGATACATCTCTCAGTGAACAGAGTTGACAAGGCTATGGGAAATGCTGA 480
DB 1097 GGGCACCAAGATACATCTCTCAGTGAACAGAGTTGACAAGGCTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTACAGCTGTGAGCTTGAAGTTCTTCCCTGATCTACCCCTGCAAG 540
DB 1157 TGGGATTAATCTTACAGCTGTGAGCTTGAAGTTCTTCCCTGATCTACCCCTGCAAG 1216
QY 541 CCAAGTTCTGTAAGAGAATGCTGAGTTCTAGCTCAGGTTTCTTACTGGAATTTAGA 600
DB 1217 CCAAGTTCTGTAAGAGAATGCTGAGTTCTAGCTCAGGTTTCTTACTGGAATTTAGA 1276
QY 601 TCTCCAGACCTGCTGCGCCACAATTCAAATTAAGGCAACAACATATACCTTCATGAA 660
DB 1277 TCTCCAGACCTGCTGCGCCACAATTCAAATTAAGGCAACAACATATACCTTCATGAA 1336
QY 661 GCACACACAGACTTTTGAAGAGACAATGACTGTGAATTGAGGCTTGAAGGAATG 720
DB 1337 GCACACACAGACTTTTGAAGAGACAATGACTGTGAATTGAGGCTTGAAGGAATG 1396
QY 721 AAGCTTTGAGGAAAGAAATATCTTGTTCAGAGCCCTTCCACACTCTTCATGTGTA 780
DB 1397 AAGCTTTGAGGAAAGAAATATCTTGTTCAGAGCCCTTCCACACTCTTCATGTGTA 1456
QY 781 ACCACTGCTTCTGGAACCTTGAGGCCAGGTAAGCTGTAATTAATGTTGTAAGAAAAC 840
```

```
DB 1457 ACCACTGCTTCTGGAACCTTGAGGCCAGGTAAGCTGTAATTAATGTTGTAAGAAAAC 1516
QY 841 TGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTTAAATATACATTTGCT 890
DB 1517 TGATTTTGAAGTTCTGATCGTTCAAGAGAAATGATTTAAATATACATTTGCT 1566
```

Search completed: May 30, 2005, 17:54:11
Job time : 4109.01 secs

CC predisposition to these diseases. The antibodies are useful as


```

Db      181 TAGTGATAAAGGCAGAGATGCTGCTCAACTCTACATGTAAGAGAGCTGCCCAT 240
Qy      241 TAACTATACCAATCCGAATGTCACACTGTGTCAAGACTAAGAAACCTGGTTTGAAGTA 300
Db      241 TAACTATACCAATCCGAATGTCACACTGTGTCAAGACTAAGAAACCTGGTTTGAAGTA 300
Qy      301 GAAAGGGGCTGGGAAAGAGAGGAGCCAACTGTGTGTCTCTCCCTCACTAGTCATT 360
Db      301 GAAAGGGGCTGGGAAAGAGAGGAGCCAACTGTGTGTCTCTCCCTCACTAGTCATT 360
Qy      361 GGGAAATTAAGCATTTGTCTCTTTGGCTGCTGCTGAGACAGAGAGCCAGAACTCTATC 420
Db      361 GGGAAATTAAGCATTTGTCTCTTTGGCTGCTGCTGAGACAGAGAGCCAGAACTCTATC 420
Qy      421 GGGGACACAGATTAACATCTCTCACTGTAACAGAGTTGACAGAGGCTTATGGAAATGCTCTGA 480
Db      421 GGGGACACAGATTAACATCTCTCACTGTAACAGAGTTGACAGAGGCTTATGGAAATGCTCTGA 480
Qy      481 TGGGATTAATCTAGCTGTGTGAGCTTCTAAGTTTCTTCCCTTCAATCTACCTGCAAG 540
Db      481 TGGGATTAATCTAGCTGTGTGAGCTTCTAAGTTTCTTCCCTTCAATCTACCTGCAAG 540
Qy      541 CCAAGTTCTGTAAAGAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGTGAATTAGA 600
Db      541 CCAAGTTCTGTAAAGAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGTGAATTAGA 600
Qy      601 TCTCCGAGCCCTGCTGCGCCACAATTAAGGACAAACATTAATCTTCCATGAA 660
Db      601 TCTCCGAGCCCTGCTGCGCCACAATTAAGGACAAACATTAATCTTCCATGAA 660
Qy      661 GCACACACAGACTTTTGAAGAGAGGACATGACGTGTAATGAGGCGCTTGAAGAAAG 720
Db      661 GCACACACAGACTTTTGAAGAGAGGACATGACGTGTAATGAGGCGCTTGAAGAAAG 720
Qy      721 AAGCTTTGAAGAGAAAGAAATACTTTGTTTCCAGCCCTTCCACACTCTTCAATGTGTA 780
Db      721 AAGCTTTGAAGAGAAAGAAATACTTTGTTTCCAGCCCTTCCACACTCTTCAATGTGTA 780
Qy      781 ACCACTGCTTCTCTGAGACCTTGAAGCCAGCTGATTAATCAATGTTGTTAAGAAAC 840
Db      781 ACCACTGCTTCTCTGAGACCTTGAAGCCAGCTGATTAATCAATGTTGTTAAGAAAC 840
Qy      841 TGAATTTAAGATTCTGATCGTTCAAGAGAAATGAATTAATATACATTTTCT 890
Db      841 TGAATTTAAGATTCTGATCGTTCAAGAGAAATGAATTAATATACATTTTCT 890

```

RESULT 3

```

ID      ABL57349 standard; cDNA; 893 BP.
XX      ABL57349.
AC      ABL57349.
XX      12-AUG-2002 (first entry)
DT      12-AUG-2002 (first entry)
XX      Breast BS265 gene EST clone 3090742H1.
DE      BS265; human; breast; cancer; tumour; metastasis;
KW      gene therapy; expressed sequence tag; EST; ss.
XX      Homo sapiens.
OS      Homo sapiens.
XX      PN      US2002034749-A1.
XX      PD      21-MAR-2002.
XX      PF      07-MAY-2001, 2001US-00850178.
XX      PR      18-NOV-1997, 97US-00972376.
XX      PR      18-NOV-1998, 98US-00193944.
XX      PA      (BILLINGEL P A.
XX      PA      (COHEN M.

```

```

PA      (COLP/) COLPITTS T L.
PA      (FRIE/) FRIEDMAN P N.
PA      (GORD/) GORDON J.
PA      (GRAN/) GRANADOS E N.
PA      (HODG/) HODGES S C.
PA      (KLAS/) KLAS M R.
PA      (KRAT/) KRATOCHVIL J D.
PA      (ROBE/) ROBERTS-RAPP L A.
PA      (RUSSEL) RUSSELL J C.
PA      (STRO/) STROUPE S D.
XX      XX
XX      PI      Billingel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI      Granados EN, Hodges SC, KLAS MR, Kratochvil JD, Roberts-Rapp LA,
PI      Russell JC, Stroupe SD;
XX      XX
XX      DR      WPI; 2002-403712/43.
XX      XX
XX      PT      New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
XX      PT      staging, monitoring, prognosticating, in vivo imaging, preventing,
XX      PT      treating, or determining the predisposition of an individual to breast
XX      PT      cancer.
XX      PS      Claim 1; Page 37; 52pp; English.
XX      XX
XX      CC      The present sequence is of BS265 gene expressed sequence tag (EST) full-
XX      CC      length sequence clone 3090742H1 (ATCC 98683). ESTs were derived from cDNA
XX      CC      libraries made from breast tumour tissues, breast non-tumour tissues and
XX      CC      numerous other tissues, and entered into a database as gene transcript
XX      CC      images. They were then evaluated to identify EST sequences that were
XX      CC      representative primarily of the breast tissue libraries, and were ranked
XX      CC      according to their abundance in target libraries and absence from
XX      CC      background libraries. Partial clones 3090742H1, g991752, g2058967 and
XX      CC      g1615448 (see ABL57345-48) represent the minimum number of clones that,
XX      CC      together with the present full-length sequence of clone 3090752H1, were
XX      CC      needed to form a contig and from which a consensus sequence (see
XX      CC      ABL57350) was derived. ESTs corresponding to the consensus sequence of
XX      CC      BS265 were found in 33.3% (9/27) of breast tissue libraries, and in 0.6%
XX      CC      (3/476) of non-breast libraries. This set of contiguous and partially
XX      CC      overlapping cDNA sequences, designated as BS265 and transcribed from
XX      CC      breast tissue, and the polypeptides encoded by them, are useful for
XX      CC      detecting, diagnosing, staging, monitoring, prognosticating, in vivo
XX      CC      imaging, preventing, treating, or determining the predisposition of an
XX      CC      individual to diseases and conditions of the breast, such as breast
XX      CC      cancer. Also provided are antibodies which specifically bind to BS265
XX      CC      proteins, and agonists or inhibitors which prevent action of the
XX      CC      proteins, and which are useful for treatment of breast disease,
XX      CC      especially tumours and metastases
XX      SQ      Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other;
XX      XX
XX      Query Match      90.6%; Score 806.4; DB 6; Length 893;
XX      Best Local Similarity 91.9%; Pred. No. 9.9e-263;
XX      Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

```

```

QY 301 GAAAAGGCGCTGGGAAAAGAGGAGCCAAATCTGTCCTTCACATTAGTCATT 360
DB 301 GAAAAGGCGCT-GGAAAAGAGGAGGACCAAAATCTGTCCTTCACATTAGTCATT 359
QY 361 GCGAATTAAGCATTTCTGTCCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB 360 GCGAATTAAGCATTTCTGTCCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 419
QY 421 GGGGACCGAGATTAATCTCTAGTGAACAGAGTTGACAAAGGCTATGAGGAATGCTGGA 480
DB 420 GGGGACCGAGATTAATCTCTAGTGAACAGAGTTGACAAAGGCTATGAGGAATGCTGGA 479
QY 481 TGGGATTAATCTCTAGCTTGTGAGCTTCAAGTTTCTTCCCTTCATTCTACCTGCAAG 540
DB 480 TGGGATTAATCTCTAGCTTGTGAGCTTCAAGTTTCTTCCCTTCATTCTACCTGCAAG 539
QY 541 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGAGTTTCTTACTGTAATTTAGA 600
DB 540 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGAGTTTCTTACTGTAATTTAGA 599
QY 601 TCTCAGAGCCCTGCGGCGCACAAATTAAGGCAACAAATATACCTTCATGAA 660
DB 600 TCTCAGAGCCCTTCTGCGCACAAATTAAGGCAACAAATATACCTTCATGAA 659
QY 661 GCACACACAGACTTTTGAAGCAGAGCAATGACTGCTGAATTTGAGGCTTGAAGAAATG 720
DB 660 GCACACACAGACTTTTGAAGCAGAGCAATGACTGCTGAATTTGAGGCTTGAAGAAATG 719
QY 721 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTTTTATGTTA 780
DB 720 AAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTTTTATGTTA 779
QY 781 ACCACTGCTCTCTGAGACCTTGGAGCAGAGTGACTGATTCATGTTTATGAAAAC 840
DB 780 ACCACTGCTCTCTGAGACCTTGGAGCAGAGTGACTGATTCATGTTTATGAAAAC 839
QY 841 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCT 890
DB 840 TGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCT 889

RESULT 4
ABL57350
ID ABL57350 standard; cDNA; 893 BP.
AC ABL57350;
XX
DT 12-AUG-2002 (first entry)
XX
DE Breast BS265 gene consensus sequence.
XX
KM BS265; human; breast; cancer; tumour; metastasis; diagnosis;
KW gene therapy; expressed sequence tag; EST; gene; ss.
XX
OS Homo sapiens.
XX
FH Key 1, 123 Location/Qualifiers
FT CDS /tag= a
FT /product= "BS265"
FT /partial
FT /note= "the CDS does not include a start codon"
XX
US2002034749-A1.
XX
PD 21-MAR-2002.
XX
PF 07-MAY-2001; 2001US-00850178.
XX
PR 18-NOV-1997; 97US-00972376.
XX
PR 18-NOV-1998; 98US-00193944.
XX

```

```

PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GORD/) GORDON J.
PA (GRAN/) GRANADOS E N.
PA (HODG/) HODGES S C.
PA (KLAS/) KLAS M R.
PA (KRAT/) KRATOCHVIL J D.
PA (ROBE/) ROBERTS-RAPP L A.
PA (RUS/) RUSSELL J C.
PA (STRO/) STROUBE S D.
XX
PI Billingsel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
PI Granados EN, Hodges SC, Klaas MR, Kratochvil JD, Roberts-Rapp LA,
PI Russell JC, Stroupe SD,
XX
DR WPI, 2002-403712/43.
XX
P-PSDB; ABB76272.
XX
PT New BS265 proteins and nucleic acids, useful for detecting, diagnosing,
PT staging, monitoring, prognosticating, in vivo imaging, preventing,
PT treating, or determining the predisposition of an individual to breast
PT cancer.
XX
PS Claim 1; Page 38; 52p; English.
XX
CC The present sequence is a consensus sequence of the human breast BS265
CC gene. Expressed sequence tags (ESTs) were derived from cDNA libraries
CC made from breast tumour tissues, breast non-tumour tissues and numerous
CC other tissues, and entered into a database as gene transcript images.
CC They were then evaluated to identify EST sequences that were
CC representative primarily of the breast tissue libraries, and were ranked
CC according to their abundance in target libraries and absence from
CC background libraries. 4 Overlapping EST clones, together with a full-
CC length sequence (see ABL57345-49), were used to form a contig from which
CC the present consensus sequence was derived. ESTs corresponding to the
CC consensus sequence were found in 33.3% (9/27) of breast tissue libraries,
CC and in 0.6% (3/476) of non-breast libraries. The set of contiguous and
CC partially overlapping cDNA sequences, designated as BS265 and transcribed
CC from breast tissue, and the polypeptides encoded by them, are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
CC imaging, preventing, treating, or determining the predisposition of an
CC individual to diseases and conditions of the breast, such as breast
CC cancer. Also provided are antibodies which specifically bind to BS265
CC proteins, and agonists or inhibitors which prevent action of the
CC proteins, and which are useful for treatment of breast disease,
CC especially tumours and metastases
XX
SQ Sequence 893 BP; 244 A; 215 C; 193 G; 241 T; 0 U; 0 Other;
XX
Query Match 90.6%; Score 806.4; DB 6; Length 893;
Best Local Similarity 91.9%; Pred. No. 9.9e-263;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
QY 1 CAAGCTGAGGCTTCTCTTCATCTGCTGAGACGTTAAGACCTCACTTTCAATA 60
DB 1 CAAGCTGAGGCTTCTCTTCATCTGCTGAGACGTTAAGACCTCACTTTCAATA 60
QY 61 GCATCTAAGAGAGGAGCTCAGCTGGGATATTTGCCCCCATTCGCGGGAATGTC 120
DB 61 GCATCTAAGAGAGGAGCTCAGCTGGGATATTTGCCCCCATTCGCGGGAATGTC 120
QY 121 TGAAGACAATTTGGTATCTCAATGAGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
DB 121 TGAAGACAATTTGGTATCTCAATGAGAGGAGTGAAGAGATACAGGCTACTACCAAC 180
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
DB 181 TAGTGATTAAGAGCCAGGAGTGTGCTCACTCTCACTGATGACAGGACGCTCCCAT 240
QY 241 TCAACTACCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTTTGAATA 300
DB 241 TCAACTACCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAACCTGTTTGAATA 300

```


Db 765 GCACACAGACGCTTTGAAAGCAGACAGACGCTGTAATGAGCCCTTGAGAAATG 824
Qy 721 AAGCTTTGAGGAGAAAGATACTTTGTTTCAGCCGCCCTTCCACACTCTTCATGTGTA 780
Db 825 AAGCTTTGAGGAGAAAGATACTTTGTTTCAGCCGCCCTTCCACACTCTTCATGTGTA 884
Qy 781 ACCACTGCTCTTCTGAGACCTTGAGCCACGCTGACTGATTAATCATGTTGTTATGAAAAC 840
Db 885 ACCACTGCTCTTCTGAGACCTTGAGCCACGCTGACTGATTAATCATGTTGTTATGAAAAC 944
Qy 841 TGATTTGAGCTTCTGATCTTCAGAGAAATGATTAATACATTTCT 890
Db 945 TGATTTGAGCTTCTGATCTTCAGAGAAATGATTAATACATTTCT 994

RESULT 6

AAA70077 standard, cDNA; 2627 BP.

AAA70077;

07-NOV-2000 (first entry)

Human ovarian carcinoma antigen polynucleotide SEQ ID NO:391.

Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis; tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.

Homo sapiens.

WO200036107-A2.

22-JUN-2000.

17-DEC-1999; 99WO-US030270.

17-DEC-1998; 98US-00215681.

17-DEC-1998; 98US-00216003.

23-JUN-1999; 99US-00318933.

24-SEP-1999; 99US-00404879.

(CORI-) CORIXA CORP.

MITCHELL JL, KING GE, ALGATE PA, FRUDAKIS TN;

WPI; 2000-431589/37.

Immunogenic portion of an ovarian carcinoma protein and the nucleic acid

encoding it, useful for the diagnosis, prevention and treatment of

cancer, preferably ovarian cancer.

Claim 1; Page 204-205; 299pp; English.

The present invention describes an isolated polypeptide comprising an

immunogenic portion of an ovarian carcinoma protein (or its variants).

Ovarian carcinoma proteins, and polynucleotides encoding them, have

cytostatic activity and can be used in gene therapy and vaccines. Ovarian

carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful

for the prevention, diagnosis and treatment of cancer, preferably ovarian

cancer. AAB69691 to AAA70077 and AAB12552 to AAB12557 represent human

exemplification of the present invention

Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 90.6%; Score 806.4; DB 3; Length 2627;

Best Local Similarity 91.9%; Pred. No. 1.9e-262;

Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

1 CAAGCTGAGGCTTCTCTTCATCTCCGCGTGAAGCTTAAGCTTCAGTTTCATA 60

1721 CAAGCTGAGGCTTCTCTTCATCTCCGCGTGAAGCTTAAGCTTCAGTTTCATA 1780

Qy 61 GCATCTAGAGAGTGGGACTCAGCTGGGGTATTTGCCCCCATCTCCGGGGATATTC 120
Db 1781 GCATCTAGAGAGTGGGACTCAGCTGGGGTATTTGCCCCCATCTCCGGGGATATTC 1840
Qy 121 TGAAGCAATTTGGTTACCTCAATGAGGAGTGGAGAGATACAGNNNNNNNNNNNN 180
Db 1841 TGAAGCAATTTGGTTACCTCAATGAGGAGTGGAGAGATACAGGCTACTACCAAC 1900
Qy 181 NNN 240
Db 1901 TAGTGATTAAGGCGAGGATGCTGCTCAACCTCCTACATGTACAGGAGCTGCCAT 1960
Qy 241 TACAACTACCAATCCGAATGCTCACTGTCTCAGACTAAGAAACCTGGTTGAGTA 300
Db 1961 TACAACTACCAATCCGAATGCTCACTGTCTCAGACTAAGAAACCTGGTTGAGTA 2020
Qy 301 GAAAAGGCGCTGGGAGAGGAGGAGCCAAATCTGCTGCTCTCCTACATTAATGTCAT 360
Db 2021 GAAAAGGCGCTGGGAGAGGAGGAGCCAAATCTGCTGCTCTCCTACATTAATGTCAT 2079
Qy 361 GGCATAATGAGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 2080 GGCATAATGAGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2139
Qy 421 GGGCACCAGATTAATCTCTCAGTGAACAGAGTTGACAGGCTTAAGGAAATGCTGCA 480
Db 2140 GGGCACCAGATTAATCTCTCAGTGAACAGAGTTGACAGGCTTAAGGAAATGCTGCA 2199
Qy 481 TGGGATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 2200 TGGGATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2259
Qy 541 CCAAGTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 600
Db 2260 CCAAGTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGAAATTTAGA 2319
Qy 601 TCTCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 2320 TCTCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2379
Qy 661 GCACACAGACTTTTGAAGCAAGAGCAATGACTGCTGAATTTGAGGCTTTGAGGAATG 720
Db 2380 GCACACAGACTTTTGAAGCAAGAGCAATGACTGCTGAATTTGAGGCTTTGAGGAATG 2439
Qy 721 AAGCTTTGAGGAGAAAGATATCTTTGTTTCCAGCCCTTCCACACTCTTCATGTGTA 780
Db 2440 AAGCTTTGAGGAGAAAGATATCTTTGTTTCCAGCCCTTCCACACTCTTCATGTGTA 2499
Qy 781 ACCACTGCTCTCTGAGACTTTGAGCCACGCTGACTGATTAATGTTGTTATGAAAAC 840
Db 2500 ACCACTGCTCTCTGAGACTTTGAGCCACGCTGACTGATTAATGTTGTTATGAAAAC 2559
Qy 841 TGATTTGAGCTTCTGATCTTCAGAGAAATGATTAATATACATTTCT 890
Db 2560 TGATTTGAGCTTCTGATCTTCAGAGAAATGATTAATATACATTTCT 2609

RESULT 7

AAH55681 standard, DNA; 2627 BP.

AAH55681;

04-SEP-2001 (first entry)

Human ovarian tumour-derived antigen O8E DNA sequence.

Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;

antigen; O8E; ds.

Homo sapiens.

WO200140269-A2.

```

XX 07-JUN-2001.
PD
XX
PF 29-NOV-2000; 2000MO-US032520.
XX
XX 30-NOV-1999; 990US-00451651.
PR 22-FEB-2000; 2000US-00510662.
PR 10-MAR-2000; 2000US-0052386.
PR 07-APR-2000; 2000US-00545068.
PR 15-MAY-2000; 2000US-00571025.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX
XX WPI; 2001-356154/37.
DR N-PSDB; AAB99204, AAB99205.
XX
XX Breat tumor polypeptides and the nucleic acids that encode them, useful
XX PT for the prevention, diagnosis and treatment of breast cancer.
XX
XX Claim 24; Page 189; 221pp; English.
XX
XX The present invention relates to human breast tumor protein coding
XX CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-
XX CC AAH55762). The breast tumor protein DNA sequences may be used in the
XX CC prevention, diagnosis and treatment of diseases associated with the
XX CC inappropriate expression of the breast tumor protein e.g. breast cancer.
XX CC The present sequence is a human ovarian tumor-derived antigen coding
XX CC sequence, which was used in an example from the present invention
XX
XX SO Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
XX
Query Match 90.6%; Score 806.4; DB 4; Length 2627;
Best Local Similarity 91.9%; Pred. No. 1.9e-262;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
XX
QY 1 CAAGCTGAGGCTTCCTTCATCCCTGAGAGAGCTAGAGCTTTCATTA 60
DB 1721 CAAGCTCTGAGGCTTCCTTCATCTGCTGAGAGAGCTTTCATTA 1780
QY 61 GCATCTAGAGCAGTGGAGCTCAGCTGGGATTTGCCCCCATCTCCGGGGAATGTC 120
DB 1781 GCATCTAGAGCAGTGGAGCTCAGCTGGGATTTGCCCCCATCTCCGGGGAATGTC 1840
QY 121 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGAAGAGATACGNNNNNNNNNNNN 180
DB 1841 TGAAGCAATTTGTTTACTCTCAATGAGGAGTGAAGAGATACGTTACTACCAAC 1900
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
DB 1901 TAGTGATTAAGGCCAGAGAGTGTCTCAACTCTCACTAGTACAGAGCTCTCCCAT 1960
QY 241 TACAACTACCAATCCGAAAGTGTCACTGTGAGAGCTAAGAAACCTGGTTTGAAGA 300
DB 1961 TACAACTACCAATCCGAAAGTGTCACTGTGAGAGCTAAGAAACCTGGTTTGAAGA 2020
QY 301 GAAAAGGGCTGGGAAAAGAGGGAGCCAAATCTGTCTGCTTCTTCACTTAATGTCATT 360
DB 2021 GAAAAGGGCTT-GGAAAAGAGGGAGCCAAATCTGTCTGCTTCTTCACTTAATGTCATT 2079
QY 361 GGGCAATTAAGCATTGCTGCTTGGCTGTGCTGAGCAGAGAGCCAGAACTTATC 420
DB 2080 GGGCAATTAAGCATTGCTGCTTGGCTGTGCTGAGCAGAGAGCCAGAACTTATC 2139
QY 421 GGGCACCAGGATTAACATCTCTCAGTAAAGAGAGTGAAGAGGCTTGGAAATGCTGA 480
DB 2140 GGGCACCAGGATTAACATCTCTCAGTAAAGAGAGTGAAGAGGCTTGGAAATGCTGA 2199
QY 481 TGGGATTAATCTTACGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTCACTGCAAG 540
DB 2200 TGGGATTAATCTTACGCTTGTGAGCTTCTAAGTTTCTTCCCTTCACTTCACTGCAAG 2259

```

```

QY 541 CCAGTCTGTAGAGAAAGGCTGAGTTCTAGCTCAGGTTTTTCTTACTCTGAATTTAGA 600
DB 2260 CCAGTCTGTAGAGAAAGGCTGAGTTCTAGCTCAGGTTTTTCTTACTCTGAATTTAGA 2319
QY 601 TCTCAGAGCCCTGCTGCGCAGCAATTCAAATTAAAGGCAACAAACATATACCTTCCATGAA 660
DB 2320 TCTCAGAGCCCTTCTGCGCAGCAATTCAAATTAAAGGCAACAAACATATACCTTCCATGAA 2379
QY 661 GCACACACAGACTTTTGAAGAGAGAGCAATAGCTCTGAATTGAGGCTTGAGAGAAAG 720
DB 2380 GCACACACAGACTTTTGAAGAGAGAGCAATAGCTCTGAATTGAGGCTTGAGAGAAAG 2439
QY 721 AAGCTTTGAAGGAAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCAATGTGTTA 780
DB 2440 AAGCTTTGAAGGAAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCAATGTGTTA 2499
QY 781 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGAGCTATTAATCATGTTTATAGAAAC 840
DB 2500 ACCACTGCTTCTCTGAGACCTTGGAGCCAGGAGCTATTAATCATGTTTATAGAAAC 2559
QY 841 TGATTTTGAAGTTTCAATGCTTCAAGAGAAATGATTAAATATCATTTCTT 890
DB 2560 TGATTTTGAAGTTTCAATGCTTCAAGAGAAATGATTAAATATCATTTCTT 2609
XX
XX RESULT 8
XX ID ABN72971 standard; DNA; 2627 BP.
XX
XX ABN72971;
XX
XX 02-JUL-2002 (first entry)
XX
XX DE Ovarian carcinoma polynucleotide OBE.
XX
XX KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200206317-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 17-JUL-2001; 2001WO-US022635.
XX
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.
XX PR 20-SEP-2000; 2000US-00667857.
XX PR 04-APR-2001; 2001US-00827271.
XX PR 18-JUN-2001; 2001US-00884441.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX DR WPI; 2002-164781/21.
XX DR P-PSDB; ABB30900, ABB30901.
XX
XX PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
XX PT protein or its variants, useful for stimulating an immune response in a
XX PT patient and treating ovarian cancer.
XX
XX PS Example 2; Page 319-320; 408pp; English.
XX
XX This invention relates to polypeptides comprising an immunogenic portion
XX CC of an ovarian carcinoma protein which acts as an immunostimulant and is
XX CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
XX CC proteins, T cell populations and antigen presenting cells that express
XX CC the polypeptides are useful for stimulating an immune response in a
XX CC patient and treating ovarian cancer. This sequence represents DNA related
XX CC to the invention

```

Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 90.6%; Score 806.4; DB 6; Length 2627;

Best Local Similarity 91.9%; Pred. No. 1.9e-262;

Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

```

QY      1 CAAGCTCTGAGGCTTCTCCTTTTCATCTCTGCTGAGACAGCTTAAGACCTTCAGTTTCAATA 60
DB      1721 CAAGCTCTGAGGCTTCTCCTTTTCATCTCTGCTGAGACAGCTTAAGACCTTCAGTTTCAATA 1780
QY      61 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 120
DB      1781 GCATCTAAGACAGTGGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAATGTC 1840
QY      121 TGAAGCAATTTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB      1841 TGAAGCAATTTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGTCTACTACCAAC 1900
QY      181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
DB      1901 TAGTGATTAAGGCGCAGGAGTGTGCTCAACCTCTACCATGTACAGACGTCTCCCAT 1960
QY      241 TACAACTACCAATCCGAAGTGTCACTGTCTAGAGACTTAAGAAACCTGGTTTGAATA 300
DB      1961 TACAACTACCAATCCGAAGTGTCACTGTCTAGAGACTTAAGAAACCTGGTTTGAATA 2020
QY      301 GAAAAGGGGCTGGGAAAGAGGGGAGCCAACTATCTGTCTGCTTCTCACTTAAGTCAAT 360
DB      2021 GAAAAGGGGCTT-GGAAAGGGGAGCCAACTATCTGTCTGCTTCTCACTTAAGTCAAT 2079
QY      361 GGCATAATAGCAATTCCTCTTTGGCTGCTGCTCTCAGACAGAGAGCCAGAACTCTATC 420
DB      2080 GGCATAATAGCAATTCCTCTTTGGCTGCTGCTCTCAGACAGAGAGCCAGAACTCTATC 2139
QY      421 GGGCACAGAGATTAATCTCTCAAGTGAAGAGAGTTGACAAAGCCCTTAGGAAATGCCGTA 480
DB      2140 GGGCACAGAGATTAATCTCTCAAGTGAAGAGAGTTGACAAAGCCCTTAGGAAATGCCGTA 2199
QY      481 TGGGATTAATCTCTCAGCTTTGAGCTTCTAAGTTTCTTCCCTCACTTACCTCGCAAG 540
DB      2200 TGGGATTAATCTCTCAGCTTTGAGCTTCTAAGTTTCTTCCCTCACTTACCTCGCAAG 2259
QY      541 CCAAGTCTGTAAAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
DB      2260 CCAAGTCTGTAAAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
QY      601 TCTCCAGACCTGCTGCGCCACAACTTAAGGCAACAAACATATACCTTCATGAA 660
DB      2320 TCTCCAGACCTGCTGCGCCACAACTTAAGGCAACAAACATATACCTTCATGAA 2379
QY      661 GCACACAGACCTTTGAAAGCAAGGACAACTGCTTGAATTGAGGCTTGAGGAATG 720
DB      2380 GCACACAGACCTTTGAAAGCAAGGACAACTGCTTGAATTGAGGCTTGAGGAATG 2439
QY      721 AAGCTTTGAAGAAAAAATTAATCTTTTTCAGCCCCCTTCCACACTCTTCATGTGTTA 780
DB      2440 AAGCTTTGAAGAAAAAATTAATCTTTTTCAGCCCCCTTCCACACTCTTCATGTGTTA 2499
QY      781 ACCACCTGCTTCTCTGAGACCTTGAAGCAAGGTGACGTATTAAGTTTGAAGAAAC 840
DB      2500 ACCACCTGCTTCTCTGAGACCTTGAAGCAAGGTGACGTATTAAGTTTGAAGAAAC 2559
QY      841 TGATTTTGAAGTTCTGATCGTTCAGAGAAATGATTAATATACATTTCTCT 890
DB      2560 TGATTTTGAAGTTCTGATCGTTCAGAGAAATGATTAATATACATTTCTCT 2609

```

RESULT 9

ADA08544

ID ADA08544 strand: cDNA; 2627 BP.

AC ADA08544;

XX

XX

DT 06-NOV-2003 (first entry)

XX Human ovarian carcinoma polynucleotide O8E.

XX ss; human; gene therapy; ovarian cancer; cancer.

KM Homo sapiens.

XX US2003091580-A1.

XX 15-MAY-2003.

XX 17-JUN-2001; 2001US-00907969.

XX 18-JUN-2001; 2001US-00884441.

XX (MITC/ MITCHAM J L.

XX (KING/ KING G E.

XX (ALGA/ ALGATE P A.

XX (FLIN/ FLING S P.

XX (RETT/ RETTER M W.

XX (FANG/ FANGER G R.

XX (VEDV/ VEDVICK T S.

XX (CART/ CARTER D.

XX (HILL/ HILL P.

XX (ALBO/ ALBONE E.

XX Mitcham JI, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;

PI Reed SG, Vedrick TS, Carter D, Hill P, Albone E;

XX WPI; 2003-532352/50.

XX New isolated O772P polypeptides and polynucleotides, useful in gene

PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian

PT cancer.

XX Example 2; SEQ ID NO 391; 371pp; English.

XX The invention relates to an isolated O772P polypeptide, which has the

CC structure fully defined in the specification. The composition containing

CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells

CC or antigen presenting cells are useful for stimulating an immune response

CC and treating ovarian cancer. Detecting the presence of the

CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian

CC carcinoma cDNAs and protein cDNAs were identified using microarray

CC technology. The present sequence represents a human ovarian carcinoma

CC antigen polynucleotide.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 1961 TACAACTACCCAAATCCGAAATGTCACACTGTGTGACAGTAAGAAACCTGGTTTGAGTA 2020
 Qy 301 GAAAGGGGCTGGGAAAGAGGGAGCCAAATCTGTCTCTCCACATTAAGTAT 360
 Db 2021 GAAAGGGGCTT-GGAAAGAGGGAGCCAAATCTGTCTCTCCACATTAAGTAT 2079
 Qy 361 GGCAAATTAAGCATTTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 420
 Db 2080 GGCAAATTAAGCATTTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 2139
 Qy 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 480
 Db 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 2199
 Qy 481 TGGATTAATCTTGAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTAACCTGGAAG 540
 Db 2200 TGGATTAATCTTGAAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTAACCTGGAAG 2259
 Qy 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGTAATTAGA 600
 Db 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGTTTCTTACTGTAATTAGA 2319
 Qy 601 TCTCCAGACCTCTGCTGGCCACAAATTAAGGCAACAAATATACCTTCATGAA 660
 Db 2320 TCTCCAGACCTCTGCTGGCCACAAATTAAGGCAACAAATATACCTTCATGAA 2379
 Qy 661 GCACACACAGATTTTGAAGCAAGGACATGACTGTGTAATTGAGGCTTGAGCAATG 720
 Db 2380 GCACACACAGATTTTGAAGCAAGGACATGACTGTGTAATTGAGGCTTGAGCAATG 2439
 Qy 721 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTTA 780
 Db 2440 AAGCTTTGAAGAAAGAAATACTTTGTTTCCAGCCCCCTTCCCACTCTTCAATGTTA 2499
 Qy 781 ACCACTGCTTCTCTGACCTTGAAGCCAGGTGATGATTAATGATTTGTAATGAAGAAC 840
 Db 2500 ACCACTGCTTCTCTGACCTTGAAGCCAGGTGATGATTAATGATTTGTAATGAAGAAC 2559
 Qy 841 TGAATTTAAGTCTGATTCGTTCAAGAGATGATTAATTAATTAATTCCT 890
 Db 2560 TGAATTTAAGTCTGATTCGTTCAAGAGATGATTAATTAATTAATTCCT 2609
 RESULT 10
 ADF08887
 ID ADF08887 standard; cDNA; 2627 BP.
 XX
 AC ADF08887;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE cDNA encoding secreted ovarian carcinoma antigen segid 391.
 XX
 KM Gene therapy; protein therapy; vaccine; antibody inhibition;
 KM breast cancer; restorative therapy; diagnostic agent; immunoassay;
 KM secreted ovarian carcinoma antigen; gene; ss.
 XX
 OS Homo sapiens.
 OS
 PN US2003124140-A1.
 XX
 PD 03-JUL-2003.
 PF 17-JUL-2002; 2002US-00198053.
 XX
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00215603.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00636801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.

PR 18-JUN-2001; 2001US-00884441.
 PR 17-JUL-2001; 2001US-00907969.
 PA (CORI-) CORIXA CORP.
 PI Bangor CS, Retter MW, Fanger GR, Hill P;
 XX
 XX WPI: 2003-897152/82.
 DR P-PSDB; ADF08888, ADF08889.
 XX
 PT Oncogenic nucleic acids useful for the prevention, diagnosis and
 PT treatment of breast cancer.
 XX
 PS Example 2; SEQ ID NO 391; 399bp; English.
 CC The invention describes nucleic acids (I) and the polypeptides (II) they
 CC encode. The nucleic acids (I) may be used for preventing, diagnosing and
 CC treating diseases related to their aberrant expression i.e. breast
 CC cancers. For example, (I) and (II) may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of (II) by expressing
 CC inactive proteins or to supplement the patient's own production of (II).
 CC Additionally, (I) may be used to produce (II), by inserting (I) into a
 CC host cell and culturing the cell to express the protein (II). (I) And its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. The host cell may also be used as antigens in the production of
 CC antibodies against (II) and in assays to identify modulators of (II)'s
 CC expression and activity. The anti-(II) antibodies, agonists and
 CC antagonists may be used to regulate expression and activity and as
 CC diagnostic agents for detecting the presence of (II) in samples (e.g. by
 CC immunoassay). This sequence represents a polynucleotide encoding a
 CC secreted ovarian carcinoma antigen.
 XX
 SQ Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;
 Query Match 90.6%; Score 806.4; DB 10; Length 2627;
 Best Local Similarity 91.9%; Pred. No. 1,9e-262;
 Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
 Qy 1 CAAGCTCTGAGGCTTCTCCCTTCCATCTGCGTGAACAGTCAAGCTTCAATTA 60
 Db 1721 CAAGCTCTGAGGCTTCTCCCTTCCATCTGCGTGAACAGTCAAGCTTCAATTA 1780
 Qy 61 GCATCTAAGACAGTGGAGCTCAGCTGGGATTTGCCCCCATCTCCGGGGGAATGTC 120
 Db 1781 GCATCTAAGACAGTGGAGCTCAGCTGGGATTTGCCCCCATCTCCGGGGGAATGTC 1840
 Qy 121 TGAAGCAATTTTGTCTTACTCAATGAAGGAGTGGAGAGATACAGNNNNNNNNNN 180
 Db 1841 TGAAGCAATTTTGTCTTACTCAATGAAGGAGTGGAGAGATACAGNNNNNNNNNN 1900
 Qy 181 NNN 240
 Db 1901 TAGTGATTAAGGCCAGGAGTGTCTCAACCTCTCAATGATGACAGAGTCTCCCAT 1960
 Qy 241 TACAACTACCCAAATCCGAAATGTCACATGTGTACAGATTAAGAAACCTGTTTGAAGTA 300
 Db 1961 TACAACTACCCAAATCCGAAATGTCACATGTGTACAGATTAAGAAACCTGTTTGAAGTA 2020
 Qy 301 GAAAGGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTCTCTCTCAATTAAGTAT 360
 Db 2021 GAAAGGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTCTCTCTCAATTAAGTAT 2079
 Qy 361 GGCAAATTAAGCATTTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 420
 Db 2080 GGCAAATTAAGCATTTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTATC 2139
 Qy 421 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 480
 Db 2140 GGGCACCAGATTAACATCTCTCAGTGAACAGAGTTGCAAGGCTATGGAAATGCTGA 2199

```
OY 481 TGGATTAATCTTACAGCTTGTAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 540
DB 2200 TGGGATTAATCTTACAGCTTGTAGCTTCTAAGTTTCTTCCCTTCAATTCACCTGCAAG 2259
OY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
OY 601 TCTCCAGACCTGCTGGCCCAATTCAAATTAAGCAACAAACATATACCTTCCATGAA 660
DB 2320 TCTCCAGACCTTCTGCGCCCAATTCAAATTAAGCAACAAACATATACCTTCCATGAA 2379
OY 661 GCACACACAGACTTTTGAAGAGCAACAGACTGCTTGAATTAAGGCTTGAAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGAGCAACAGACTGCTTGAATTAAGGCTTGAAGAAATG 2439
OY 721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTTA 780
DB 2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTTA 2499
OY 781 ACCACTGCTTCTGAGACCTTGGAGCAAGGTAAGTATTAATGTTATAGAAAC 840
DB 2500 ACCACTGCTTCTGAGACCTTGGAGCAAGGTAAGTATTAATGTTATAGAAAC 2559
OY 841 TGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAATATACATTTCT 890
DB 2560 TGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAATATACATTTCT 2609
```

RESULT 11

ADG46174
ID ADG46174 standard; cDNA; 2627 BP.

AC ADG46174;

DT 26-FEB-2004 (first entry)

DE Human ovarian carcinoma polynucleotide #387.

KM Human; ovarian carcinoma; gene; 88; OBE; ovarian cancer;
secreted tumour antigen; cytostatic; O772P.

OS Homo sapiens.

PN US2003165504-A1.

PD 04-SEP-2003.

PF 04-APR-2001; 2001US-00827271.

PR 17-DEC-1998; 98US-00215681.

PR 17-DEC-1998; 98US-00216003.

PR 23-JUN-1999; 99US-00338933.

PR 24-SEP-1999; 99US-00404879.

PR 17-JUL-2000; 2000US-00617747.

PR 10-AUG-2000; 2000US-00636801.

PR 20-SEP-2000; 2000US-00667857.

PA (RETT/) RETTER M W.

PA (FANG/) FANGER G R.

PI Recter MW, Fanger GR;

DR MPI, 2003-898035/82.

PT New isolated OBE or O772P polypeptides, useful for diagnosing,
preventing, treating and monitoring cancer, e.g. ovarian cancer,
stimulating the immune response in patient.

PS Example 2; SEQ ID NO 391; 290bp; English.

CC The invention relates to human ovarian carcinoma polypeptides, designated
OBE or O772P, and the polynucleotides encoding them. The invention also

CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC methods for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polynucleotide of the invention.

Sequence 2627 BP; 754 A; 605 C; 584 G; 684 T; 0 U; 0 Other;

Query Match 90.6%; Score 806.4; DB 10; Length 2627;

Best Local Similarity 91.9%; Pred. No. 1.9e-262;

Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

```
OY 1 CAAAGCTGAGAGCTTCTCCCTTCCATCCCTGGGAGAGAGCTAGAGCTCAGTTTCAATA 60
DB 1721 CAAAGCTGAGAGCTTCTCCCTTCCATCCCTGGGAGAGAGCTAGAGCTCAGTTTCAATA 1780
OY 61 GCATCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 1781 GCATCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1840
OY 121 TGAAGACAAATTTGGTTAAGTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 1841 TGAAGACAAATTTGGTTAAGTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1900
OY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
DB 1901 TAGTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1960
OY 241 TACAATCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 300
DB 1961 TACAATCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 2020
OY 301 GAAAAGGGGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 2021 GAAAAGGGGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2079
OY 361 GGGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 2080 GGGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2139
OY 421 GGGACACAGATTAATCTCTCAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 2140 GGGACACAGATTAATCTCTCAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2199
OY 481 TGGGATTAATCTTCAAGCTTGTAGCTTGAATTTCTTCCCTTCAATTCACCTGCAAG 540
DB 2200 TGGGATTAATCTTCAAGCTTGTAGCTTGAATTTCTTCCCTTCAATTCACCTGCAAG 2259
OY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
DB 2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 2319
OY 601 TCTCCAGACCTGCTGGCCCAATTCAAATTAAGCAACAAACATATACCTTCCATGAA 660
DB 2320 TCTCCAGACCTTCTGCGCCCAATTCAAATTAAGCAACAAACATATACCTTCCATGAA 2379
OY 661 GCACACACAGACTTTTGAAGAGCAACAGACTGCTTGAATTAAGGCTTGAAGAAATG 720
DB 2380 GCACACACAGACTTTTGAAGAGCAACAGACTGCTTGAATTAAGGCTTGAAGAAATG 2439
OY 721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTTA 780
DB 2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACTTTCATGTGTTA 2499
OY 781 ACCACTGCTTCTGAGACCTTGGAGCAAGGTAAGTATTAATGTTATAGAAAC 840
DB 2500 ACCACTGCTTCTGAGACCTTGGAGCAAGGTAAGTATTAATGTTATAGAAAC 2559
OY 841 TGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAATATACATTTCT 890
```


XX WO2004053079-A2.
 XX 24-JUN-2004.
 XX 08-DEC-2003; 2003WO-US038855.
 XX 06-DEC-2002; 2002US-0431301P.
 XX 06-DEC-2002; 2002US-0431321P.
 XX 30-JUN-2003; 2003US-0484584P.
 XX 07-NOV-2003; 2003US-0518607P.
 XX (DIAD-) DIADEXUS INC.
 XX Macina RA, Turner LR, Sun Y, Liu S, Chen H;
 XX WPI; 2004-468850/44.
 XX P-P8DB; ADP81235, ADP81236.
 XX New ovarian specific nucleic acid molecules and polypeptides useful for
 XX diagnosing, preventing or treating ovarian cancer, for producing
 XX transgenic animals or cells, or for research purposes.
 XX Claim 1; SEQ ID NO 109; 754bp, English.
 XX The invention relates to novel isolated nucleic acid molecules and
 XX polypeptides present in normal and neoplastic ovarian cells. These
 XX comprise a nucleic acid sequence encoding any of the 167 amino acid
 XX sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
 XX specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
 XX the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
 XX in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
 XX further comprises: a method for determining the presence of a ovarian
 XX specific nucleic acid (OSNA) in a sample; a vector comprising the above
 XX nucleic acid molecule; a host cell comprising the vector; a method for
 XX producing a polypeptide encoded by the nucleic acid molecule; a
 XX polypeptide encoded by the nucleic acid molecule cited above; an antibody
 XX or its fragment that specifically binds to the above polypeptide; a
 XX method for determining the presence of an ovarian specific protein in a
 XX sample; a method for diagnosing or monitoring the presence and metastases
 XX of ovarian cancer in a patient; a kit for detecting a risk of cancer or
 XX presence of cancer in a patient, the kit comprising a means for
 XX determining the presence of the above nucleic acid molecule or
 XX polypeptide; a method of treating a patient with ovarian cancer; and a
 XX vaccine comprising the above polypeptide or nucleic acid encoding the
 XX polypeptide. The isolated nucleic acid molecules and polypeptides have
 XX cytostatic activity. The isolated polypeptides may be used to create a
 XX vaccine. The isolated nucleic acid molecules and polypeptides can be used
 XX for diagnosing or monitoring the presence and metastases of ovarian
 XX cancer and treating ovarian cancer. This polynucleotide sequence
 XX represents an ovarian specific gene of the invention.
 XX Sequence 2690 BP; 760 A; 611 G; 603 G; 716 T; 0 U; 0 Other;
 XX
 XX Query Match 90.6%; Score 806.4; DB 12; Length 2690;
 XX Best Local Similarity 91.9%; Pred. No. 1.9e-262;
 XX Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
 XX
 QY 1 CAAGCTGAGGCTTCCTTCCTCCATGCTGAGCAGCTAAGCCTCAGTTTCATTA 60
 Db 1801 CAAGCTCGAGGCTTCCTTCCTCCATGCTGAGCAGCTAAGCCTCAGTTTCATTA 1860
 QY 61 GCATCTAGAGAGAGTGGAGCTCAGCTGGGTGATTTCCGCCCATCTCCGGGGAGATGTC 120
 Db 1861 GCATCTAGAGAGAGTGGAGCTCAGCTGGGTGATTTCCGCCCATCTCCGGGGAGATGTC 1920
 QY 121 TGAAGACAATTTTGGTACCTTCATGAGGAGCTGAGAGATACAGNNNNNNNNNNNN 180
 Db 1921 TGAAGACAATTTTGGTACCTTCATGAGGAGCTGAGAGATACAGGCTACTACCAAC 1980
 QY 181 NNN 240
 Db 1981 TAGTGATTAAGGCGAGGATGCTGCTCAACTCTTACCATGTACAGAGCGTCTCCCAT 2040

QY 241 TACAACCTACCCCAATCCGAAGTGTCAACTGTGTGAGACTAAGAAACCTGGTTTGA 300
 Db 2041 TACAACCTACCCCAATCCGAAGTGTCAACTGTGTGAGACTAAGAAACCTGGTTTGA 2100
 QY 301 GAAAAAGGCTGGGAGAGAGGAGCCCAAAATGTGTCTCTCTCACTTACTGATT 360
 Db 2101 GAAAAAGGCTGGGAGAGAGGAGCCCAAAATGTGTCTCTCTCACTTACTGATT 2159
 QY 361 GGGCAATAGAGATTCGTCTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
 Db 2160 GGGCAATAGAGATTCGTCTCTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2219
 QY 421 GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGAGAAATGCTCTGA 480
 Db 2220 GGGCAACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGAGAAATGCTCTGA 2279
 QY 481 TGGGATTAATCTTCAGCTTGTGAGCTTGAATTTCTTCCCTTCATCTACCTCTGACAG 540
 Db 2280 TGGGATTAATCTTCAGCTTGTGAGCTTGAATTTCTTCCCTTCATCTACCTCTGACAG 2339
 QY 541 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGCTTCTTACTCTGAATTTAGA 600
 Db 2340 CCAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTCAGCTTCTTACTCTGAATTTAGA 2399
 QY 601 TCTCCAGACCCCTGCTGCGCCCAATTCMAATTAAGCAACAAATATACCTTCATGAA 660
 Db 2400 TCTCCAGACCCCTGCTGCGCCCAATTCMAATTAAGCAACAAATATACCTTCATGAA 2459
 QY 661 GCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTAGAGCCCTTGAGGAATG 720
 Db 2460 GCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTAGAGCCCTTGAGGAATG 2519
 QY 721 AAGCTTGAAGAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCATGATGTTA 780
 Db 2520 AAGCTTGAAGAAAGAAATATCTTGTTCAGGCCCTTCCACACTCTTCATGATGTTA 2579
 QY 781 ACCACTGCTTCTGAGACTTTGAGCCAGCCAGGCTGATGATTTATTAATGTTATGAA 840
 Db 2580 ACCACTGCTTCTGAGACTTTGAGCCAGCCAGGCTGATGATTTATTAATGTTATGAA 2639
 QY 841 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCTCT 890
 Db 2640 TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCTCT 2689
 XX
 XX RESULT 14
 XX ID AAD32519 standard; DNA; 3357 BP.
 XX AC AAD32519;
 XX DT 18-JUN-2002 (first entry)
 XX
 XX Human B7-H8 gene.
 XX
 XX Human; B7-1like protein; inflammation; tissue damage; immune disorder;
 XX Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis;
 XX diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer;
 XX rheumatoid arthritis; cardiovascular disorder; nervous system disorder;
 XX myocardial ischaemia; ulcerative colitis; reproductive system disorder;
 XX Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis;
 XX diabetes mellitus; Grave's disease; Paget's disease; liver disorder;
 XX gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia;
 XX dysphagia; hepatomegaly; neurological disease; infectious disease;
 XX epilepsy; gene therapy; B7-H8 protein; chromosome 1; gene; ds.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 419..1267
 XX FT /*tag= a
 XX FT /product= "Human B7-H8 protein"

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2005, 08:54:34 ; Search time 164.951 Seconds
(without alignments)
8828.602 Million cell updates/sec

Title: US-09-763-978B-16

Perfect score: 890

Sequence: 1 caagctctgagcgtctctcct.....tgataataatacattctcct 890

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/6CTUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	806.4	90.6	2627	3	US-09-404-879A-391 Sequence 391, App
2	806.4	90.6	2627	4	US-09-667-857-391 Sequence 391, App
3	794.4	89.3	1567	3	US-09-404-879A-74 Sequence 74, Appl
4	794.4	89.3	1567	4	US-09-338-933-74 Sequence 74, Appl
5	794.4	89.3	1567	4	US-09-215-681-74 Sequence 74, Appl
6	794.4	89.3	1567	4	US-09-216-003A-74 Sequence 74, Appl
7	794.4	89.3	1567	4	US-09-667-857-74 Sequence 74, Appl
8	446.6	50.2	461	3	US-09-404-879A-27 Sequence 27, Appl
9	446.6	50.2	461	4	US-09-338-933-27 Sequence 27, Appl
10	446.6	50.2	461	4	US-09-215-681-27 Sequence 27, Appl
11	446.6	50.2	461	4	US-09-216-003A-27 Sequence 27, Appl
12	446.6	50.2	461	4	US-09-667-857-27 Sequence 27, Appl
13	364.8	41.0	695	3	US-09-040-984-15 Sequence 15, Appl
14	364.8	41.0	695	3	US-09-123-912-15 Sequence 15, Appl
15	364.8	41.0	695	3	US-09-643-597-15 Sequence 15, Appl
16	364.8	41.0	695	4	US-09-480-884A-15 Sequence 15, Appl
17	364.8	41.0	695	4	US-09-542-615A-15 Sequence 15, Appl
18	364.8	41.0	695	4	US-09-606-421B-15 Sequence 15, Appl
19	364.8	41.0	695	4	US-09-221-107-15 Sequence 15, Appl
20	364.8	41.0	695	4	US-09-466-396A-15 Sequence 15, Appl
21	364.8	41.0	695	4	US-09-476-496A-15 Sequence 15, Appl
22	364.8	41.0	695	4	US-09-630-940B-15 Sequence 15, Appl
23	364.8	41.0	695	4	US-09-285-479-15 Sequence 15, Appl
24	52.4	5.3	59828	4	US-09-949-016-16238 Sequence 16238, A
25	47.6	5.3	1082	2	US-08-909-965C-12 Sequence 12, Appl
26	46.2	5.2	77661	4	US-09-949-016-12770 Sequence 12770, A
27	46.2	5.2	77663	4	US-09-949-016-13751 Sequence 13751, A

28	45.2	5.1	601	4	US-09-949-016-88942 Sequence 88942, A
C 29	44	4.9	162465	4	US-09-949-016-14264 Sequence 14264, A
C 30	43	4.8	146401	4	US-09-949-016-16151 Sequence 16151, A
C 31	41.2	4.6	112623	4	US-09-949-016-14374 Sequence 14374, A
C 32	40.6	4.6	601	4	US-09-949-016-160158 Sequence 160158, A
C 33	40.2	4.5	601	4	US-09-949-016-43835 Sequence 43835, A
C 34	40.2	4.5	601	4	US-09-949-016-52452 Sequence 52452, A
C 35	40.2	4.5	601	4	US-09-949-016-52452 Sequence 52452, A
C 36	40.2	4.5	601	4	US-09-949-016-52497 Sequence 52497, A
C 37	40.2	4.5	49164	4	US-09-949-016-12985 Sequence 12985, A
C 38	40.2	4.5	49164	4	US-09-949-016-12986 Sequence 12986, A
C 39	40.2	4.5	49164	4	US-09-949-016-13262 Sequence 13262, A
C 40	40.2	4.5	49164	4	US-09-949-016-13263 Sequence 13263, A
C 41	40.2	4.5	87863	4	US-09-949-016-14402 Sequence 14402, A
C 42	39.8	4.5	82494	4	US-09-949-016-16537 Sequence 16537, A
C 43	39.8	4.5	115814	4	US-09-949-016-16205 Sequence 16205, A
C 44	39.6	4.4	178883	4	US-09-949-016-12733 Sequence 12733, A
C 45	39.6	4.4	178884	4	US-09-949-016-13039 Sequence 13039, A

ALIGNMENTS

RESULT 1									
US-09-404-879A-391									
Sequence 391, Application US/09404879A									
Patent No. 6468546									
GENERAL INFORMATION:									
APPLICANT: Mitcham, Jennifer L.									
APPLICANT: King, Gordon E.									
TITLE OF INVENTION: ALGATE, PAUL A.									
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND									
FILE REFERENCE: 210121.462C2									
CURRENT APPLICATION NUMBER: US/09/404,879A									
NUMBER OF SEQ ID NOS: 1999-09-24									
SOFTWARE: FASTSQ for Windows Version 3.0									
SEQ ID NO 391									
LENGTH: 2627									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-404-879A-391									
Query Match									
Best Local Similarity 90.6%; Score 806.4; DB 3; Length 2627;									
Matches 818; Conservativity 91.9%; Pred. No. 4.3e-246;									
Mismatch 71; Indels 1; Gaps 1;									
QY	1	CAAGCTGAGGCTTCTCTTCCATCCGCGGAGACGTAAGACCTGAGTTTCAATA	60						
DB	1721	CAAGCTGAGGCTTCTCTTCCATCCGCGGAGACGTAAGACCTGAGTTTCAATA	1780						
QY	61	GCATCTAGAGCAGTGGACTCAGCTGGGTGATTTGCCCCCATCTCCGGGGATGTC	120						
DB	1781	GCATCTAGAGCAGTGGACTCAGCTGGGTGATTTGCCCCCATCTCCGGGGATGTC	1840						
QY	121	TGAAGCAATTTTGGTTACTCAATGAGGAGTGAGAGATACGNNNNNNNNNN	180						
DB	1781	TGAAGCAATTTTGGTTACTCAATGAGGAGTGAGAGATACGNNNNNNNNNN	1840						
QY	1841	TGAAGCAATTTTGGTTACTCAATGAGGAGTGAGAGATACGNNNNNNNNNN	1900						
DB	1841	TGAAGCAATTTTGGTTACTCAATGAGGAGTGAGAGATACGNNNNNNNNNN	1900						
QY	181	NN	240						
DB	181	NN	240						
QY	1901	TGTTGATTAAGCCAGGAGATCTGCTCACTCTCAATGATACAGAGCTCTCCCAAT	1960						
DB	1901	TGTTGATTAAGCCAGGAGATCTGCTCACTCTCAATGATACAGAGCTCTCCCAAT	1960						
QY	241	TACCACTACCAATCCGAGTGTCACTGTGACAGACTAAGAAACCTGTTTGAGTA	300						
DB	241	TACCACTACCAATCCGAGTGTCACTGTGACAGACTAAGAAACCTGTTTGAGTA	300						
QY	1961	TACCACTACCAATCCGAGTGTCACTGTGACAGACTAAGAAACCTGTTTGAGTA	2020						
DB	1961	TACCACTACCAATCCGAGTGTCACTGTGACAGACTAAGAAACCTGTTTGAGTA	2020						
QY	301	GAAAAGGCTTGGGAAAGGGGAGCCAAATCTGTCTCTTCTCACTTAATGATTC	360						
DB	301	GAAAAGGCTTGGGAAAGGGGAGCCAAATCTGTCTCTTCTCACTTAATGATTC	360						
QY	2021	GAAAAGGCTTGGGAAAGGGGAGCCAAATCTGTCTCTTCTCACTTAATGATTC	2079						
DB	2021	GAAAAGGCTTGGGAAAGGGGAGCCAAATCTGTCTCTTCTCACTTAATGATTC	2079						
QY	361	GGAATATAGCATTCGTCTTTGGCTGCTCTCAGCAGAGAGGAGAACTCTATC	420						
DB	361	GGAATATAGCATTCGTCTTTGGCTGCTCTCAGCAGAGAGGAGAACTCTATC	420						

Db	2080	GGCAATATAGCATTTCTGTCCTCTTGGCTGCTGCTCAGACACAGAGGCCAAGACTTATC	21338
QY	421	GGGCAACGAGTAACATCTCTCAGTGAACAGATTGACAGGCTTATGGAAATGCTCGA	480
Db	2140	GGGCAACGAGTAACATCTCTCAGTGAACAGATTGACAGGCTTATGGAAATGCTCGA	2199
QY	481	TGGATTATCTTCAGCTTGTTGAGTTCTTAAGTTCTTCCCTCATTTCAACCTCGAAG	540
Db	2200	TGGATTATCTTCAGCTTGTTGAGTTCTTAAGTTCTTCCCTCATTTCAACCTCGAAG	2259
QY	541	CCAAGTCTGTAAAGAAATGCTGAGTTAGCTCAGATTTTCTTACTCGAATTTTGA	600
Db	2260	CCAAGTCTGTAAAGAAATGCTGAGTTCTTAAGTCTGAGATTTTCTTACTCGAATTTTGA	2319
QY	601	TCTCCAGACCTGCTGCGCCACAATTCAAATTAAGCAACAACATATACCTTCATGAA	660
Db	2320	TCTCCAGACCTGCTGCGCCACAATTCAAATTAAGCAACAACATATACCTTCATGAA	2379
QY	661	GCAACACACAGACTTTTGAAGCAGAGAACATATGACTGTTGAATTGAGGCTTTGAGAAATG	720
Db	2380	GCAACACACAGACTTTTGAAGCAGAGAACATATGACTGTTGAATTGAGGCTTTGAGAAATG	2439
QY	721	AAGCTTTGAAGAAAAGAACTTTGTTCCAGGCCCCCTCCACACACTTCATATGTTA	780
Db	2440	AAGCTTTGAAGAAAAGAACTTTGTTCCAGGCCCCCTCCACACACTTCATATGTTA	2499
QY	781	ACCACTGCTTCTCTGACCTTGGAGCCACGGTGACTGTATTACATGTTGTTATAGAAAAC	840
Db	2500	ACCACTGCTTCTCTGACCTTGGAGCCACGGTGACTGTATTACATGTTGTTATAGAAAAC	2559
QY	841	TGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAAATATACATTTCTCT	890
Db	2560	TGATTTTGAAGTTCTGATCTGTTCAAGAGAAATGATTAAATATACATTTCTCT	2609

```

RESULT 2
US-09-667-857-391
; Sequence 391, Application US/09667857
; Patent No. 669664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Retteer, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Patrick
; TITLE OF INVENTION: DIAGNOSIS AND METHODS FOR THE THERAPY AND
; TITL OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-667-857-391

```

Query Match	90.6%	Score 806.4	DB 4	Length 2627
Best Local Similarity	91.9%	Pred. 4.3e-246		
Matches 818	Conservative	0	Mismatches 71	Indels 1
			Gaps	1
Qy	1	CAAGCTCGAAGCTTCTCTTTCATCTCGGCTGACAGCTAAGACTCAGTTTCATTA	60	
Db	1721	CAAGCTCGAAGCTTCTCTTTCATCTCGGCTGACAGCTAAGACTCAGTTTCATTA	1780	
Qy	61	GCATCTAAGACAGTGGACTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGGAAATGTC	120	

[illegible]

```

1 RESULT 3
2 US-09-404-879A--74
3
4 ; Sequence 74, Application US/09404879A
5 ; Patent No. 6468546
6 ; GENERAL INFORMATION:
7 ; APPLICANT: Mitcham, Jennifer L.
8 ; APPLICANT: King, Gordon E.
9 ; APPLICANT: Algate, Paul A.
10 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
11 ; FILE REFERENCE: 210121.462C2
12 ; CURRENT APPLICATION NUMBER: US/09/404,879A
13 ; CURRENT FILING DATE: 1999-09-24
14 ; NUMBER OF SEQ ID NOS: 193
15 ; SOFTWARE: FastSeq for Windows Version 3.0
16 ; SEQ ID NO 74
17 ; LENGTH: 1567
18 ; TYPE: DNA
19 ;

```

ORGANISM: Homo sapien
US-09-404-879A-74

Query Match 89.3%; Score 794.4; DB 3; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

```
QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCTAAGAGACTGAGTTTCAAT 60
DB 679 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCTAAGAGACTGAGTTTCAAT 738
QY 61 GCATCTAGAGCACTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 120
DB 739 GCATCTAGAGCACTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGCAATTTTGGTTTACTCTCATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB 799 TGAAGCAATTTT-GTTACTCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 857
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
DB 858 TAGTGATTAAGGCCAGGAGTGTCTCAACCTCTCAATGATACAGAGCTCTCCCAT 917
QY 241 TACAATCACTCCCAATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGGTTTGAAT 300
DB 918 TACAATCACTCCCAATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGGTTTGAAT 977
QY 301 GAAAAGGGCTGGGAAAAGGGGAGCCAAATCTGTCTCTCTCTCTCATTAATGTCATT 360
DB 978 GAAAAGGGGCTT-GGAAAAGGGGAGCCAAATCTGTCTCTCTCTCATTAATGTCATT 1036
QY 361 GGGAAATTAAGCAATCTGTCTGTGCTGTGCTGCTGAGCAGAGAGCCAGACTATAC 420
DB 1037 GGGAAATTAAGCAATCTGTCTGTGCTGTGCTGCTGAGCAGAGAGCCAGACTATAC 1096
QY 421 GGGCAACAGAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTTATGGGAAATGCTGA 480
DB 1097 GGGCAACAGAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCACTGTGAGCTTTGAGCTTTCTTAAGTTTCTTCCCTCATTTACTCCGCAAG 540
DB 1157 TGGGATTAATCTTCACTGTGAGCTTTGAGCTTTCTTCCCTCATTTACTCCGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTCTGAATTTAGA 600
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTCTGAATTTAGA 1276
QY 601 TCTCCAGACCTGCTGCGCAATTCATTAAGGCAACAAACATATACCTTCCATGAA 660
DB 1277 TCTCCAGACCTTCTGCGCAATTCATTAAGGCAACAAACATATACCTTCCATGAA 1336
QY 661 GCACACACAGACTTTTGAAGCAAGACATAGCTCTGAATTTAGGCTTGAAGAAATG 720
DB 1337 GCACACACAGACTTTTGAAGCAAGACATAGCTCTGAATTTAGGCTTGAAGAAATG 1396
QY 721 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGA 780
DB 1397 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGA 1456
QY 781 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATTTATCATGTTGTTATAGAAAC 840
DB 1457 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATTTATCATGTTGTTATAGAAAC 1516
QY 841 TGAATTTAAGATTCTGATGTTCAAGAGATGATTAATATACATTTCT 890
DB 1517 TGAATTTAAGATTCTGATGTTCAAGAGATGATTAATATACATTTCT 1566
```

RESULT 4
US-09-338-933-74
Sequence 74, Application US/09338993
Patent No. 6488931
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapien
US-09-338-933-74

Query Match 89.3%; Score 794.4; DB 4; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

```
QY 1 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCTAAGAGACTGAGTTTCAAT 60
DB 679 CAAGCTCTGAGGCTTCTCTTCCATCCCTGCGAGCTAAGAGACTGAGTTTCAAT 738
QY 61 GCATCTAGAGCACTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 120
DB 739 GCATCTAGAGCACTGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCCGGGGAAATGTC 798
QY 121 TGAAGCAATTTTGGTTTACTCTCATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB 799 TGAAGCAATTTT-GTTACTCTCATGAGGAGTGAAGAGATACAGTCTACTACCAAC 857
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
DB 858 TAGTGATTAAGGCCAGGAGTGTCTCAACCTCTCAATGATACAGAGCTCTCCCAT 917
QY 241 TACAATCACTCCCAATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGGTTTGAAT 300
DB 918 TACAATCACTCCCAATCCGAAGTGTCAACTGTGTGAGAGCTAAGAAACCTGGTTTGAAT 977
QY 301 GAAAAGGGCTGGGAAAAGGGGAGCCAAATCTGTCTCTCTCTCATTAATGTCATT 360
DB 978 GAAAAGGGGCTT-GGAAAAGGGGAGCCAAATCTGTCTCTCTCTCATTAATGTCATT 1036
QY 361 GGGAAATTAAGCAATCTGTCTGTGCTGTGCTGCTGAGCAGAGAGCCAGACTATAC 420
DB 1037 GGGAAATTAAGCAATCTGTCTGTGCTGTGCTGCTGAGCAGAGAGCCAGACTATAC 1096
QY 421 GGGCAACAGAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTTATGGGAAATGCTGA 480
DB 1097 GGGCAACAGAGATTAACATCTCTCAGTGAACAGAGTTGACAGGCTTATGGGAAATGCTGA 1156
QY 481 TGGGATTAATCTTCACTGTGAGCTTTGAGCTTTCTTAAGTTTCTTCCCTCATTTACTCCGCAAG 540
DB 1157 TGGGATTAATCTTCACTGTGAGCTTTGAGCTTTCTTCCCTCATTTACTCCGCAAG 1216
QY 541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTCTGAATTTAGA 600
DB 1217 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTGAGTTTCTTACTCTGAATTTAGA 1276
QY 601 TCTCCAGACCTGCTGCGCAATTCATTAAGGCAACAAACATATACCTTCCATGAA 660
DB 1277 TCTCCAGACCTTCTGCGCAATTCATTAAGGCAACAAACATATACCTTCCATGAA 1336
QY 661 GCACACACAGACTTTTGAAGCAAGACATAGCTCTGAATTTAGGCTTGAAGAAATG 720
DB 1337 GCACACACAGACTTTTGAAGCAAGACATAGCTCTGAATTTAGGCTTGAAGAAATG 1396
QY 721 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGA 780
DB 1397 AAGCTTTGAAGAAAGAAATACCTTGTTCACGCCCCCTTCCACACTCTTCAATGTGA 1456
QY 781 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATTTATCATGTTGTTATAGAAAC 840
DB 1457 ACCACTGCTTCTCTGAGACCTTGAAGCAAGTGAATTTATCATGTTGTTATAGAAAC 1516
```


Db 1457 ACCACTGCTTCCTGAGACCTTGAGCCAGCGTAGCTGATTAATACATGTTGTTATAGAAAAC 1516
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
Db 1517 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 1566

RESULT 5
US-09-215-681-74
; Sequence 74, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-74

Query Match 89.3%; Score 794.4; DB 4; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

Qy 1 CAAGCTTGAGGCTTCCTCTCCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 60
Db 679 CAAGCTTGAGGCTTCCTCTCCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 738
Qy 61 GCATCTAGAGCAGTGGAGCTGAGTGGGGTGAATTTGCCCCCATCTCCGGGGATGTC 120
Db 739 GCATCTAGAGCAGTGGAGCTGAGTGGGGTGAATTTGCCCCCATCTCCGGGGATGTC 798
Qy 121 TGAACACATTTTGGTTACCTCAATGAGAGAGTGAAGAGATACAGNNNNNNNNNN 180
Db 799 TGAACACATTTT-GTTACTCAATGAGAGAGTGAAGAGATACAGTCACTACCAAC 857
Qy 181 NNN 240
Db 858 TAGTGATTAAGAGCCAGAGATGCTGCTCAACTCTCACTAGTACAGACGCTCCCAT 917
Qy 241 TACAACCTAACCTCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGGTTTGAATA 300
Db 918 TACAACCTAACCTCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGGTTTGAATA 977
Qy 301 GAAAAGGCGCTGGGAAAAGAGGGGAGCCAACTGTCCTCTCTCACTAGTCAAT 360
Db 978 GAAAAGGCGCT-GGAAAAGGGGAGCCAACTGTCCTCTCTCACTAGTCAAT 1036
Qy 361 GGCATAATAGCATCTGCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 420
Db 1037 GGCATAATAGCATCTGCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 1096
Qy 421 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGA 480
Db 1097 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGA 1156
Qy 481 TGGGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTTCCCTTCACTTACCTCGCAG 540
Db 1157 TGGGATTAATCTTCACTGTTGAGCTTCTAAGTTCTTTCCCTTCACTTACCTCGCAG 1216
Qy 541 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 600
Db 1217 CCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGA 1276
Qy 601 TCTTCAGACCTGCTGCGCACAAATTAATTAAGCAACAAACATATATACCTTCATGAA 660

Db 1277 TCTCAGACCCCTTCCTGCGCACAAATTAATTAAGCAACAAACATATACCTTCATGAA 1336
Qy 661 GCACACAGACTTTTGAAGAACAGACATGAGCTGTAATGAGGCTTGAGGAATG 720
Db 1337 GCACACAGACTTTTGAAGAACAGACATGAGCTGTAATGAGGCTTGAGGAATG 1396
Qy 721 AAGCTTGAAGAAAAGAAATCTTGTTCAGCCCCCTTCCACACTCTTCATGTGTA 780
Db 1397 AAGCTTGAAGAAAAGAAATCTTGTTCAGCCCCCTTCCACACTCTTCATGTGTA 1456
Qy 781 ACCACTGCTTCCTGAGACCTTGAGCCAGCGTAGCTGATTAATACATGTTTATAGAAAAC 840
Db 1457 ACCACTGCTTCCTGAGACCTTGAGCCAGCGTAGCTGATTAATACATGTTTATAGAAAAC 1516
Qy 841 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 890
Db 1517 TGATTTAGAGTTCTGATCGTTCAAGAGATGATTAATATACATTTCT 1566

RESULT 6

US-09-216-003A-74
; Sequence 74, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-216-003A-74

Query Match 89.3%; Score 794.4; DB 4; Length 1567;
Best Local Similarity 91.8%; Pred. No. 2.2e-242;
Matches 817; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

Qy 1 CAAGCTTGAGGCTTCCTCTCCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 60
Db 679 CAAGCTTGAGGCTTCCTCTCCATCCGCTGAGACAGCTAAGACTCAGTTTCAATA 738
Qy 61 GCATCTAGAGCAGTGGAGCTGAGTGGGGTGAATTTGCCCCCATCTCCGGGGATGTC 120
Db 739 GCATCTAGAGCAGTGGAGCTGAGTGGGGTGAATTTGCCCCCATCTCCGGGGATGTC 798
Qy 121 TGAACACATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
Db 799 TGAACACATTTT-GTTACTCAATGAGGAGTGAAGAGATACAGTCACTACCAAC 857
Qy 181 NNN 240
Db 858 TAGTGATTAAGAGCCAGAGATGCTGCTCAACTCTCACTAGTACAGACGCTCCCAT 917
Qy 241 TACAACCTAACCTCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGGTTTGAATA 300
Db 918 TACAACCTAACCTCCGAAGTGTCAACTGTCTCAGAGCTAAGAAACCTGGTTTGAATA 977
Qy 301 GAAAAGGCGCTGGGAAAAGAGGGGAGCCAACTGTCCTCTCTCACTAGTCAAT 360
Db 978 GAAAAGGCGCT-GGAAAAGGGGAGCCAACTGTCCTCTCTCACTAGTCAAT 1036
Qy 361 GGCATAATAGCATCTGCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 420
Db 1037 GGCATAATAGCATCTGCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 1096
Qy 421 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGGCTTATGGAAATGCTGA 480

Db	1097	GGGCAACCGATACATCTTCAGTGAACAAGTTGACAGGCTTATGGAAATGGCTGA	1156
Qy	481	TGGATTATCTTCAGCTGTGTAGCTTCTAAGTTCTTCCCTCATTTCACTCCGCAAG	540
Db	1157	TGGGTTATCTTCAGCTGTGTAGCTTCTAAGTTCTTCCCTCATTTCACTCCGCAAG	1216
Qy	541	CCAACTTCTGTAAAGAAATCCCTGAGTTCTAGCTCAAGTTTCTTACTGAAATTTAGA	600
Db	1217	CCAACTTCTGTAAAGAAATCCCTGAGTTCTAGCTCAAGTTTCTTACTGAAATTTAGA	1276
Qy	601	TCTCCAGCCCTGCTGGCCCAATTTCAATTAAGGCAACAATATACCTTCATGAA	660
Db	1277	TCTCCAGCCCTTCTCTGGCCCAATTTCAATTAAGGCAACAATATACCTTCATGAA	1336
Qy	661	GCACACACAGACTTTTGAAGCAAGACAAATGACTGCTGAAATTAGGCGCTTGAGAAATG	720
Db	1337	GCACACACAGACTTTTGAAGCAAGACAAATGACTGCTGAAATTAGGCGCTTGAGAAATG	1396
Qy	721	AAGCTTTGAAGAAAAGAATACTTGTGTTCCAGCCCCCTTCCCACTCTTCATGTGTGA	780
Db	1397	AAGCTTTGAAGAAAAGAATACTTGTGTTCCAGCCCCCTTCCCACTCTTCATGTGTGA	1456
Qy	781	ACCACTGCTTCTCGGACCTTGGAGCCACGGTGACTGTATTAACATGTTGTTATAGAAAAC	840
Db	1457	ACCACTGCTTCTCGGACCTTGGAGCCACGGTGACTGTATTAACATGTTGTTATAGAAAAC	1516
Qy	841	TGATTTTGAAGTTCTGATCGTTTCAAGAAATGATTTAAATATACATTTTCT	890
Db	1517	TGATTTTGAAGTTCTGATCGTTTCAAGAAATGATTTAAATATACATTTTCT	1566

RESULT 7
US-09-66

; Sequence 74, Application US/09667857

; GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Retter, Marc W.

APPLICANT: Reed, Steven G.

APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND PREVENTION OF DYSMOTRIC SYNDROMES

FILE REFERENCE: 210121.462C5

CURRENT FILING DATE: 2000-09-20

```

; NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0

```

; SEQ ID NO 74
; LENGTH: 1563

TYPE: DNA

US-09-667-857-74

Query Match	89.3%	Score 794.4	DB 4	Length 1567
Best Local Similarity	91.8%	Pred. No. 2.2e-242		
Matches 817; Conservative	0	Mismatches 71	Indels 2	Gaps 2

Qy CAAGCTCGAGGCTTCCTCTTCACATCCGACGAGACACTAAGACTCATGTTTCAATA 60
Db CAAAGCTCGAGGCTTCCTCTTCACATCCGACGAGACACTAAGACTCATGTTTCAATA 738
Qy - 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 120
Db GCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCCCCCATCTCCGGGGAAATGTC 798
Qy TGAAACAATTTGGTTACCTCAATGAGGAGTGGAGAGGATACAGNNNNNNNNNNNNNN 180

[illegible]

RESULT 8

US-03-404-875A-21/C
: Sequence 27, Application US/09404879A

Patent NO. 6468546
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION:	DIAGNOSIS OF OVARIAN CANCER
INVENTOR:	COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C2

CURRENT FILING DATE: 1999-09-24

```

; SOFTWARE: FastSeq for Windows Version 3.0

```

LENGTH: 461

```

; TYPE: DNA
; ORGANISM: Homo sapiens

```

FEATURE:

LOCATION: (1) ... (461)

OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-27

Query Match 50.2%; Score 446.6; DB 3; Length 461;
Best Local Similarity 98.9%; Pred. No. 7.1e-132;
Matches 457; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAGGCGCTATGGAAATGCTGATGGAT 486
DB 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAAGGCGCTATGGAAATGCTGATGGAT 403
QY 487 TATCTTCAGCTTGTGAGCTTTAAAGTTTCTTCCCTCATTTCACTGCAAGCCAACT 546
DB 402 TATCTTCAGCTTGTGAGCTTTAAAGTTTCTTCCCTCATTTCACTGCAAGCCAACT 343
QY 547 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
DB 342 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
QY 607 GACCTGCTGCGCCAAATTCATAATTAAAGCAACAATATACCTTCATGAGCAAC 666
DB 282 GACCTGCTGCGCCAAATTCATAATTAAAGCAACAATATACCTTCATGAGCAAC 223
QY 667 ACAGCTTTTGAAGCAAGCAATGACTGCTTGAATTGAGGCTTTGAGAAATGAGCTT 726
DB 222 ACAGCTTTTGAAGCAAGCAATGACTGCTTGAATTGAGGCTTTGAGAAATGAGCTT 163
QY 727 TGAAGAAAGAAATCTTGTTCAGAGCCCTCCACACTCTTCATGTTAAACACT 786
DB 162 TGAAGAAAGAAATCTTGTTCAGAGCCCTCCACACTCTTCATGTTAAACACT 103
QY 787 GCCTTCCTGACCTTGAAGCCAGCTGATGATTAACATGTTTAAAGAAATGATTT 846
DB 102 GCCTTCCTGACCTTGAAGCCAGCTGATGATTAACATGTTTAAAGAAATGATTT 43
QY 847 TAGAGTTCTGATCGTTCAAGGAATGATTAATATACCTTC 888
DB 42 YAGAGTTCTGATCGTTCAAGGAATGATTAATATACCTTC 1

RESULT 9
US-09-338-933-27/C
Sequence 27, Application US/09338933
Patent No. 6488931

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(461)
OTHER INFORMATION: n = A,T,C or G
US-09-338-933-27

Query Match 50.2%; Score 446.6; DB 4; Length 461;
Best Local Similarity 98.9%; Pred. No. 7.1e-132;
Matches 457; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAGGCGCTATGGAAATGCTGATGGAT 486
DB 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAAGGCGCTATGGAAATGCTGATGGAT 403
QY 487 TATCTTCAGCTTGTGAGCTTTAAAGTTTCTTCCCTCATTTCACTGCAAGCCAACT 546

DB 402 TATCTTCAGCTTGTGAGCTTTAAAGTTTCTTCCCTCATTTCACTGCAAGCCAACT 343

QY 547 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
DB 342 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283

QY 607 GACCTGCTGCGCCAAATTCATAATTAAAGCAACAATATACCTTCATGAGCAAC 666
DB 282 GACCTGCTGCGCCAAATTCATAATTAAAGCAACAATATACCTTCATGAGCAAC 223

QY 667 ACAGCTTTTGAAGCAAGCAATGACTGCTTGAATTGAGGCTTTGAGAAATGAGCTT 726
DB 222 ACAGCTTTTGAAGCAAGCAATGACTGCTTGAATTGAGGCTTTGAGAAATGAGCTT 163

QY 727 TGAAGAAAGAAATCTTGTTCAGAGCCCTCCACACTCTTCATGTTAAACACT 786
DB 162 TGAAGAAAGAAATCTTGTTCAGAGCCCTCCACACTCTTCATGTTAAACACT 103

QY 787 GCCTTCCTGACCTTGAAGCCAGCTGATGATTAACATGTTTAAAGAAATGATTT 846
DB 102 GCCTTCCTGACCTTGAAGCCAGCTGATGATTAACATGTTTAAAGAAATGATTT 43

QY 847 TAGAGTTCTGATCGTTCAAGGAATGATTAATATACCTTC 888
DB 42 YAGAGTTCTGATCGTTCAAGGAATGATTAATATACCTTC 1

RESULT 10
US-09-215-681-27/C
Sequence 27, Application US/09215681A
Patent No. 6528253

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(461)
OTHER INFORMATION: n = A,T,C or G
US-09-215-681-27

Query Match 50.2%; Score 446.6; DB 4; Length 461;
Best Local Similarity 98.9%; Pred. No. 7.1e-132;
Matches 457; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 427 CAGGATTAACATCTCTCAGTGAACAGAGTTGACAGGCGCTATGGAAATGCTGATGGAT 486
DB 461 CAGGATTAACATCTCTCAGTGAACAGAGTTG-CAAGGCGCTATGGAAATGCTGATGGAT 403
QY 487 TATCTTCAGCTTGTGAGCTTTAAAGTTTCTTCCCTCATTTCACTGCAAGCCAACT 546
DB 402 TATCTTCAGCTTGTGAGCTTTAAAGTTTCTTCCCTCATTTCACTGCAAGCCAACT 343
QY 547 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 606
DB 342 TCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCA 283
QY 607 GACCTGCTGCGCCAAATTCATAATTAAAGCAACAATATACCTTCATGAGCAAC 666
DB 282 GACCTGCTGCGCCAAATTCATAATTAAAGCAACAATATACCTTCATGAGCAAC 223

```

RESULT 11
US-09-216-003A-27/c
; Sequence 27, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (367)
; OTHER INFORMATION: where n is a, c, g or t
US-09-216-003A-27

```

```

RESULT 12
; Sequence 27, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Kiting, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-667-857-27

```

Query Match	50.2%;	Score 446.6;	DB 4;	Length 461;
Best Local Similarity	98.9%;	Pred. No. 7.1e-112;		
Matches	457;	Conservative	2;	Mismatches 2; Indels 1; Gaps 1;
QY	427	CAGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCCTATGGGAAATGCTGATGGAT	486	
Db	461	CAGATTAACATCTCTCAGTGAACAGAGTTG-CAAGGCTTAGGAAATGCTGATGGAT	403	
QY	487	TATCTAGAGCTGTGTGAGCTTCTAAGTTCTTTCCTTCATTTACCCGTGCAAGCAAGT	546	
Db	402	TATCTTAGCTTGTGTGAGCTTCTAAGTTCTTTCCTTCATTTACCCGTGCAAGCAAGT	343	
QY	547	TCTGTAAAGAAATGCTGAGTTCTAGCTCAGTTTTCTTACTGTGAATTTAGATCTTCA	606	
Db	342	TCTGTAAAGAAATGCTGAGTTCTACTCAGGTTTTCTTACTGTGAATTTAGATCTTCA	283	
QY	607	GACCTCCGCGGCCACAATTCAAATTAAAGCAACAAACATATACCTTCGATGAGCAAC	666	
Db	282	GACCTTCCTCGGCCACATTTCAATTAAAGCAACAAACATATACCTTCGATGAGCAAC	223	
QY	667	ACAGACTTTTGAAGAAGCAATGAATGACTGTTGAATTGAGGCCCTTGAGGATGAAGCTT	726	
Db	222	ACAGACTTTTGAAGAAGCAATGAATGACTGTTGAATTGAGGCCCTTGAGGATGAAGCTT	163	
QY	727	TGAAGAAAAGAAATCTTGTTCACACCCCTCCACACTCTTCAATGTGTTAAACAT	786	
Db	162	TGAAGAAAAGAAATCTTGTTCACACCCCTCCACACTCTTCAATGTGTTAAACAT	103	
QY	787	GCTTCTCTGACCTTGAGGCCACGCGTACTGTATTAATCATGTGTATATGAATCTGATT	846	
Db	102	GCTTCTCTGACCTTGAGGCCACGCGTACTGTATTAATCATGTGTATATGAATCTGATT	43	
QY	847	TAGAGTTCTGATGCTTCAAGAGATGATTAATTAATTAATTC	888	
Db	42	YAGAGTTCTGATGCTTCAAGAGATGATTAATTAATTAATTC	1	

```
RESULT 13
US-09-040-984-15
; Sequence 15, Application US/09040984
; Patent No. 6210883
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF LUNG CANCER
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,984
; FILING DATE: 18-MAR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-282-6031
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-040-984-15

Query Match      41.0%; Score 364.8; DB 3; Length 695;
Best Local Similarity 77.4%; Pred. No. 1e-105;
Matches 486; Conservative 0; Mismatches 131; Indels 11; Gaps 7;

QY      238 CATTCACCTACCACTCCGAGTGTCACTGTGACGACGAAAGAAACCCGTGTTTGA 297
DB      61 CATTCACCTACCACTCCGAGTGTCACTGTGACGACGAAAGAAACCCGTGTTTGA 120
QY      238 GTAGAAAAGGCGCTGGGAAAGAGGAGGAGCAAAATCTGTCTGCTTCACTTAATGTC 357
DB      121 TTAAGAAAAGGCGCT--GAAAGAAAGGAGGAGCAAAATCTGTCTGCTTCACTTAATGTC 178
QY      358 ATTGGCAATTAAGCAATTCTGTTCTTTGGCTGCTGCTGCTGACGACAGAGAGCAACTCT 417
DB      179 NTTGGCAATTAAGCAATTCTGTTCTTTGGCTGCTGCTGCTGACGAGCAAAAGCAACTCTN 238
QY      418 ATCGGGACCAAGATAAATCTCTGAGTAAGAGTAAGAGCAAGGCGTAATGGGAATGGC 477
DB      239 ATCTNGGC--CCAGGATATACATCTCNCATTAACNAATTAAGNCAAGGCGNNTGGGAATGGC 297
QY      478 TGATGGGATTAATCTTCAGCTGTGTGAGCTTCTTAAGTTTCTTCCCTTCATTTACCCCTGC 537
DB      288 NGATGGGATTAATCTTCAGCTGTGTGAGCTTCTTAAGTTTCTTCCCTTCATTTACCCCTGC 357
QY      538 AAGCCAAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTT 597
DB      358 CAGCCNAGTTCTGTAAGAGAAATGCGCNGAATTCNAACCCGGTTTCTACTCNGAATTT 417
QY      598 AGATCTCAGACCCGCGCGGCGCAATCAAAAT--AAGGCAACAAACATATACCTTCCA 656
DB      418 AGATCTCNAAGAACTTCTCGGCCACNATTCNAATTNANGNCAAGNACANATNCTTCCA 477
```

```
QY      657 TGAAGCACACAGACTTTTGAAGCAAGCAATGACTGTGTAATTGAGGCTTGAGG 716
DB      478 TTAATNCAC--CCACNTTTGAMNGCCANAGCAATGACTGCTNNAATGAAGGCTTGAAG 536
QY      717 AATGAGCTTTGAAGAGAAAGATATCTTTGTTTTCAGACGCCCTTCCACACTCTTCAGT 776
DB      537 GAANNA--CTTTGAAGAGAAAAAACTTTGTTTCGCGCCCTT---CCAACTTCTGT 591
QY      777 GTTAACGACTGCTTCTGTG--ACCTTGAGGCAAGTACTGTATTAATGATGTTGTTATAG 835
DB      592 GTTANACCTGCTTCTTGNAAACCTTGAAGCCCGNAGACGTGTATCATGTGTTCTAN 651
QY      836 AAAACTGATTTTGAAGTTCTGATCGTTT 863
DB      652 NAAACNACNCTTNAATTCNATCTTCC 679

RESULT 14
US-09-123-912-15
; Sequence 15, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (105)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (172)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (176)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (179)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (189)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (203)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (212)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (219)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (221)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (229)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (231)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (238)
```

1	OTHER INFORMATION: Where n is a, c, g or t	1	NAME/KEY: modified_base
2	NAME/KEY: modified_base	2	LOCATION: (458)
3	LOCATION: (242)	3	OTHER INFORMATION: Where n is a, c, g or t
4	OTHER INFORMATION: Where n is a, c, g or t	4	NAME/KEY: modified_base
5	NAME/KEY: modified_base	5	LOCATION: (463)
6	LOCATION: (261)	6	OTHER INFORMATION: Where n is a, c, g or t
7	OTHER INFORMATION: Where n is a, c, g or t	7	NAME/KEY: modified_base
8	NAME/KEY: modified_base	8	LOCATION: (467)
9	LOCATION: (266)	9	OTHER INFORMATION: Where n is a, c, g or t
10	OTHER INFORMATION: Where n is a, c, g or t	10	NAME/KEY: modified_base
11	NAME/KEY: modified_base	11	LOCATION: (470)
12	LOCATION: (270)	12	OTHER INFORMATION: Where n is a, c, g or t
13	OTHER INFORMATION: Where n is a, c, g or t	13	NAME/KEY: modified_base
14	NAME/KEY: modified_base	14	LOCATION: (479)
15	LOCATION: (278)	15	OTHER INFORMATION: Where n is a, c, g or t
16	OTHER INFORMATION: Where n is a, c, g or t	16	NAME/KEY: modified_base
17	NAME/KEY: modified_base	17	LOCATION: (481)
18	LOCATION: (285)	18	OTHER INFORMATION: Where n is a, c, g or t
19	OTHER INFORMATION: Where n is a, c, g or t	19	NAME/KEY: modified_base
20	NAME/KEY: modified_base	20	LOCATION: (484)
21	LOCATION: (286)	21	OTHER INFORMATION: Where n is a, c, g or t
22	OTHER INFORMATION: Where n is a, c, g or t	22	NAME/KEY: modified_base
23	NAME/KEY: modified_base	23	LOCATION: (493)
24	LOCATION: (298)	24	OTHER INFORMATION: Where n is a, c, g or t
25	OTHER INFORMATION: Where n is a, c, g or t	25	NAME/KEY: modified_base
26	NAME/KEY: modified_base	26	LOCATION: (499)
27	LOCATION: (311)	27	OTHER INFORMATION: Where n is a, c, g or t
28	OTHER INFORMATION: Where n is a, c, g or t	28	NAME/KEY: modified_base
29	NAME/KEY: modified_base	29	LOCATION: (505)
30	LOCATION: (324)	30	OTHER INFORMATION: Where n is a, c, g or t
31	OTHER INFORMATION: Where n is a, c, g or t	31	NAME/KEY: modified_base
32	NAME/KEY: modified_base	32	LOCATION: (518)
33	LOCATION: (337)	33	OTHER INFORMATION: Where n is a, c, g or t
34	OTHER INFORMATION: Where n is a, c, g or t	34	NAME/KEY: modified_base
35	NAME/KEY: modified_base	35	LOCATION: (520)
36	LOCATION: (350)	36	OTHER INFORMATION: Where n is a, c, g or t
37	OTHER INFORMATION: Where n is a, c, g or t	37	NAME/KEY: modified_base
38	NAME/KEY: modified_base	38	LOCATION: (523)
39	LOCATION: (363)	39	OTHER INFORMATION: Where n is a, c, g or t
40	OTHER INFORMATION: Where n is a, c, g or t	40	NAME/KEY: modified_base
41	NAME/KEY: modified_base	41	LOCATION: (540)
42	LOCATION: (384)	42	OTHER INFORMATION: Where n is a, c, g or t
43	OTHER INFORMATION: Where n is a, c, g or t	43	NAME/KEY: modified_base
44	NAME/KEY: modified_base	44	LOCATION: (584)
45	LOCATION: (391)	45	OTHER INFORMATION: Where n is a, c, g or t
46	OTHER INFORMATION: Where n is a, c, g or t	46	NAME/KEY: modified_base
47	NAME/KEY: modified_base	47	LOCATION: (595)
48	LOCATION: (395)	48	OTHER INFORMATION: Where n is a, c, g or t
49	OTHER INFORMATION: Where n is a, c, g or t	49	NAME/KEY: modified_base
50	NAME/KEY: modified_base	50	LOCATION: (597)
51	LOCATION: (405)	51	OTHER INFORMATION: Where n is a, c, g or t
52	OTHER INFORMATION: Where n is a, c, g or t	52	NAME/KEY: modified_base
53	NAME/KEY: modified_base	53	LOCATION: (609)
54	LOCATION: (411)	54	OTHER INFORMATION: Where n is a, c, g or t
55	OTHER INFORMATION: Where n is a, c, g or t	55	NAME/KEY: modified_base
56	NAME/KEY: modified_base	56	LOCATION: (626)
57	LOCATION: (424)	57	OTHER INFORMATION: Where n is a, c, g or t
58	OTHER INFORMATION: Where n is a, c, g or t	58	NAME/KEY: modified_base
59	NAME/KEY: modified_base	59	LOCATION: (611)
60	LOCATION: (427)	60	OTHER INFORMATION: Where n is a, c, g or t
61	OTHER INFORMATION: Where n is a, c, g or t	61	NAME/KEY: modified_base
62	NAME/KEY: modified_base	62	LOCATION: (626)
63	LOCATION: (443)	63	OTHER INFORMATION: Where n is a, c, g or t
64	OTHER INFORMATION: Where n is a, c, g or t	64	NAME/KEY: modified_base
65	NAME/KEY: modified_base	65	LOCATION: (628)
66	LOCATION: (448)	66	OTHER INFORMATION: Where n is a, c, g or t
67	OTHER INFORMATION: Where n is a, c, g or t	67	NAME/KEY: modified_base
68	NAME/KEY: modified_base	68	LOCATION: (651)
69	LOCATION: (453)	69	OTHER INFORMATION: Where n is a, c, g or t
70	OTHER INFORMATION: Where n is a, c, g or t	70	NAME/KEY: modified_base
71	NAME/KEY: modified_base	71	LOCATION: (652)
72	LOCATION: (455)	72	OTHER INFORMATION: Where n is a, c, g or t
73	OTHER INFORMATION: Where n is a, c, g or t	73	NAME/KEY: modified_base

Result No.	Score	Query Match	Length	DB	ID	Description
1	806.4	90.6	893	9	US-09-850-178-5	Sequence 5, Appli
2	806.4	90.6	863	9	US-09-850-179-6	Sequence 6, Appli
3	806.4	90.6	2627	9	US-09-778-320-207	Sequence 207, App
4	806.4	90.6	2627	9	US-09-910-689-207	Sequence 207, App
5	806.4	90.6	2627	9	US-09-884-441-391	Sequence 391, App
6	806.4	90.6	2627	10	US-09-907-969-391	Sequence 391, App
7	806.4	90.6	2627	10	US-09-821-271-391	Sequence 391, App
8	806.4	90.6	2627	13	US-10-010-742-207	Sequence 207, App
9	806.4	90.6	2627	15	US-10-198-053-391	Sequence 391, App
10	806.4	90.6	2627	18	US-10-714-389-207	Sequence 207, App
11	806.4	90.6	2627	18	US-10-717-236-207	Sequence 207, App

12	806.4	90.6	2627	17	US-10-060-790-391	Sequence 391, Appl
13	806.4	90.6	3357	19	US-10-023-339-2	Sequence 2, Appl1
14	806	90.6	2603	9	US-09-896-728-1	Sequence 1, Appl1
15	804.8	90.4	2626	9	US-09-877-065-7	Sequence 7, Appl1
16	795.4	89.4	2591	9	US-08-850-178-23	Sequence 23, Appl1
17	794.4	89.3	1567	9	US-09-884-441-74	Sequence 74, Appl1
18	794.4	89.3	1567	10	US-09-907-969-74	Sequence 74, Appl1
19	794.4	89.3	1567	10	US-09-827-271-74	Sequence 74, Appl1
20	794.4	89.3	1567	15	US-10-198-053-74	Sequence 74, Appl1
21	794.4	89.3	1567	19	US-10-860-790-74	Sequence 74, Appl1
22	782.8	88.6	2626	17	US-10-023-339-9	Sequence 9, Appl11
23	785.4	82.6	846	10	US-09-814-353-21446	Sequence 21446, A
24	639.4	71.8	725	9	US-09-850-178-30	Sequence 30, Appl1
25	617.2	69.3	1811	14	US-10-097-340-106	Sequence 106, Appl
26	617.2	69.3	1811	14	US-10-097-340-331	Sequence 331, Appl
27	617.2	69.3	1811	15	US-10-173-993-163	Sequence 163, Appl
28	617.2	69.3	1811	17	US-10-173-999-71	Sequence 71, Appl1
29	518.4	58.2	563	9	US-09-867-701-3948	Sequence 3948, A
30	492.4	55.3	524	9	US-09-867-701-3301	Sequence 2301, Ap
31	489.4	55.0	555	9	US-09-833-790-388	Sequence 388, App
32	468.4	52.6	1596	14	US-10-198-846-13583	Sequence 13583, A
33	465.6	52.3	578	10	US-09-814-853-17682	Sequence 17682, A
34	464.6	52.2	486	9	US-09-867-701-1482	Sequence 1482, Ap
35	450.8	50.7	1891	14	US-10-097-340-347	Sequence 347, App
36	446.6	50.2	461	9	US-09-884-441-27	Sequence 27, Appl
37	446.6	50.2	461	10	US-09-907-969-27	Sequence 27, Appl
38	446.6	50.2	461	10	US-09-827-271-27	Sequence 27, Appl
39	446.6	50.2	461	15	US-10-198-053-27	Sequence 27, Appl
40	446.6	50.2	461	19	US-10-860-790-27	Sequence 27, Appl
41	446.4	50.2	491	9	US-09-850-178-3	Sequence 3, Appl1
42	438.4	49.3	442	9	US-09-867-701-2832	Sequence 2832, Ap
43	423	47.5	598	9	US-09-867-701-1498	Sequence 1498, Ap
44	422.8	47.5	757	10	US-09-814-353-5006	Sequence 5006, Ap
45	422.8	47.5	757	10	US-09-814-353-11298	Sequence 11298, A

ALIGNMENTS

```

RESULT 1
US-09-850-178-5
Sequence 5, Application US/09850178
Patent No. US20020034749A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colipits, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Russell, John C.
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Kلاس, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Stroupe, Stephen D.
APPLICANT: Gordon, Julian
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
FILE REFERENCE: 625. US.P1
CURRENT APPLICATION NUMBER: US/09/850,178
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastrSeq for Windows Version 4.0
SEQ ID NO: 5
LENGTH: 893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-850-178-5
Query Match 90.6%, Score 806.4, DB 9, Length 893

```

Best Local Similarity 91.9%; Pred. No. 2.9e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

```
QY 1 CAAGCTCGAAGGCTTCCTCTCCATCCGCGCTGAGCAAGCTTAAGACCTCAGTTTTCATA 60
Db 1 CAAGCTCGAAGGCTTCCTCTCCATCCGCGCTGAGCAAGCTTAAGACCTCAGTTTTCATA 60
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
QY 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
QY 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
Db 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
QY 181 TAGTGGATTAAGGCCAGGAGATCTGCTCAACTCTCCATGATACAGAGCTCTCCCAT 240
Db 181 TAGTGGATTAAGGCCAGGAGATCTGCTCAACTCTCCATGATACAGAGCTCTCCCAT 240
QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
Db 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
Db 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
QY 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
Db 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
QY 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
Db 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
QY 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
Db 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
QY 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
Db 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
QY 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
Db 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
QY 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
Db 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
QY 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
QY 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
QY 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
Db 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
QY 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
Db 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
QY 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
Db 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
QY 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
Db 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
QY 661 GCACACACAGATCTTTGAAAGCAGACATGATGCTTGAATGAGGCTTGAAGAA 720
Db 661 GCACACACAGATCTTTGAAAGCAGACATGATGCTTGAATGAGGCTTGAAGAA 720
QY 661 GCACACACAGATCTTTGAAAGCAGACATGATGCTTGAATGAGGCTTGAAGAA 720
Db 661 GCACACACAGATCTTTGAAAGCAGACATGATGCTTGAATGAGGCTTGAAGAA 720
QY 721 AAGCTTTGAAGGAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
Db 721 AAGCTTTGAAGGAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
QY 721 AAGCTTTGAAGGAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
Db 721 AAGCTTTGAAGGAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTTTCATGTTA 780
QY 781 ACCACTGCTTCTGAGACCTTGAAGCAGCTGATCTATTAATGATGTTTGAAGAA 840
Db 781 ACCACTGCTTCTGAGACCTTGAAGCAGCTGATCTATTAATGATGTTTGAAGAA 840
QY 781 ACCACTGCTTCTGAGACCTTGAAGCAGCTGATCTATTAATGATGTTTGAAGAA 840
Db 781 ACCACTGCTTCTGAGACCTTGAAGCAGCTGATCTATTAATGATGTTTGAAGAA 840
QY 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATCATTTTCT 890
Db 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATCATTTTCT 890
QY 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATCATTTTCT 890
Db 841 TGAATTTAGAGTTCTGATGTTCAAGAGAAATGATTAATATCATTTTCT 890
```

RESULT 2

US-09-850-178-6
; Sequence 6, Application US/09850178
; Patent No. US20020034749A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colipitics, Tracey L.

```
; APPLICANT: Friedman, Paula N.  
; APPLICANT: Russell, John C.  
; APPLICANT: Granados, Edward N.  
; APPLICANT: Hodges, Steven C.  
; APPLICANT: Klass, Michael R.  
; APPLICANT: Kralovich, Jon D.  
; APPLICANT: Roberts-Rapp, Lisa  
; APPLICANT: Stroupe, Stephen D.  
; APPLICANT: Gordon, Julian  
; TITLE OF INVENTION: REAGENTS AND METHODS OF THE BREAST  
; TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST  
; FILE REFERENCE: 6251.US.PI  
; CURRENT APPLICATION NUMBER: US/09/850.178  
; PRIOR FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: US 08/972,376  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 6  
; LENGTH: 893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-850-178-6
```

Query Match 90.6%; Score 806.4; DB 9; Length 893;
Best Local Similarity 91.9%; Pred. No. 2.9e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

```
QY 1 CAAGCTCGAAGGCTTCCTCTCCATCCGCGCTGAGCAAGCTTAAGACCTCAGTTTTCATA 60
Db 1 CAAGCTCGAAGGCTTCCTCTCCATCCGCGCTGAGCAAGCTTAAGACCTCAGTTTTCATA 60
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
QY 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
Db 61 GCATCTAGAGCAGTGGGACTCAGCTGGGGTGAATTCGCCCCCATCTCGGGGGAATGTC 120
QY 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
QY 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
Db 121 TGAAGACAATTTTGGTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
QY 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
Db 181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
QY 181 TAGTGGATTAAGGCCAGGAGATCTGCTCAACTCTCCATGATACAGAGCTCTCCCAT 240
Db 181 TAGTGGATTAAGGCCAGGAGATCTGCTCAACTCTCCATGATACAGAGCTCTCCCAT 240
QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
Db 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
Db 241 TACAACCTACCCCAATCCGAAGTGTCACTGTCTCAGAGACTAAGAAACCTGTTTGA 300
QY 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
Db 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
QY 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
Db 301 GAAAAGGGCTTGGGAAAGAGGGAGCCAAATCTGTCTGCTTCTCTCAATTAGTCA 360
QY 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
Db 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
QY 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
Db 361 GGGCAATTAAGCATCTGTCTCTTGGGCTGTGCTCTCAGAGCAGAGAGCCAGAACTATC 420
QY 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
Db 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
QY 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
Db 421 GGGCAACAGATATACATCTCTCAGTGAACAGAGTTGACAGAGCCATAGGGAATCC 480
QY 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
QY 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
Db 481 TGGGATTAATCTTCAAGCTTGTGAAGCTTCTTAAGTTCTTCTCTCAATTAGTCA 540
QY 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
Db 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
QY 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
Db 541 CCAAGTTCTGTAAGGAATGCTGATCTAGCTCAGGTTTCTTACTCTGAATTTTGA 600
QY 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
Db 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
QY 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
Db 601 TCTCCAGACCTGCTGCGCACATTCATTAATTAAGCAACCAATATACCTTCCATGA 660
QY 661 GCACACACAGATCTTTGAAAGCAGACATGATGCTTGAATGAGGCTTGAAGAA 720
Db 661 GCACACACAGATCTTTGAAAGCAGACATGATGCTTGAATGAGGCTTGAAGAA 720
```



```
Db      660 GCACACAGACATTTTGAAGCAAGACATGACTGTTGAATGAGGCTTGAGGAAATG 719
      721 AAGCTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTTTA 780
      720 AAGCTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTTTA 779
      781 ACCACTGCTTCTTCCAGCTTGGAGCCAGGAGTACTGATATTAATGTTTATAGAAAC 840
      780 ACCACTGCTTCTTCCAGCTTGGAGCCAGGAGTACTGATATTAATGTTTATAGAAAC 839
      841 TGATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 890
      840 TGATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 889
```

```
RESULT 3
US-09-778-320-207
; Sequence 207, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-320-207
```

```
Query Match      90.6%; Score 806.4; DB 9; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
```

```
      1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCACTTAAGACCTCACTTTCATA 60
      1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCACTTAAGACCTCACTTTCATA 1780
      61 GCATCTAGAGCACTGAGGAGTCAAGCTGAGGATTTGCCCCCATCTCGGGGGAATGTC 120
      1781 GCATCTAGAGCACTGAGGAGTCAAGCTGAGGATTTGCCCCCATCTCGGGGGAATGTC 1840
      121 TGAAGCAATTTTGTCTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
      1841 TGAAGCAATTTTGTCTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 1900
      181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240
      1901 TAGTGATTAAGGCCCAAGGATGCTGCTCAACTCTTACATGTAAGAGAGTCTCCCAT 1960
      241 TACAATACCAATCGAAGTGTCACTGTGCAAGACTTAAGAAACCTGGTTTGAAGTA 300
      1961 TACAATACCAATCGAAGTGTCACTGTGCAAGACTTAAGAAACCTGGTTTGAAGTA 2020
      301 GAAAAGGCGCTGGAAGAGGAGGCAACAATCTGTCTGCTCTTCACTTATGATCAT 360
      2021 GAAAAGGCGCT-GAAAAGGAGGAGGCAACAATCTGTCTGCTCTTCACTTATGATCAT 2079
      361 GGAATTAAGCATTTCTGCTCTTGTGCTGCTGCTTCAAGACAGAGAGCCAACTCTATC 420
      2080 GGAATTAAGCATTTCTGCTCTTGTGCTGCTGCTGCTTCAAGAGAGCCAACTCTATC 2139
```

```
      421 GGGCACCAGGATTAATCATCTCTCAGTGAAGAGTTGACAAGGCTTAAGGAAATGCTGA 480
      2140 GGGCACCAGGATTAATCATCTCTCAGTGAAGAGTTGACAAGGCTTAAGGAAATGCTGA 2199
      481 TGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTCTTTCCCTTCACTTACCTGCAAG 540
      2200 TGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTCTTTCCCTTCACTTACCTGCAAG 2259
      541 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTGTAATTTAGA 600
      2260 CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAAGTTTCTTACTGTAATTTAGA 2319
      601 TCTCCAGACCCCTGCTGGCCACAATTCATTAAGGCAACAACATATACCTTCCATGAA 660
      2320 TCTCCAGACCCCTGCTGGCCACAATTCATTAAGGCAACAACATATACCTTCCATGAA 2379
      661 GCACACAGACATTTTGAAGCAAGGACATGACTGTTGAATTAAGGCTTGAAGAAATG 720
      2380 GCACACAGACATTTTGAAGCAAGGACATGACTGTTGAATTAAGGCTTGAAGAAATG 2439
      721 AAGCTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTTTA 780
      2440 AAGCTTGAAGAAAAGAAATACCTTTGTTCCAGCCCCCTTCCCACTCTTCAATGTTTA 2499
      781 ACCACTGCTTCTTCCAGCTTGGAGCCAGGAGTACTGTTATACATGTTGTTATAGAAAC 840
      2500 ACCACTGCTTCTTCCAGCTTGGAGCCAGGAGTACTGTTATACATGTTGTTATAGAAAC 2559
      841 TGATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 890
      2560 TGATTTAGAGTTCTGATCGTTCAAGAAATGATTAATATACATTTCT 2609
```

```
RESULT 4
US-09-910-689-207
; Sequence 207, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-689-207
```

```
Query Match      90.6%; Score 806.4; DB 9; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;
```

```
      1 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCACTTAAGACCTCACTTTCATA 60
      1721 CAAGCTCTGAGGCTTCTCTTCCATCTGCGTGAAGCACTTAAGACCTCACTTTCATA 1780
      61 GCATCTAGAGCACTGAGGAGTCAAGCTGAGGATTTGCCCCCATCTCGGGGGAATGTC 120
      1781 GCATCTAGAGCACTGAGGAGTCAAGCTGAGGATTTGCCCCCATCTCGGGGGAATGTC 1840
      121 TGAAGCAATTTTGTCTTACTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNNNN 180
```

[illegible]

```

RESULT 5
US-09-884-441-391
; Sequence 391, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-884-441-391

```

Query Match	90.6%;	Score 806.4;	DB 9;	Length 2627;
Best Local Similarity	91.9%;	Pred. No. 5.4e-260;		

[illegible]

RESULT 6
US-09-907-969-391
; Sequence 391, Application US/099079665001
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.

```

? APPLICANT: Fanger, Gary Richard
? APPLICANT: Reed, Steven G.
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Carter, Darrick
? APPLICANT: Hill, Paul
? APPLICANT: Albone, Earl
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
? FILE REFERENCE: 210121.462C8
? CURRENT APPLICATION NUMBER: US/09/907,969
? CURRENT FILING DATE: 2001-07-17
? NUMBER OF SEQ ID NOS: 596
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 391
? LENGTH: 2627
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-907-969-391

```

[illegible]

Db 2440 AAGCTTGAAGAAAAGAAATACTTTGTTTCACAGCCCCCTTCCACACATCTTCAATGTETA 2499

Qy 781 AACACGTCCCTCCGAGCACTTGGAGCCAGGTAGCTATTAACATGTTGTTAAGAAAC 840

Db 2500 AACACGTCCCTCCGAGCACTTGGAGCCAGGTAGCTATTAACATGTTGTTAAGAAAC 2559

Qy 841 TGAATTTAGAGCTTGATCGTTCAAGAGATGATTAATTAATTAACATTTCT 890

Db 2560 TGAATTTAGAGCTTGATCGTTCAAGAGATGATTAATTAATTAACATTTCT 2609

```

RESULT 7
US-09-827-271-391
: Sequence 391, Application US/09827271
: Publication No. US20030165504A1
: GENERAL INFORMATION:
: APPLICANT: Retter, Marc W.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C6
: CURRENT APPLICATION NUMBER: US/09/827,271
: CURRENT FILING DATE: 2001-04-04
: NUMBER OF SEQ ID NOS: 461
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 391
: LENGTH: 2627
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-827-271-391

```

Query Match	90.6%;	Score 806.4;	DB 10;	Length 2627;
Best Local Similarity	91.9%;	Pred. No. 5,4e-260;		
Matches 818;	Conservative 0;	Mismatches 71;	Indels 1;	Gaps 1;
QY 1	CAAGCTCTGAGGCTCTTCCTCTTCCATCTCTCGTGGACAGCTTAAGACTCACTGATTTTCATATA	60		
Db 1721	CAAGCTCTGAGGCTCTTCCTCTTCCATCTCTCGTGGACAGCTTAAGACTCACTGATTTTCATATA	1780		
QY 61	GCATCTTAGAGCAGTGGGAGCTCAGCTGGGGGATTTTGGCCCCCATCTCCGGGGGAATGTC	120		
Db 1781	GCATCTTAGAGCAGTGGGAGCTCAGCTGGGGGATTTTGGCCCCCATCTCCGGGGGAATGTC	1840		
QY 121	TGAAGCAATTTTGGTTAACCCTCAATGAGGGAGTGGAGAGATACAGNNNNNNNNNNNNNN	180		
Db 1841	TGAAGCAATTTTGGTTAACCCTCAATGAGGGAGTGGAGAGATACAGTGTCTACTACCAAC	1900		
QY 181	NN	240		
Db 1901	TAGTGATTAAGGCCAGGGATGCTGCTCAACTTCCTCAATGATACAGAGCTCTCCCAT	1960		
QY 241	TACAACCTACCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTGGTTTGGAGTA	300		
Db 1961	TACAACCTACCCCAATCCGAAGTGTCAACTGTGTGAGAGCTTAAGAAACCTGGTTTGGAGTA	2020		
QY 301	GAAAAGGCGCTGGGAAAAGAGGGGAGCCCAAAATCTGTCTGTCTTCTCACATTAATGTCATT	360		
Db 2021	GAAAAGGCGCT -GAAAAGAGGGGAGCCCAAAATCTGTCTGTCTTCTCACATTAATGTCATT	2079		
QY 361	GGCAAAATTAAGCATTTCTGTCTTCTTGGCTGTGCTGCTCAGCAGCAGAGAGCCAGACTCTATC	420		
Db 2080	GGCAAAATTAAGCATTTCTGTCTTCTTGGCTGTGCTCAGCAGCAGAGAGCCAGACTCTATC	2139		
QY 421	GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTATGGGAAATGCTCTGA	480		
Db 2140	GGGACACAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTATGGGAAATGCTCTGA	2199		
QY 481	TGGATTATATTAGACTGTGTGAGCTTCTTAAGTTTCTTTCCCTCAATTCTAACCTGCAAG	540		
Db 2200	TGGATTATATTAGACTGTGTGAGCTTCTTAAGTTTCTTTCCCTCAATTCTAACCTGCAAG	2259		
QY 541	CCAAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTTCTTACTGTGAATTTAGA	600		

Db 2260 CCAAGTCTGTGAAGAAATGCGTCTAGCTCAGGTTTCTTACTGTGAATTAGA 2319
Qy 601 TCTCCAGACCTGCGCTGGCCACATTTCAATTAAAGCAACAACATATACCTTCCATGNA 660
Db 2320 TCTCCAGACCTTCTGCGCCACATTTCAATTAAAGCAACAACATATACCTTCCATGNA 2379
Qy 661 GCACACAGACATTTTGAAGCAAGCAACATGCTGTTGAATTGAGGCTTGAAGAAATG 720
Db 2380 GCACACAGACATTTTGAAGCAAGCAACATGCTGTTGAATTGAGGCTTGAAGAAATG 2439
Qy 721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACATTTATGTTTA 780
Db 2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACATTTATGTTTA 2499
Qy 781 ACCACTGCTTCTGAGACCTTGGAGCCAGGTCATGTTATCATGTTTATAGAAAAC 840
Db 2500 ACCACTGCTTCTGAGACCTTGGAGCCAGGTCATGTTATCATGTTTATAGAAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAAATATACATTTCT 2609

RESULT 8

US-10-010-742-207
; Sequence 207, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yudi
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongrong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-742-207

Query Match 90.6%; Score 806.4; DB 13; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

Qy 1 CAAGCTCGAGGCTTCTCTTCCATCTCGGCTGACACCTTAAGACTTCAATTA 60
Db 1721 CAAGCTCGAGGCTTCTCTTCCATCTCGGCTGACACCTTAAGACTTCAATTA 1780
Qy 61 GCATCTAGAGCAGTGGAGTCACTGAGGCTGATTTGCCCCCATCTCCGGGGGATGTC 120
Db 1781 GCATCTAGAGCAGTGGAGTCACTGAGGCTGATTTGCCCCCATCTCCGGGGGATGTC 1840
Qy 121 TGAAGACAATTTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNN 180
Db 1841 TGAAGACAATTTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNN 1900
Qy 181 NNN 240
Db 1901 TAGTGATTAAGGCCAGGAGTCTGCTCAACTCTTACATGTACAGAGCTCTCCCAT 1960

Qy 241 TACAATCCCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTGGTTTGAGTA 300
Db 1961 TACAATCCCAATCCGAAGTGTCACTGTGTCAAGACTTAAGAAACCTGGTTTGAGTA 2020
Qy 301 GAAAAGGCGCTGGGAAAGAGGGAGCCCAAAATCTGTCTGTCTTCTCAATTAAGTCA 360
Db 2021 GAAAAGGCGCTGGGAAAGAGGGAGCCCAAAATCTGTCTGTCTTCTCAATTAAGTCA 2079
Qy 361 GGCAAATAGAGATCTGTCTCTTTGGCTGTGCTCCAGACAGAGAGCCAGAACTCTATC 420
Db 2080 GGCAAATAGAGATCTGTCTCTTTGGCTGTGCTCCAGACAGAGAGCCAGAACTCTATC 2139
Qy 421 GGGCACCGAGATTAATCTCTCACTGAGAAACAAGTTGAACAAGGCTTATGGAAATGCC 480
Db 2140 GGGCACCGAGATTAATCTCTCACTGAGAAACAAGTTGAACAAGGCTTATGGAAATGCC 2199
Qy 481 TGGGATTAATCTTCACTGAGTTGAGGCTTGAAGTTCTTCCCTCATCTACCTGCAAG 540
Db 2200 TGGGATTAATCTTCACTGAGTTGAGGCTTGAAGTTCTTCCCTCATCTACCTGCAAG 2259
Qy 541 CCAAGTCTGTGAAGAAATGCTGAGTCTTCACTGAGTCTGAGTTTCTTACTGTGAATTAGA 600
Db 2260 CCAAGTCTGTGAAGAAATGCTGAGTCTTCACTGAGTCTGAGTTTCTTACTGTGAATTAGA 2319
Qy 601 TCTCCAGACCTGCTGGCCACATTTCAATTAAAGCAACAACATATACCTTCCATGNA 660
Db 2320 TCTCCAGACCTTCTGCGCCACATTTCAATTAAAGCAACAACATATACCTTCCATGNA 2379
Qy 661 GCACACAGACATTTTGAAGCAAGCAACATGACTGTTGAATTGAGGCTTGAAGAAATG 720
Db 2380 GCACACAGACATTTTGAAGCAAGCAACATGACTGTTGAATTGAGGCTTGAAGAAATG 2439
Qy 721 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACATTTATGTTTA 780
Db 2440 AAGCTTTGAAGAAAGAAATATCTTTGTTCCAGCCCCCTTCCACACATTTATGTTTA 2499
Qy 781 ACCACTGCTTCTGAGACCTTGGAGCCAGGTCATGTTATCATGTTTATAGAAAAC 840
Db 2500 ACCACTGCTTCTGAGACCTTGGAGCCAGGTCATGTTATCATGTTTATAGAAAAC 2559
Qy 841 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAAATATACATTTCT 890
Db 2560 TGATTTAGAGTTCTGATGTTCAAGAGAAATGATTAAATATACATTTCT 2609

RESULT 9

US-10-198-053-391
; Sequence 391, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 391
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-391

Query Match 90.6%; Score 806.4; DB 15; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

Qy 1 CAAGCTCGAGGCTTCTCTTCCATCTCGGCTGACACCTTAAGACTTCAATTA 60
|||||

Db 2560 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTCTT 2609

RESULT 11

US-10-717-296-207

; Sequence 207, Application US/10717296

; Publication No. US20040142361A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Jiang, Yuhui

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.491C8

; CURRENT APPLICATION NUMBER: US/10/717,296

; CURRENT FILING DATE: 2003-11-19

; NUMBER OF SEQ ID NOS: 313

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 207

; LENGTH: 2627

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-717-296-207

Query Match 90.6%; Score 806.4; DB 18; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTCGAGGCTTCTCTTCCATCCCTGGCGTGAAGCACTTAAGCCTCAGTTTCATA 60

Db 1721 CAAGCTCGAGGCTTCTCTTCCATCCCTGGCGTGAAGCACTTAAGCCTCAGTTTCATA 1780

QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 120

Db 1781 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 1840

QY 121 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180

Db 1841 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 1900

QY 181 NNN 240

Db 1901 TAGTGATTAAGGCCAGGAGTGTCTCAACCTCTACATATTAAGAGCTCTCCCAT 1960

QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAAACCTGTTTGAAGTA 300

Db 1961 TACAACCTACCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAAACCTGTTTGAAGTA 2020

QY 301 GAAAAGGCGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGTCATT 360

Db 2021 GAAAAGGCGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGTCATT 2079

QY 361 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 420

Db 2080 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 2139

QY 421 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGGAATGCTGA 480

Db 2140 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGGAATGCTGA 2199

QY 481 TGGGATTATCTTCACTGTTGAGCTTCTTAAGTTCTTTCCCTTCACTTACCTTCGACAG 540

Db 2200 TGGGATTATCTTCACTGTTGAGCTTCTTAAGTTCTTTCCCTTCACTTACCTTCGACAG 2259

QY 541 CCAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTGA 600

Db 2260 CCAAGTTCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTCTGAATTTGA 2319

QY 601 TCTCCAGACCTGCTGGCCCAATTAATTAAGGCAACAACATATACCTTCATGAA 660

Db 2320 TCTCCAGACCTGCTGGCCCAATTAATTAAGGCAACAACATATACCTTCATGAA 2379

QY 661 GCACACACAGATTTTGAAGCAAGACATGATGCTTGAATGAGGCTTTGAGGAATG 720

Db 2380 GCACACACAGATTTTGAAGCAAGACATGACTCTGTAATTGAGGCTTTGAGGAATG 2439

QY 721 AAGCTTTGAAGAAAAGAAATCTTGTTCAGCCGCCCTTCCACACTCTTCATGTGTTA 780

Db 2440 AAGCTTTGAAGAAAAGAAATCTTGTTCAGCCGCCCTTCCACACTCTTCATGTGTTA 2499

QY 781 ACCACTGCTTCTGAGACTTTGAGCCAGGCTGACTGATTAATGTTGTTATAGAAAAC 840

Db 2500 ACCACTGCTTCTGAGACTTTGAGCCAGGCTGACTGATTAATGTTGTTATAGAAAAC 2559

QY 841 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTCTT 890

Db 2560 TGAATTTAGAGTTCTGATCGTTCAAGAGATGATTAAATATACATTCTT 2609

RESULT 12

US-10-860-790-391

; Sequence 391, Application US/10860790

; Publication No. US20050031634A1

; GENERAL INFORMATION:

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Hill, Paul

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C11

; CURRENT APPLICATION NUMBER: US/10/860,790

; CURRENT FILING DATE: 2004-06-02

; NUMBER OF SEQ ID NOS: 624

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 391

; LENGTH: 2627

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-860-790-391

Query Match 90.6%; Score 806.4; DB 19; Length 2627;
Best Local Similarity 91.9%; Pred. No. 5.4e-260;
Matches 818; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCTCGAGGCTTCTCTTCCATCCCTGGCGTGAAGCACTTAAGCCTCAGTTTCATA 60

Db 1721 CAAGCTCGAGGCTTCTCTTCCATCCCTGGCGTGAAGCACTTAAGCCTCAGTTTCATA 1780

QY 61 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 120

Db 1781 GCATCTAGAGCAGTGGGAGCTCAGCTGGGGTGAATTTGCCCCCATCTCGGGGGAATGTC 1840

QY 121 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180

Db 1841 TGAAGACAATTTGGTTACTCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 1900

QY 181 NNN 240

Db 1901 TAGTGATTAAGGCCAGGAGTGTCTCAACCTCTACATATTAAGAGCTCTCCCAT 1960

QY 241 TACAACCTACCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAAACCTGTTTGAAGTA 300

Db 1961 TACAACCTACCCCAATCCGAAGTGTCACTGTGTCAAGACTAAGAAAACCTGTTTGAAGTA 2020

QY 301 GAAAAGGCGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGTCATT 360

Db 2021 GAAAAGGCGCTTGGGAAAAGGGGAGCCAAACAATCTGTCTGCTTCTCTCACTTAATGTCATT 2079

QY 361 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 420

Db 2080 GGCATAATAGCATCTGTCTCTTTGGCTGCTCCTCAGACAGAGAGCCAGAACTCTATC 2139

QY 421 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGGAATGCTGA 480

Db 2140 GGGCACAAGATTAACATCTCTCAGTGAACAGAGTTGAACAAGGCTTAAGGGAATGCTGA 2199

Qy	481	TGGGATPAPCTTACACTGTGGAGCTTCAGTTCTTCCCTCATCTPACCCGCAAG	540
Db	2200	TGGGATPAPCTTACACTGTGGAGCTTCAGTTCTTCCCTCATCTPACCCGCAAG	2259
Qy	541	CCAGTTCGTGAGAGAAATGCTGAGTTCAGCTCAGTCTTCTTACTCTGAATTAGA	600
Db	2260	CCAAGTTCGTGAGAGAAATGCTGAGTTCAGCTCAGTCTTCTTACTCTGAATTAGA	2319
Qy	601	TCTCCAGACCTGCTGGCCACAAATTCAATTAAAGCAACAACATATACCTTCAGTAA	660
Db	2320	TCTCCAGACCTTCTCTGGCCACAATTCAAAATTAAAGCAACAACATATACCTTCAGTAA	2379
Qy	661	GCACACACAGCTTTGAAAGCAAGGACAAATGACCTGTAATTGAGGCTTGGAGAAATG	720
Db	2380	GCACACACAGCTTTGAAAGCAAGGACAAATGACCTGTAATTGAGGCTTGGAGAAATG	2439
Qy	721	AAGCTTTGAAGAAAGAAATGACTTGTGTTCCAGCCCCCTTCCACACCTTCATGTGTTA	780
Db	2440	AAGCTTTGAAGAAAGAAATGACTTGTGTTCCAGCCCCCTTCCACACCTTCATGTGTTA	2499
Qy	781	ACCACTGCTTCTCTGGACCTTGGAGCCACGGTGACTGTATTACATGTTGTTATGAAAAC	840
Db	2500	ACCACTGCTTCTCTGGACCTTGGAGCCACGGTGACTGTATTACATGTTGTTATGAAAAC	2559
Qy	841	TGATTTTGAAGATTCTGATCTTCAAGAGAAATGATTAATATACATTTTCTT	890
Db	2560	TGATTTTGAAGATTCTGATCTTCAAGAGAAATGATTAATATACATTTTCTT	2609

[illegible]

OY	241	TACAACTAACCCAAATCCGAATGTCACATGTGTACAGACTAAGAAACCCGTGTTTAGTA	300
Db	2297	TACAACTAACCCAAATCCGAATGTCACATGTGTACAGACTAAGAAACCCGTGTTTAGTA	2356
OY	301	GAAAAAGGCGCTGGGAAAGAGGGGAGCCAAATACTGTCTAGTCTCTCAATTAAGTCAAT	360
Db	2357	GAAAAAGGCGCT - GAAAAAGAGGGGAGCCAAATACTGTCTGTGCTTCCATTAAGTCAAT	2415
OY	361	GGCAATTAAGCAATCTGTCTCTTTGGTGTGCTCAGCAACAGAGGCCAGAACTATAC	420
Db	2416	GGCAATTAAGCAATCTGTCTCTTTGGTGTGCTCAGCAACAGAGGCCAGAACTATAC	2475
OY	421	GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAGGCCATATGGGAAATGCTCA	480
Db	2476	GGGCAACAGAGTAACATCTCTCAGTGAACAGAGTTGACAAGGCCATATGGGAAATGCTCA	2535
OY	481	TGGGATTAATCTCAGCTGTGTAGCTTCTAAGTTCTTTTCCCTCAATTCACCTGCAAG	540
Db	2536	TGGGATTAATCTCAGCTGTGTAGCTTCTAAGTTCTTTTCCCTCAATTCACCTGCAAG	2595
OY	541	CCAAGTTCTGTGAAGAGAAATGCTCGAGTTTACGTCAAGTTTTCTAATCTGAATTTAGA	600
Db	2596	CCAAGTTCTGTGAAGAGAAATGCTCGAGTTTACGTCAAGTTTTCTAATCTGAATTTAGA	2655
OY	601	TCTCCAGACCCGTGCTGGCCACAATTCAAATTAAGCAACAAACATTAACCTTCCATGAA	660
Db	2656	TCTCCAGACCCCTTCTGTGCGCACATTCAAATTAAGCAACAAACATTAACCTTCCATGAA	2715
OY	661	GCACACACAGACTTTTGAAGCAGAGCAATGACTGTGAATTAAGGCGCTTGAGGATG	720
Db	2716	GCACACACACACTTTTGAAGCAGAGCAATGACTGTGAATTAAGGCGCTTGAGGATG	2775
OY	721	AAGCTTTGAAGGAAAGAAATACTTTGTTTCCAGCCCTCCACACTCTTCATGTGTTA	780
Db	2776	AAGCTTTGAAGGAAAGAAATACTTTGTTTCCAGCCCTCCACACTCTTCATGTGTTA	2835
OY	781	ACCACTGCTCTTCTGACACTTGGAGCCACGGTACGTATTAATGATGTTGTTATAGAAAC	840
Db	2836	ACCACTGCTCTTCTGAGACTTTGGAGCCACGGTACGTATTAATGATGTTGTTATAGAAAC	2895
OY	841	TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATTAACATTTCCCT	890
Db	2896	TGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAATTAACATTTCCCT	2945

```

RESULT 14
US-09-896-738-1
; Sequence 1, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Pang, Wei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)..(901)
US-09-896-738-1

Query Match          90.6%; Score 806; DB 9; Length 2603;
Best Local Similarity 91.8%; Pred. No. 7,4e-260;
Matches 81%; Conservatve 1; Mismatches 71; Indels 1; Gaps 1;

```



```

QY      1 CAAGCTGAGGCTTCTCCTTTCATCTGCGTGACAGTAAAGCTCAGTTTCAATA 60
DB      1691 CAAGCTGAGGCTTCTCCTTTCATCTGCGTGACAGTAAAGCTCAGTTTCAATA 1750
QY      61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGCCCCCATCTCCGGGGATGTC 120
DB      1751 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGCCCCCATCTCCGGGGATGTC 1810
QY      121 TGAACAATTTTGGTTACCTCAATGAGGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB      1811 TGAACAATTTTGGTTACCTCAATGAGGGAGTGAAGAGATACAGNNNNNNNNNNNN 1870
QY      181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
DB      1871 TAGTGATTAAGAGCCAGGGATGCTGCTCAACTCTCACTAGTACAGAGCTCTCCCAT 1930
QY      241 TACAACTACCCCAATCCGAAGTGTCAACTGTGTACAGACTAAGAAACCTGGTTTGAAGTA 300
DB      1931 TACAACTACCCCAATCCGAAGTGTCAACTGTGTACAGACTAAGAAACCTGGTTTGAAGTA 1990
QY      301 GAAAAGGGGCTGGGAAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACTAGTCAAT 360
DB      1991 GAAAAGGGGCTGGGAAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACTAGTCAAT 2049
QY      361 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB      2050 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2109
QY      421 GGGCACACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGAGAAATGCTCGA 480
DB      2110 GGGCACACAGATTAACATCTCTCAGTGAACAGAGTTGACAGAGCCCTATGAGAAATGCTCGA 2169
QY      481 TGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTTCTTCCCTTCACTACCTGCAAG 540
DB      2170 TGGGATTAATCTTCAAGCTTGTGAGCTTCAAGTTTCTTCCCTTCACTACCTGCAAG 2229
QY      541 CCAAGTTCTGTAAAGAAATGCTGATCTAGCTCAGGTTTCTTACTGTGAATTTAGA 600
DB      2230 CCAAGTTCTGTAAAGAAATGCTGATCTAGCTCAGGTTTCTTACTGTGAATTTAGA 2289
QY      601 TCTCCAGACCTTCTGCTGCGCACAAATTCAAATTAAGCAACAAATATACCTTCATGAA 660
DB      2290 TCTCCAGACCTTCTGCTGCGCACAAATTCAAATTAAGCAACAAATATACCTTCATGAA 2349
QY      661 GCACACAGACTTTTGAAGAGAGCAATGACTGCTGAATGAGGCTTGAGGAATG 720
DB      2350 GCACACAGACTTTTGAAGAGAGCAATGACTGCTGAATGAGGCTTGAGGAATG 2409
QY      721 AAGCTTTGAAGAAAGAAATACCTTGTTCAGCCCCCTTCCACACTCTTCATGTGTA 780
DB      2410 AAGCTTTGAAGAAAGAAATACCTTGTTCAGCCCCCTTCCACACTCTTCATGTGTA 2469
QY      781 ACCACTGCTTCTTGAAGAGAGCAATGACTGCTGAATGAGGCTTGAGGAATG 840
DB      2470 ACCACTGCTTCTTGAAGAGAGCAATGACTGCTGAATGAGGCTTGAGGAATG 2529
QY      841 TGAATTTAGAGTTCTGATGCTTCAAGAGAAATGATTAATATACATTTCT 890
DB      2530 TGAATTTAGAGTTCTGATGCTTCAAGAGAAATGATTAATATACATTTCT 2579

```

RESULT 15

```

US-09-877-065-7
; Sequence 7, Application US/09877065
; Patent No. US20020051990A1
; GENERAL INFORMATION:
; APPLICANT: OPLE, ERIC
; APPLICANT: MCLACHLAN, KAREN
; APPLICANT: HEAD, CHERYL J.
; TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR
; FILE REFERENCE: 037003-0280631

```

```

; CURRENT APPLICATION NUMBER: US/09/877, 065
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,451
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1303)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (1384)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-877-065-7

```

```

Query Match      90.4%; Score 804.8; DB 9; Length 2626;
Best Local Similarity 91.8%; Pred. No. 1.9e-259;
Matches 817; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

```

```

QY      1 CAAGCTGAGGCTTCTCCTTTCATCTGCGTGACAGTAAAGCTCAGTTTCAATA 60
DB      1699 CAAGCTGAGGCTTCTCCTTTCATCTGCGTGACAGTAAAGCTCAGTTTCAATA 1758
QY      61 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGCCCCCATCTCCGGGGATGTC 120
DB      1759 GCATCTAGAGCAGTGGAGCTCAGCTGGGGTATTTGCCCCCATCTCCGGGGATGTC 1818
QY      121 TGAACAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 180
DB      1819 TGAACAATTTTGGTTACCTCAATGAGGAGTGAAGAGATACAGNNNNNNNNNNNN 1878
QY      181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAT 240
DB      1879 TAGTGATTAAGAGCCAGGGATGCTGCTCAACTCTCACTAGTACAGAGCTCTCCCAT 1938
QY      241 TACAACTACCCCAATCCGAAGTGTCAACTGTGTACAGACTAAGAAACCTGGTTTGAAGTA 300
DB      1939 TACAACTACCCCAATCCGAAGTGTCAACTGTGTACAGACTAAGAAACCTGGTTTGAAGTA 1998
QY      301 GAAAAGGGGCTGGGAAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACTAGTCAAT 360
DB      1999 GAAAAGGGGCTGGGAAAGAGGGGAGCCAAACAATCTGTCTGCTTCTCACTAGTCAAT 2057
QY      361 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 420
DB      2058 GGCATAATAGCATCTGTCTCTTTGGCTGCTGCTCAGACAGAGAGCCAGAACTCTATC 2117
QY      421 GGGCACACAGATTAACATCTCAGTGAACAGAGTTGACAGAGCCATGAGGAATGCTCGA 480
DB      2118 GGGCACACAGATTAACATCTCAGTGAACAGAGTTGACAGAGCCATGAGGAATGCTCGA 2177
QY      481 TGGGATTAATCTTCAAGCTTGTGAGCTTGAAGTTTCTTCCCTTCACTACCTGCAAG 540
DB      2178 TGGGATTAATCTTCAAGCTTGTGAGCTTGAAGTTTCTTCCCTTCACTACCTGCAAG 2237
QY      541 CCAAGTTCTGTAAAGAAATGCTGATCTAGCTCAGGTTTCTTACTCGAATTTAGA 600
DB      2238 CCAAGTTCTGTAAAGAAATGCTGATCTAGCTCAGGTTTCTTACTCGAATTTAGA 2297
QY      601 TCTCCAGACCTTCTGCTGCGCACAAATTCAAATTAAGCAACAAATATACCTTCATGAA 660
DB      2298 TCTCCAGACCTTCTGCTGCGCACAAATTCAAATTAAGCAACAAATATACCTTCATGAA 2357
QY      661 GCACACAGACTTTTGAAGAGAGCAATGACTGCTGAATGAGGCTTGAGGAATG 720
DB      2358 GCACACAGACTTTTGAAGAGAGCAATGACTGCTGAATGAGGCTTGAGGAATG 2417
QY      721 AAGCTTTGAAGAAAGAAATCTTGTTCAGAGCCCTTCCACACTCTTCATGTGTA 780

```


Db 2418 AACCTTGAAGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTTCATGTGTA 2477
QY 781 AACACTGCCCTTCTTGACCTTGAAGCCACGCTGACTGTATTACATGTGTATAGAAAC 840
Db 2478 AACACTGCCCTTCTTGACCTTGAAGCCACGCTGACTGTATTACATGTGTATAGAAAC 2537
QY 841 TGATTTAGAGTCTGATCGTTCAGAGAAATGATTAATATACATTTCCT 890
Db 2538 TGATTTAGAGTCTGATCGTTCAGAGAAATGATTAATATACATTTCCT 2587

Search completed: May 31, 2005, 10:07:43
Job time : 613.64 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: May 30, 2005, 08:48:09 ; Search time 3461.52 Seconds

(without alignments)
9786.800 Million cell updates/sec

Title: US-09-763-978B-16

Perfect score: 890

Sequence: 1 caagcctcagagcttcctcct.....tgatataatatacttcct 890

Scoring table: IDENTITY_NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	779.4	87.6	2431	3	CR603772 full-length
2	671.8	75.5	1018	5	EX337228 BX337228
3	639.4	71.8	691	6	CB241729 UI-CF-FNO
4	639.4	71.8	700	5	BU632767 UI-H-FEI-
5	638.4	71.7	691	6	CA314865 UI-CF-FNO
6	638.4	71.7	737	6	CA314445 UI-CF-FNO
7	634.6	71.3	691	5	BU608696 UI-CF-FNO
8	628.4	70.6	660	6	CB852239 UI-CF-FNO
9	621.8	69.9	660	6	CA426580 UI-H-FEI-
10	615.4	69.1	679	6	CA312678 UI-CF-FNO
11	566.4	63.6	594	6	CA503188 UI-CF-FNO
12	550.4	61.8	556	1	AI684143 k79G04.x
13	549.6	61.8	556	6	CD632169 56084071H
14	542.6	61.0	560	6	CD632170 56084071J
15	530.8	59.6	557	5	BM982674 UI-CF-FNO
16	518.4	58.2	563	1	AA404225 zc43h04.x
17	509.4	57.2	529	2	AM615203 hg78a06.x
18	492.4	55.3	524	1	AA171844 z098e08.s
19	480	53.9	482	1	AI683712 tw53a09.x
20	476.4	53.5	481	2	AM470108 kx229h08.x
21	464.6	52.1	486	1	AA075579 zm88h04.b
22	463.8	52.1	485	1	AI859795 zm88h04.b
23	438.4	49.3	442	1	AA291512 zc40f01.s
24	430.4	48.4	436	1	AI638559 ts50a07.x

C	25	427	48.0	447	1	AI686571 tx08d03.x
C	26	423	47.5	598	1	AA075632 zm88h04.x
C	27	417.8	46.9	426	1	AA411046 zw40c07.s
C	28	417.4	46.9	426	1	AI828762 zw45f01.x
C	29	416.4	46.8	422	1	AA434329 zw45g07.t
C	30	412.4	46.3	424	2	BE819515 RC2-BN033
C	31	401.6	45.1	416	1	AI539668 LP71e07.x
C	32	384.4	43.2	391	1	AA404609 zt43h04.s
C	33	375.4	42.2	398	1	AI858190 w146b08.x
C	34	367.2	41.3	374	1	AA706376 ag91h05.t
C	35	365.8	41.1	392	2	AM073686 xD01d04.x
C	36	361	40.6	530	4	BI963964 i663c03.y
C	37	356.2	40.0	382	2	AM172459 xj39d04.x
C	38	347.4	39.0	349	1	AA554431 n114f07.s
C	39	336	37.8	553	5	BU742690 UI-E-B01-
C	40	335	37.6	352	1	AA953518 on8b02.b
C	41	330	37.1	737	7	CN259810 17006f001
C	42	326.8	36.7	355	6	CA314209 UI-CF-FNO
C	43	325.4	36.6	450	7	H51315 YP07f05.B1
C	44	289.2	32.5	352	1	AA503020 ng20d05.s
C	45	279.4	31.4	259	2	AM150534 xg32906.x

ALIGNMENTS

RESULT 1
CR603772
LOCUS
DEFINITION
full-length cDNA clone CS0D1039YG21 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION
CR603772
VERSION
CR603772.1 GI:50484579
KEYWORDS
HTC; CNSLT_CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact: Feng Liang Email: fliang@life.rockefeller.edu
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 2431
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

FEATURES
source
1. 2431
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YG21"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 87.6% Score 779.4; DB 3; Length 2431;
Best local Similarity 91.7% Pred. No. 7.7e-223;
Matches 791; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 CAAGCCTCAGAGCTTCCTTCCTCCATCGCTGACACCTAAGACCTCAGTTTCAATA 60
1570 CAAGCCTCAGAGCTTCCTTCCTCCATCGCTGACACCTAAGACCTCAGTTTCAATA 1629

|||||
Db 270 ATTAGATCTCCAGACCTTCTCGGCACCAATTCAATTAAGCAACAATATACCTT 211
Qy 654 CCAATGAGCACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTAAGGCTTG 713
Db 210 CCAATGAGCACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTAAGGCTTG 151
Qy 714 AGAATGAGCTTTGAAGAAAGATCTTTGTTTCACGCCCCCTCCACACTCTCA 773
Db 150 AGAATGAGCTTTGAAGAAAGATCTTTGTTTCACGCCCCCTCCACACTCTCA 91
Qy 774 TGTGTTAACCACTGCTTCTCGACCTTGAGCCAGCGTACTGATTAATGATTTGAT 833
Db 90 TGTGTTAACCACTGCTTCTCGACCTTGAGCCAGCGTACTGATTAATGATTTGAT 31
Qy 834 AGAAACTGATTTTGAAGTTCTGATCTTC 863
Db 30 AGAAACTGATTTTGAAGTTCTGATCTTC 1

RESULT 3
CB241729/c
LOCUS CB241729 691 bp mRNA linear EST 12-FEB-2003
DEFINITION UI-CF-FN0-afz-p-01-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
ACCESSION CB241729
VERSION CB241729.1 GI:28363373
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia: Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 691)
JOURNAL Normalization and subtraction: two approaches to facilitate gene
MEDLINE Genome Res. 6 (9), 791-806 (1996)
PUBMED 97044477
COMMENT 8889548
Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Gene Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 618-691. >MER20#DNA/MER1_type (matched complement)
PolyA+tes.

FEATURES
source
1. 691
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FN0-afz-p-01-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (71 phage resistant)"
/clone_lib="UI-CF-FN0"
/notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
normalized human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:

bento-soares@uiowa.edu
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FN0
TAG_SEQ=GAGCTGTAGGC"

ORIGIN
Query Match 71.8%; Score 639.4; DB 6; Length 691;
Best Local Similarity 99.7%; Pred. No. 7.6e-181;
Matches 651; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 238 CATTACACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGGTTTGA 297
Db 670 CATTACACTACCAATCCGAAGTGTCACTGTGTGAGCACTAAGAAACCTGGTTTGA 611
Qy 298 GTGAAAAGGCGCTGGGAAAAGAGGAGCCAAATCTGTCTCTCTCAATTAATGTC 357
Db 610 GTGAAAAGGCGCT -GGAAAAGAGGAGCCAAATCTGTCTCTCTCAATTAATGTC 552
Qy 358 ATTGGCAATTAAGCATTTGCTCTTTTGGCTGCTGCTGAGCAGAGAGCCAGAACTCT 417
Db 551 ATTGGCAATTAAGCATTTGCTCTTTTGGCTGCTGCTGAGCAGAGAGCCAGAACTCT 492
Qy 418 ATCGGACACAGAGATTAATCTCTCAGTGAACAGAGTTGACAGAGGCTATGGAATGCG 477
Db 491 ATCGGACACAGAGATTAATCTCTCAGTGAACAGAGTTGACAGAGGCTATGGAATGCG 432
Qy 478 TGAATGGATTAATTTAGCTTTGAGCTTTCTAAGTTTCTTTCCCTTCAATTCACCTGC 537
Db 431 TGAATGGATTAATTTAGCTTTGAGCTTTCTAAGTTTCTTTCCCTTCAATTCACCTGC 372
Qy 538 AAGCCAAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTAGGTTTCTTACTGTAATTT 597
Db 371 AAGCCAAAGTTCTGTAGAGAAATGCTGAGTTCTAGCTAGGTTTCTTACTGTAATTT 312
Qy 598 AGATCTCCAGACCTTCTGCGCACAATTAATTAAGCAACAATATACCTTCAT 657
Db 311 AGATCTCCAGACCTTCTGCGCACAATTAATTAAGCAACAATATACCTTCAT 252
Qy 658 GAAGCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTAAGGCTTTAGGA 717
Db 251 GAAGCACACACAGACTTTTGAAGCAAGCAATGACTGTTGAATTAAGGCTTTAGGA 192
Qy 718 ATGAGCTTTGAAGAAAGAAATTAATCTTTTCCAGCCCCCTTCCACACTCTTCATGTC 777
Db 191 ATGAGCTTTGAAGAAAGAAATTAATCTTTTCCAGCCCCCTTCCACACTCTTCATGTC 132
Qy 778 TTACCACTGCTTCTCTGAGCTTGAGCCAGGTTGATTAATCATGTTGTTATAGAA 837
Db 131 TTACCACTGCTTCTCTGAGCTTGAGCCAGGTTGATTAATCATGTTGTTATAGAA 72
Qy 838 AACTGATTTTGAAGTTCTGATGTTCAAGAGAAATGATTAATTAATTAATTCCT 890
Db 71 AACTGATTTTGAAGTTCTGATGTTCAAGAGAAATGATTAATTAATTAATTCCT 19
RESULT 4
BU632767/c
LOCUS BU632767 700 bp mRNA linear EST 23-SEP-2002
DEFINITION UI-H-FBI-bdy-k-03-0-UI.s1 NCI CGAP FBI Homo sapiens cDNA clone
ACCESSION BU632767
VERSION BU632767.1 GI:23300022
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 623-700, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 PolyA=yes.

FEATURES

source
 1..700
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FE1-bdy-k-03-0-UI"
 /tissue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FE1"
 /note="Organ: Chondrosarcoma; Vector: pTT73-Pac
 (Pharmacia) with a modified polylinker; Site 1: Ecor I;
 Site 2: Not I; NCI CGAP FE1 is a normalized cDNA library
 derived from a pool of mRNA obtained from 3 cell lines
 from grade II chondrosarcoma tissues. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an Ecor I
 adaptor, digested with Not I, and cloned directionally
 into pTT73-pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 CGCTACGGAC. The cell lines were provided by Dr James
 Martin from the University of Iowa.
 TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
 TAG_LIB=UI-H-FE1
 TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match 71.8%; Score 639.4; DB 5; Length 700;
 Best Local Similarity 99.7%; Pred. No. 7.6e-181;
 Matches 651; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Oy 238 CATTAACACTACCCATCCGAAGTGCACCTGTGACAGACTAAGAAACCTGGTTTGA 297
 Db 675 CATTAACACTACCCATCCGAAGTGCACCTGTGACAGACTAAGAAACCTGGTTTGA 616
 Oy 238 GTAGAAAAGGGCCTGGGAAAAGAGGGAGCCAAATCTGTCTGCTCTCTCATTTATGTC 357
 Db 615 GTAGAAAAGGGCCT-GGAAAAGAGGGAGCCAAATCTGTCTGCTCTCTCATTTATGTC 557
 Oy 358 ATTGGCAATTAAGCATTTCTCTTTGGCTGCTGCTCCTAGACACAGAGGCCAGAACTCT 417
 Db 556 ATTGGCAATTAAGCATTTCTCTTTGGCTGCTGCTCCTAGACACAGAGGCCAGAACTCT 497
 Oy 418 ATCGGGGACCCAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTATGGGAATGCC 477
 Db 496 ATCGGGGACCCAGGATTAACATCTCTCAGTGAACAGAGTTGACAAAGCCTATGGGAATGCC 437
 Oy 478 TGATGGGATTAATCTTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTACCCCTGC 537
 Db 436 TGATGGGATTAATCTTCAGCTTGTGAGCTTCTAAGTTCTTCCCTTCATTTACCCCTGC 377
 Oy 538 AAGCCAGTTCTGTAAAGAGAAATGCCCTGAGTTCTAAGCTCAGGTTTCTTACTCTGAATTT 597
 Db 376 AAGCCAGTTCTGTAAAGAGAAATGCCCTGAGTTCTAAGCTCAGGTTTCTTACTCTGAATTT 317
 Oy 598 AGATCTCCAGACCCGCGCTGGCCACAATTCAAATTAAGGCAACAACATATCCTTCAT 657
 Db 316 AGATCTCCAGACCCCTTCCTGGCCACAATTCAAATTAAGGCAACAACATATCCTTCAT 257

FEATURES

source

Oy 658 GAAGCACACACAGACTTTTGAAGCAAGACAAATGACTGCTTGAATTGAGGCTTTGAGCA 717
 Db 256 GAAGCACACACAGACTTTTGAAGCAAGACAAATGACTGCTTGAATTGAGGCTTTGAGCA 197
 Oy 718 ATGAAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTTTATGTC 777
 Db 196 ATGAAGCTTTGAAGAAAAGAAATACTTTGTTCCAGCCCCCTTCCACACTTTATGTC 137
 Oy 778 TTAAACCACTGCTCTCTGCTGAGCCTTGAGCCACGAGTGAATTAATCATGTTATTAGAA 837
 Db 136 TTAAACCACTGCTCTCTGCTGAGCCTTGAGCCACGAGTGAATTAATCATGTTATTAGAA 77
 Oy 838 AACTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 890
 Db 76 AACTGATTTTGAAGTTCTGATCGTTCAAGAGATGATTAAATATACATTTCT 24
 RESULT 5
 CA314865/c
 LOCUS
 DEFINITION
 UI-CF-FN0-afi-e-12-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
 UI-CF-FN0-afi-e-12-0-UI 3', mRNA sequence.
 ACCESSION
 CA314865
 VERSION
 CA314865.1 GI:24532963
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL
 Genome Res. 6 (9), 791-806 (1996)
 MEDLINE
 97044477
 PUBMED
 8889548
 COMMENT
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.regen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 618-691, >MER20#DNA/MER1_type (matched complement)
 Seq primer: M13 FORWARD
 PolyA=yes.
 Location/Qualifiers
 1..691
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FN0-afi-e-12-0-UI"
 /tissue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (TI phage resistant)"
 /clone_lib="UI-CF-FN0"
 /note="Organ: Lung; Vector: pTT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 UI-CF-FN0 is a subcloned cDNA library derived from two
 normalized Human Lung epithelial cell libraries (EN1 and
 DUL) The library was subcloned according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_SEQ=CGCTACGGAC"

ORIGIN

TAG LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

Query Match 71.7%; Score 638.4; DB 6; Length 691;
Best Local Similarity 99.5%; Pred. No. 1.5e-180;
Matches 650; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 238 CATTACAACTACCAATCCCAATGTCATCTGTCTAGAGCACTAAGAAACCTGGTTTGA 297
DB 670 CATTACAACTACCAATCCCAATGTCATCTGTCTAGAGCACTAAGAAACCTGGTTTGA 611
QY 298 GTAGAAAAGGGCTGGGAAAGAGGGAGCAACAATCTGTCTGCTTCTCATTAGTC 357
DB 610 GTAGAAAAGGGCTT-GGAAAGAGGGAGCCAAATCTGTCTGCTTCTCATTAGTC 552
QY 358 ATTGGCAATTAAGCAATTTCTGTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 417
DB 551 ATTGGCAATTAAGCAATTTCTGTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 492
QY 418 ATGGGGACCAAGATTAACATCTCTCACTGAACAAGATGACAGAGCTATGGAAATGCC 477
DB 491 ATGGGGACCAAGATTAACATCTCTCACTGAACAAGATGACAGAGCTATGGAAATGCC 432
QY 478 TGATGGGATTAATCTTCAAGCTTGTAGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 537
DB 431 TGATGGGATTAATCTTCAAGCTTGTAGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 372
QY 538 AAGCCAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 597
DB 371 AAGCCAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 312
QY 598 AGATCTCCAGACCTCTGCGCCCAATTAAGGCAACAATTAAGGCAACAATTAAGGCAACA 657
DB 311 AGATCTCCAGACCTCTGCGCCCAATTAAGGCAACAATTAAGGCAACAATTAAGGCAACA 252
QY 658 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTAGAGCCCTTGAAGA 717
DB 251 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTAGAGCCCTTGAAGA 192
QY 718 ATGAACTTTGAAGAAAGAAATACTTTGTTTTCAGAGCCCTTCCAGACTCTTCAATG 777
DB 191 ATGAACTTTGAAGAAAGAAATACTTTGTTTTCAGAGCCCTTCCAGACTCTTCAATG 132
QY 778 TTAACCACTGCTCTCTGACCTTTGAGCCAGCGTGAATTAATGTTTGAATGA 837
DB 131 TTAACCACTGCTCTCTGACCTTTGAGCCAGCGTGAATTAATGTTTGAATGA 72
QY 838 AACTGATTTTGAATGCTGATGCTTCAAGAAATGAATTAATTAATTAATTAATTAATTA 890
DB 71 AACTGATTTTGAATGCTGATGCTTCAAGAAATGAATTAATTAATTAATTAATTAATTA 19

RESULT 6
CA133445 737 bp mRNA linear EST 04-NOV-2002
LOCUS CA133445/c
DEFINITION UI-CF-FNO-aeY-b-10-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
ACCESSION CA133445
VERSION CA133445.1 GI:24531543
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB

McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.researchgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this CDNA
sequence: 618-737, >MER20#DNA/MER1_type (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..737
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-aeY-b-10-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="PH108 (Life Technologies) (T1 phage resistant)"
/clone_1ib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DN1). The library was subtracted according to
Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TNG TISSUE=Lung Epithelial cells tissue nos 359-368
TAG LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 71.7%; Score 638.4; DB 6; Length 737;
Best Local Similarity 99.5%; Pred. No. 1.5e-180;
Matches 650; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 238 CATTACAACTACCAATCCCAATGTCATCTGTCTAGAGCACTAAGAAACCTGGTTTGA 297
DB 670 CATTACAACTACCAATCCCAATGTCATCTGTCTAGAGCACTAAGAAACCTGGTTTGA 611
QY 298 GTAGAAAAGGGCTGGGAAAGAGGGAGCAACAATCTGTCTGCTTCTCATTAGTC 357
DB 610 GTAGAAAAGGGCTT-GGAAAGAGGGAGCCAAATCTGTCTGCTTCTCATTAGTC 552
QY 358 ATTGGCAATTAAGCAATTTCTGTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 417
DB 551 ATTGGCAATTAAGCAATTTCTGTCTTTGGCTGCTGCTCAGACAAGAGCCAGAACTCT 492
QY 418 ATGGGGACCAAGATTAACATCTCTCACTGAACAAGATGACAGAGCTATGGAAATGCC 477
DB 491 ATGGGGACCAAGATTAACATCTCTCACTGAACAAGATGACAGAGCTATGGAAATGCC 432
QY 478 TGATGGGATTAATCTTCAAGCTTGTAGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 537
DB 431 TGATGGGATTAATCTTCAAGCTTGTAGAGCTTCTAAGTTTCTTCCCTTCACTTACCCTGC 372
QY 538 AAGCCAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 597
DB 371 AAGCCAGTTCTGTAAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTAATTT 312
QY 598 AGATCTCCAGACCTCTGCGCCCAATTAAGGCAACAATTAAGGCAACAATTAAGGCAACA 657
DB 311 AGATCTCCAGACCTCTGCGCCCAATTAAGGCAACAATTAAGGCAACAATTAAGGCAACA 252
QY 658 GAAGCACACACAGACTTTTGAAGCAAGACATGACTGCTTGAATTTAGAGCCCTTGAAGA 717

Db 251 GAAGACACACAGACTTTTGAAGACAGACATGACTGTAATGAGCCCTTGAGGA 192
QY 718 ATGAAGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 777
Db 191 ATGAAGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 132
QY 778 TTAACCACTGCTTCTTGAGACCTTGAGACCGGAGCTGATTTAATCATGTTGTATAGA 837
Db 131 TTAACCACTGCTTCTTGAGACCGGAGCGGAGCTGATTTAATCATGTTGTATAGA 72
QY 838 AACCTATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 890
Db 71 AACTGATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 19

RESULT 7

BU608696/c 691 bp mRNA linear EST 21-FEB-2003
LOCUS UI-CF-FN0-aeg-c-07-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
DEFINITION UI-CF-FN0-aeg-c-07-0-UI 3', mRNA sequence.

ACCESSION BU608696
VERSION BU608696.1 GI:23274911

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 691)
AUTHORS Ronaldo, M. P., Lennon, G. and Soares, M. B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548

COMMENT

Contact: McCray, PB

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171

Email: pauli-mccray@iowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.research.com) or from Open Biosystems

(www.openbiosystems.com).

The following repetitive elements were found in this cDNA
sequence: 618-691, >MER20#DNA/MER1_type (matched complement)

Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..691

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-FN0-aeg-c-07-0-UI"

/tissue_type="Human Lung Epithelial cells"

/lab_host="PHIOB (Life technologies) (T1 phage resistant)"

/clone_11b="UI-CF-FN0"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI) The library was subtracted according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG TISSUE=Human Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CF-FN0
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 71.3%; Score 634.6; DB 5; Length 691;
Best Local Similarity 99.2%; Pred. No. 2.1e-179;
Matches 648; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 238 CATTACAATCCCAATCCGAATGTCATCTGTGACGACTAAGAAAACCTGGTTTGA 297
Db 670 CATACAAATCAATCCCAATCCGAATGTCATCTGTGACGACTAAGAAAACCTGGTTTGA 611
QY 298 GTAGAAAAGGGGCTGGGAAAGGGGAGCCAAATCGTGTGCTTCTCCTCATTAATGC 357
Db 610 GTAGAAAAGGGGCTGGGAAAGGGGAGCCAAATCGTGTGCTTCTCCTCATTAATGC 552
QY 358 ATTGGCAATATAGCAATTCGTCTCTTTGGCTGCTGCTCAGACAGAGCCAGAACTCT 417
Db 551 ATTGGCAATATAGCAATTCGTCTCTTTGGCTGCTGCTCAGACAGAGCCAGAACTCT 492
QY 418 ATGGGGCACCAGATATCATCTCTCAGTGAACAGAGTTGACAAAGGCTTAGGAAATGCC 477
Db 491 ATGGGGCACCAGATATCATCTCTCAGTGAACAGAGTTGACAAAGGCTTAGGAAATGCC 432
QY 478 TGATGGATATATCTTACAGCTTGTGAGCTTGAAGTTCTTCCCTTCATCTACCTGCG 537
Db 431 TGATGGATATATCTTACAGCTTGTGAGCTTGAAGTTCTTCCCTTCATCTACCTGCG 372
QY 538 AAGCCAAATCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTT 597
Db 371 AAGCCAAATCTGTGAAGAAATGCTGAGTTCTAGCTCAGGTTTCTTACTGTGAATTT 312
QY 598 AGATCTCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Db 311 AGATCTCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
QY 658 GAAGCACACACAGACTTTTGAAGCAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Db 251 GAAGCACACACAGACTTTTGAAGCAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
QY 718 ATGAAGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 777
Db 191 ATGAAGCTTTGAAGAAAGAAATACCTTTGTTCCAGCCCCCTTCCACACTCTCATGTG 132
QY 778 TTAACCACTGCTTCTTGAGACCTTGAGACCGGAGCTGATTTAATCATGTTGTATAGA 837
Db 131 TTAACCACTGCTTCTTGAGACCGGAGCGGAGCTGATTTAATCATGTTGTATAGA 72
QY 838 AACCTATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 890
Db 71 AACTGATTTTGAAGTTGATGCTTCAAGAGAAATGATTAATATCATTTCTT 19

RESULT 8

CB852239/c

LOCUS CB852239/6

DEFINITION UI-CF-FN0-aeg-c-07-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone

UI-CF-FN0-aeg-c-07-0-UI 3', mRNA sequence.

ACCESSION CB852239

VERSION CB852239.1 GI:30047206

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 660)

AUTHORS Ronaldo, M. P., Lennon, G. and Soares, M. B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

CONTACT: McCray, PB

COMMENT

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.regen.com) or from Open Biosystems (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source location/Qualifiers
 1. 660
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-FNO-aff-m-01-0-UI"
 /issue_type="Human Lung Epithelial cells"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-FNO is a subcloned CDNA library derived from two normalized Human lung epithelial cell libraries (BN1 and DU1). The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu
 TAG_SEQ=None found"

ORIGIN

Query Match 70.6%; Score 628.4; DB 6; Length 660;
 Best Local Similarity 99.5%; Pred. No. 1.5e-177;
 Matches 640; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 248 ACCCAATCCGAAGTGTCACTGTCAGACTAAGAAACCTGATTTAGTGAAGG 307
 660 ACCCAATCCGAAGTGTCACTGTCAGACTAAGAAACCTGATTTAGTGAAGG 601
 308 GCGTGGAAAGAGGGAGCCCAAAATCTGTCTGCTTCTCAGATTAGTGGCAAT 367
 600 GCGT-GGAAAGAGGGAGCCCAAAATCTGTCTGCTTCTCAGATTAGTGGCAAT 542
 368 AAGCATTTCTCTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
 541 AAGCATTTCTCTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
 428 AGGATAACATCTCTCAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 487
 481 AGGATAACATCTCTCAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 422
 488 ATCTTCAGCTTTGTAAGCTTCTAAGTTTCTTCTTCTTCTTCTTCTTCTTCTT 547
 421 ATCTTCAGCTTTGTAAGCTTCTAAGTTTCTTCTTCTTCTTCTTCTTCTTCTT 362
 548 CTGTAGAAGAAATGCTGAGTTCAGTCAAGTTTCTTACTGTAATTAAGTTCAG 607
 361 CTGTAGAAGAAATGCTGAGTTCAGTCAAGTTTCTTACTGTAATTAAGTTCAG 302
 608 ACCCTGCTGGCCACAAATTAAGGCAAAATTAAGGCAAAATTAAGGCAAAAT 667
 301 ACCCTGCTGGCCACAAATTAAGGCAAAATTAAGGCAAAATTAAGGCAAAAT 242
 668 CAGACTTTGAAAGCAAGCAATGACTGCTTGAATTAAGGCAATTAAGGCAAT 727
 241 CAGACTTTGAAAGCAAGCAATGACTGCTTGAATTAAGGCAATTAAGGCAAT 182
 728 GAAGAGAAAGAAATCTTTGTTTCCAGCCCTTCCCACTCTTCAATGTTTAAAC 787
 181 GAAGAGAAAGAAATCTTTGTTTCCAGCCCTTCCCACTCTTCAATGTTTAAAC 122
 788 CTTCTGAGACTTGGAGCCAGGTGATGATTAATGATTTATTAAGAAATGATTT 847

Db 121 CCTTCTGAGCCTTGGAGCCAGGTGATTAATGATTTATTAAGAAATGATTT 62
 QY 848 AGAGTTCTGATCGTTCAAGAAATGATTTAATTAATTAATTAATTAATTTCT 890
 Db 61 AGAGTTCTGATCGTTCAAGAAATGATTTAATTAATTAATTAATTTCT 19

RESULT 9

CA426580/c 660 bp mRNA linear EST 07-NOV-2002
 LOCUS UI-H-FBI-beh-p-14-0-UI.s1 NCI CGAP FBI Homo sapiens CDNA clone
 DEFINITION UI-H-FBI-beh-p-14-0-UI 3', mRNA sequence.
 ACCESSION CA426580
 VERSION CA426580.1 GI:24789306
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 660)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: James Martin
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source location/Qualifiers
 1. 660
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FBI-beh-p-14-0-UI"
 /issue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP_FBI"
 /note="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FBI is a normalized CDNA library derived from a pool of mRNA obtained from 3 cell lines from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is CCGTACGAC. The cell lines were provided by Dr James Martin from the University of Iowa.
 TAG TISSUE=human grade 2 chondrosarcoma cell line pool
 TAG_LIB=UI-H-FBI
 TAG_SEQ=CGTACGAC"

ORIGIN

Query Match 69.9%; Score 621.8; DB 6; Length 660;
 Best Local Similarity 99.4%; Pred. No. 1.5e-175;
 Matches 634; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 253 ATCCGAAGTGTCACTGTCAGACTAAGAAACCTGTTTGAAGTGAAGGCGCTG 312
 Db 660 ATCCGAAGTGTCACTGTCAGACTAAGAAACCTGTTTGAAGTGAAGGCGCT- 602

OY	313	GGAAAGAGGGGAGCCAAATAATCTGTCTGCTTCCCAATAATAGCATTTGGCAATTAAGCA	372
Db	601	GGAAAGAGGGGAGCCAAATAATCTGTCTGCTTCCCAATAATAGCATTTGGCAATTAAGCA	542
OY	373	TTCTGTCTCTTTGGCTGTGCTGCCTCAGCA CAGAGAGCCAGAACTCATCGGGCA CCGAGAT	432
Db	541	TTCTGTCTCTTTGGCTGTGCTGCCTCAGCA CAGAGAGCCAGAACTCATCGGGCA CCGAGAT	482
OY	433	AACATCTCTCAGTGAACAGAGTTGACAAAGCCCTATGGGAAATGCTGATGGGATTAATCTT	492
Db	481	AACATCTCTCAGTGAACAGAGTTGACAAAGCCCTATGGGAAATGCTGATGGGATTAATCTT	422
OY	493	CAGCTTTGTTAGCTTCTTAAGTTCTTTCCCTGATTAATTAACCTGGAACCCGAATTCGTGA	552
Db	421	CAGCTTTGTTAGCTTCTTAAGTTCTTTCCCTGATTAATTAACCTGGAACCCGAATTCGTGA	362
OY	553	AGAGAAATGSCCGAGTCTTAGCTCAGTGTTCCTTACTCTGAATTAGATCTCCAGACCT	612
Db	351	AGAGAAATGSCCGAGTCTTAGCTCAGTGTTCCTTACTCTGAATTAGATCTCCAGACCT	302
OY	613	GCTTGGCCACAATTCAAAATTAAAGCAACAAACATATTAACCTTTCATGAAGCA CACACAGAC	672
Db	301	TCCTGGCCACAATTCAAAATTAAAGCAACAAACATATTAACCTTTCATGAAGCA CACACAGAC	242
OY	673	TTTTTAAAGCAAGGACATGA CTGCTTGAATTGAAGCCCTTGAAGAAATGAACCTTTGAAGG	732
Db	241	TTTTTAAAGCAAGGACATGA CTGCTTGAATTGAAGCCCTTGAAGAAATGAACCTTTGAAGG	182
OY	733	AAAAAATATCTTTGTTTCCAGGCCCTTCCCA CACTTTCATATGTTTAACCACTGCCTTC	792
Db	181	AAAAAATATCTTTGTTTCCAGGCCCTTCCCA CACTTTCATATGTTTAACCACTGCCTTC	122
OY	793	CTGACCTTGGAGCCACGGTGA CTGTATTAACA TGTGTTATAGAAAACGTATTTTGAAGT	852
Db	121	CTGACCTTGGAGCCACGGTGA CTGTATTAACA TGTGTTATAGAAAACGTATTTTGAAGT	62
OY	853	TCTGATCGTTCAAGGAATGATTAATATATCACTTTTCCT	890
Db	61	TCTGATCGTTCAAGGAATGATTAATATATCACTTTTCCT	24

RESULT 10	CA312678	679 bp	mRNA	linear	EST 04-NOV-2002
LOCUS	CA312678/c				
DEFINITION	CA312678	UI-CF-FNO-afl-m-11-0-UI-s1	UI-CF-FNO	Homo sapiens	CDNA clone
ACCESSION	CA312678	CA312678.1	GI:24530776		
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
MEDLINE					
PUBMED					
COMMENT					

University of Iowa
20224 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel.: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research

Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLY=Yes.

```

FEATURES
source
Location/Qualifiers
1. .679
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afl-m-11-0-UI"
/tissue_type="Human lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI1). The library was subtracted according to according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@iowa.edu
TAG_TISSUE=Human lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

```

ORIGIN

Query Match	69.1%;	Score 615.4;	DB 6;	Length 679;
Best Local Similarity	97.4%;	Pred. No. 1.3e-173;		
Matches 636; Conservative	0;	Mismatches 16;	Indels 1;	Gaps 1

OY	238	CATTACAACTACCCCAATCCGAAGTGTCAACTGTGTGACAGACTAAGAAACCCGTGTTTGA	297
Db	670	CATTACAAAGTACCCCAATCCGAAGTGTCAACTGTGTGACAGGCTTAAGAAACCCGTGTTTGA	611
OY	298	GTAGAAAAGGACCTGGGAAAGAGGGGAGCCAACAATCTGTCTGCTTCTCACTTAGTC	357
Db	610	GCAGAAAAGGGGCTTGGAAAGAGGAGCCCAACAATCTGTCTGCTTCTCTCACTTAGTC	552
OY	358	ATTGGCAATTAAGCAATTCTGTCTCTTTGGCTGTGCTCCCTCAGACAGAGAGCCAGAACTTC	417
Db	551	ATTGGCAATTAACCAATTCCTGTCTGTGTGGCTGTGCTCCCTCAGACAGAGAACCAAGAACTTC	492
OY	418	ATCGGCACACAGAAATACATCTCTTCAGTGAACAGAGTTGACACAGGCTATGGGAATGCG	477
Db	491	ATCGGCACACAGGAATACATATTCAGTGAACAGAGTTGACACAGGCTATGGGAATGCG	432
OY	478	TGATGGGATTATCTTCACTGTGTGAGCTTCTAAGTTCTTCCCTTCAATCTTACCCTGC	537
Db	431	TGATGGGATTATCTTCACTGTGTGAGCTTCTAAGTTCTTCCCTTCAATCTTACCCTGC	372
OY	538	AAGCCAAATTCGTGAAGAAATGCGTGAAGTTCTGACGAGTTTCTTACTCTGAATTT	597
Db	371	AAACCAATTCGTGAAGAAATGCGTGAAGTTCTGACGAGTTTCTTACTCTGAATTT	312
OY	598	AGATTTCCAGACCTGCTGCGCCACAATTCAAATTAAAGCAACAACATATACCTTCCAT	657
Db	311	AGATTTCCAGACCTGCTGCGCCACAATTCAAATTAAAGCAACAACATATACCTTCCAT	252
OY	658	GAAGCACACACAGACTTTTGAAGCAAGACATATGCTTGAATTGAGCGCTTGAGGA	717
Db	251	GAAGCACACACAGACTTTTGAAGCAAGACATATGCTTGAATTGAGCGCTTGAGGA	192
OY	718	ATGAAGCTTTGAAGAAAAGAAATCTTGTTCAGGCCCTTCCCACTCTTCATGTG	777
Db	191	ATGAAGCTTTGAAGAAAAGAAATCTTGTTCAGGCCCTTCCCACTCTTCATGTG	132
OY	778	TTAACCATGCTCTCTGACCTTGAGCCACGAGGACTGTATATCATGTTTATAGAA	837
Db	131	TTAACCATGCTCTCTGACCTTGAGCCACGAGGACTGTATATCATGTTTATAGAA	72
OY	838	AACTGATTTAGAGTTCTGATGCTTCAAGAGATGATTAATATACATTTCTCT	890

DB	71	AACTGATTTAGAGTTCTGATCGTTCAGAGAAATGATTAATAATGATTTCT	19
RESULT 11	CA503188	594 bp	mRNA
LOCUS	CA503188/c		linear
DEFINITION	UI-CF-FNO-0-afp-p-10-0-UI-s1 UI-CF-FNO Homo sapiens cDNA clone		EST 14-NOV-2002
ACCESSION	CA503188		
VERSION	CA503188.1	GI:24994142	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
REFERENCE	1 (bases 1 to 594)		
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	97044477		
PUBMED	8889548		
COMMENT	Contact: McCray, PB University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171 Email: paul-mccray@iowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa cDNA library preparation: Dr. M. Bento Soares, University of Iowa cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com). Seq primer: M13 FORWARD PolyA=yes.		
FEATURES	Location/Qualifiers		
source	1..594		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="UI-CF-FNO-0-afp-p-10-0-UI"		
	/tissue_type="Human lung Epithelial cells"		
	/lab_host="DH10B (Life Technologies) (T1 phage resistant)"		
	/clone_lib="UI-CF-FNO"		
	/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; UI-CF-FNO is a subcloned cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DUL) The library was subcloned according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: benito-soares@iowa.edu		
	TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368		
	TAG_LIB=UI-CF-FNO		
	TAG_SEQ=GCCTGTAGGC"		
ORIGIN			
Query Match	63.6%; Score 566.4; DB 6; Length 594;		
Best Local Similarity	99.0%; Pred. No. 7e-159;		
Matches 570; Conservative	0; Mismatches 6; Indels 0; Gaps 0;		
DB	315 AAAGAGGGAGCCAAACAATCTGCTCTGCTTCTCACTTAGTCATTGGCAATTAAGATT	374	
594 AAAGAGGGAGCCAAACAATCTGCTCTGCTTCTCACTTAGTCATTGGCAATTAAGATT	535		
375 CTGTCCTCTTTGGCTGCTGCTCCTCAGACAGAGACAGAACTCTATCGGACACAGATTA	434		
DB	534 CTGTCCTCAATGGCTGCTGCTCCTCAGACAGAGACAGAACTCTATCGGACACAGATTA	475	
435 CATCTCTAGTGAAACAGAGTTGACAGAGGCTTATGGGAAATCCCTGATGGATTAATCTTCA	494		

	DB	474	CATCTTCAGTGAACAAGTTGACAAAGCCTTAGGGAAATGCCTGATGGATTATCTTCA	415		
OY		495	GCTTGTTAGCTTTAAGTTTTCTTCCCTTCATTCTAACCTGCAGCAAGTCTGTAG	554		
Db		414	GCTTGTTAGCTTTAAGTTTTCTTCCGTTCACTTAACCCTGCAGCAAGCTTGTAG	355		
OY		555	AGAAATGCTCGATTTCTAGCTCAGGTTTTCTACTGTGAATTAGAATCTCACAGCCTGC	614		
Db		354	AGAAATGCTCGATTTCTAGCTCAGGTTTTCTACTGTGAATTAGAATCTCACAGCCTTC	295		
OY		615	CTGGCCAATTTCAAATTTAAGGCAACAACATAATFACCTTCATGAGACACACAGACTT	674		
Db		294	CTGGCCAATTTCAAATTTAAGGCAACAACATAATFACCTTCATGAGACACACAGACTT	235		
OY		735	TGAAGCAAGCAAGCATGACTGCTTGAATTGAGGCCCTTGAGAATGAAGCTTTGAAGAA	734		
Db		234	TGAAGCAAGCAAGCATGACTGCTTGAATTGAGGCCCTTGAGAATGAAGCTTTGAAGAA	175		
OY		855	TGATCGTTCAAGAGAAATGATTTAATATACATTTTCTT	890		
Db		114	GGACCTTGAGCCACGGGTGACTGATTAACATGTGTATGAAAACATGATTTAGAGTTC	55		
OY		54	TGATCGTTCAAGAGAAATGATTTAATATACATTTTCTT	19		
RESULT 12 Al684143/c						
LOCUS		Al684143	556 bp	mRNA linear EST 16-DEC-1999		
DEFINITION		xrjg9g4.xl NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2275830 3'				
ACCESSION		Al684143				
VERSION		Al684143.1				
KEYWORDS		EST.				
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 556) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapsb-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/bdnp/image/image.html Insert Length: 2042 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 417. Location/Qualifiers 1..556 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2275830" /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors" /lab_host="DH10B" /clone_lib="NCI_CGAP_Ut1" /note="Organ: uterus; Vector: pCMV-SPORT6, Site 1: SalI;				
JOURNAL COMMENT						
REFERENCE AUTHORS TITLE						
FEATURES SOURCE						

ORIGIN

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

Query Match 61.8%; Score 550.4; DB 1; Length 556;

Best Local Similarity 99.8%; Pred. No. 4.5e-154;

Matches 551; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 339 CTGCTTCCATCATAGTATGATGGCAATATGATCATTTCTCTTGGCTGCTGCTG 398
DB 556 CTGCTTCCATCATAGTATGATGGCAATATGATCATTTCTCTTGGCTGCTGCTG 497
QY 399 CACAGAGAGCCAGAACTCTATCGGGACCCAGAGATTAATCTCTCACTGAAGAGTTGAC 458
DB 496 CACAGAGAGCCAGAACTCTATCGGGACCCAGAGATTAATCTCTCACTGAAGAGTTGAC 437
QY 459 AAGGCTTATGGAAATGCTGATGGGATTAATCTCTCACTGTTGAGCTTCAAGTTTCTT 518
DB 436 AAGGCTTATGGAAATGCTGATGGGATTAATCTCTCACTGTTGAGCTTCAAGTTTCTT 377
QY 519 TCCCTTCAATTCACCTGCAAGCCAAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTGAG 578
DB 376 TCCCTTCAATTCACCTGCAAGCCAAAGTTCTGTAAGAGAAATGCTGAGTTCTAGCTGAG 317
QY 579 GTTTTCTTACTGATTTAGATCTTCAGACCCCTGCTGCGCAATTCATTAATTAAGGA 638
DB 316 GTTTTCTTACTGATTTAGATCTTCAGACCCCTGCTGCGCAATTCATTAATTAAGGA 257
QY 639 ACAAACATATACCTTCCATGAAACACACACAGACTTTTGAAGCAAGACATGACTGT 698
DB 256 ACAAACATATACCTTCCATGAAACACACACAGACTTTTGAAGCAAGACATGACTGT 197
QY 699 TGAATTTAGAGCCCTTGAAGATGAGCTTTGAAGAAAGATACCTTTGTTCCAGCCCC 758
DB 196 TGAATTTAGAGCCCTTGAAGATGAGCTTTGAAGAAAGATACCTTTGTTCCAGCCCC 137
QY 759 TTCCCAACACTCTTCATGTTGTTAACCACTGCTCTCTGCACTTGAAGCCACGGTACTGT 818
DB 136 TTCCCAACACTCTTCATGTTGTTAACCACTGCTCTCTGCACTTGAAGCCACGGTACTGT 77
QY 819 ATTACATGTTGTTTAAAGAAACTGATTTTGAAGTTTGAATGTTCAAGAGATGATTA 878
DB 76 ATTACATGTTGTTTAAAGAAACTGATTTTGAAGTTTGAATGTTCAAGAGATGATTA 17
QY 879 TATACATTTCT 890
DB 16 TATACATTTCT 5

```

RESULT 13
 LOCUS CD632169 568 bp mRNA linear EST 12-JAN-2004
 DEFINITION 56084071H1 FLP Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD632169
 VERSION CD632169.1 GI:40280436
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes

JOURNAL
 COMMENT Genomics 84 (1), 205-210 (2004)
 Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.

FEATURES
 Source 1..568
 Location/Qualifiers

ORIGIN

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="FLP"
 /note="Vector: pDrive Cloning Vector"

Query Match 61.8%; Score 549.6; DB 6; Length 568;

Best Local Similarity 99.3%; Pred. No. 7.9e-154;

Matches 552; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 335 CTGCTGCTTCTCATATGATGATGGCAATATGATCATTTCTGTTCTTTGGCTGCTGCC 394
DB 11 CAGTGTGCTTCTCATATGATGATGGCAATATGATCATTTCTGTTCTTTGGCTGCTGCC 70
QY 395 TCAGCAGAGAGCCAGAACTCTATCGGGACCCAGAGATTAATCTCTCACTGAAGAGTTGAC 454
DB 71 TCAGCAGAGAGCCAGAACTCTATCGGGACCCAGAGATTAATCTCTCACTGAAGAGTTGAC 130
QY 455 TGACAGAGCCCTATGGAAATGCTGATGGGATTAATCTCTCACTGTTGAGCTTCAAGTT 514
DB 131 TGACAGAGCCCTATGGAAATGCTGATGGGATTAATCTCTCACTGTTGAGCTTCAAGTT 190
QY 515 TCTTTCCCTTCAATTTACCTGCAAGCCCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGC 574
DB 191 TCTTTCCCTTCAATTTACCTGCAAGCCCAAGTTCTGTAAGAGAAATGCTGAGTTCTAGC 250
QY 575 TCAGGTTTCTTACTGTAATTTAGATCTTCAGACCCCTGCTGCGCAATTCATTAATTA 634
DB 251 TCAGGTTTCTTACTGTAATTTAGATCTTCAGACCCCTGCTGCGCAATTCATTAATTA 310
QY 635 GCGCAACAAACATATACCTTCCATGAAACACACAGACTTTTGAAGCAAGACATGAC 694
DB 311 GCGCAACAAACATATACCTTCCATGAAACACACAGACTTTTGAAGCAAGACATGAC 370
QY 695 TGCCTTGAATGAGGCTTGAAGATGAGCTTTGAAGAAAGATACCTTTGTTCCAGC 754
DB 371 TGCCTTGAATGAGGCTTGAAGATGAGCTTTGAAGAAAGATACCTTTGTTCCAGC 430
QY 755 CCCCTTCCCAACACTCTTCATGTTGTTAACCACTGCTCTCTGCACTTGAAGCCACGGTACTGT 814
DB 431 CCCCTTCCCAACACTCTTCATGTTGTTAACCACTGCTCTCTGCACTTGAAGCCACGGTACTGT 490
QY 815 CTGATTAATGATGTTTAAAGAACTGATTTTGAAGTTTGAATGTTCAAGAGATGAT 874
DB 491 CTGATTAATGATGTTTAAAGAACTGATTTTGAAGTTTGAATGTTCAAGAGATGAT 550
QY 875 TAAATATACATTTCT 890
DB 551 TAAATATACATTTCT 566

```

RESULT 14
 LOCUS CD632170/c 560 bp mRNA linear EST 12-JAN-2004
 DEFINITION 56084071J1 FLP Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD632170
 VERSION CD632170.1 GI:40280437
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes

JOURNAL
 COMMENT Genomics 84 (1), 205-210 (2004)
 Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.

FEATURES
 Source 1..568
 Location/Qualifiers

FEATURES
source
1. 560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/notes="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 61.0%; Score 542.6; DB 6; Length 560;
Best Local Similarity 99.3%; Pred. No. 1e-151;
Matches 545; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

335 CTGTGCTGCTCCACATGATGCGCAATTAAGCATCTGCTCTTGGCTGCGCC 394
549 CAGTGTGCTTCTCACTTATGTCATGCGCAATTAAGCATCTGCTCTTGGCTGCGCC 490
395 TCAGCAGAGAGAGCAGAACTCTATCGGCGACGAGTAACATCTCTAGTGAACAGAT 454
489 TCAGCAGAGAGAGCAGAACTCTATCGGCGACGAGTAACATCTCTAGTGAACAGAT 430
455 TCAGCAGAGAGAGCAGAACTCTATCGGCGACGAGTAACATCTCTAGTGAACAGAT 514
429 TCAGCAGAGAGAGCAGAACTCTATCGGCGACGAGTAACATCTCTAGTGAACAGAT 370
515 TCTTCCCTTCATTTCACTTCACTGAGCAGAGTCTGTAAGAGAAAGCCGAGTCTAGC 574
369 TCTTCCCTTCATTTCACTTCACTGAGCAGAGTCTGTAAGAGAAAGCCGAGTCTAGC 310
575 TCAGTGTGCTTCTCACTGATTAATGATCTCAGACCCGCTGCGCAATTCGAATTA 634
309 TCAGTGTGCTTCTCACTGATTAATGATCTCAGACCCGCTGCGCAATTCGAATTA 250
635 GGCACAAACATATACCTTCATGAGACACACACACATTTTGAAGCAAGCAATGAC 694
249 GGCACAAACATATACCTTCATGAGACACACACACATTTTGAAGCAAGCAATGAC 190
695 TGCTTAATTAAG 754
189 TGCTTAATTAAG 130
755 CCCCTTCCACACTCTTCACTGATTAATGATCTCAGACCCGCTGCGCAATTCGA 814
129 CCCCTTCCACACTCTTCACTGATTAATGATCTCAGACCCGCTGCGCAATTCGA 70
815 CTGATTAATTAAG 874
69 CTGATTAATTAAG 10
875 TAAATATAC 883
9 TAAATATAC 1

RESULT 15
BM982674 557 bp mRNA linear EST 21-FEB-2003
LOCUS BM982674
DEFINITION UI-CF-EN1-acq-n-01-0-UI-s1 UI-CF-EN1 Homo sapiens cDNA clone
VERSION UI-CF-EN1-acq-n-01-0-UI-3', mRNA sequence.
ACCESSION BM982674
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548

COMMENT

Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
1. 557
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="UI-CF-EN1-acq-n-01-0-UI"
/issue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG: TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG: LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 59.6%; Score 530.8; DB 5; Length 557;
Best Local Similarity 99.6%; Pred. No. 3.6e-148;
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

357 CATTGGCAATTAAGACATCTGCTCTTGGCTGCTGCTCAGACAGAGACCAAGATTC 416
557 CATTGGCAATTAAGACATCTGCTCTTGGCTGCTGCTCAGACAGAGACCAAGATTC 498
417 TATCGGCGACAGAGATTAACATCTCTAGGGAACAGAGTTGACAAAGCCATAGGAAATGC 476
497 TATCGGCGCGCCAGAGATTAACATCTCTAGGGAACAGAGTTGACAAAGCCATAGGAAATGC 438
477 CTGATGGAGTTATCTTCACTGATTAATGATCTCTTCCCTTCACTTCACTTCACTTCACT 516
437 CTGATGGAGTTATCTTCACTGATTAATGATCTCTTCCCTTCACTTCACTTCACTTCACT 378
537 CAAGCCAACTTCTGTAAGAGAAATGCTGAGTTTCTGAGTTTCTTCACTTCACTTCACT 596
377 CAAGCCAACTTCTGTAAGAGAAATGCTGAGTTTCTGAGTTTCTTCACTTCACTTCACT 318
597 TAGATTCAGAGCCCTGCTGCGCAATTAAGCAACAAACATTAATTAATTAATTAATTAAT 656
317 TAGATTCAGAGCCCTGCTGCGCAATTAAGCAACAAACATTAATTAATTAATTAATTAAT 258
657 TGAAGCACACAGACTTTTGAAGCAAGCAATGATGCTTGAATTAATTAATTAATTAATTAAT 716

Db	257	TGAAGCACACACAGACTTTGAAGCAAGACAAATGACTGCTGAATTGAGGCTTGAGG	198
Qy	717	AATGAAGCTTTGAAGGAAAAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGT	776
Db	197	AATGAAGCTTTGAAGGAAAAAATACTTTGTTCCAGCCCCCTTCCACACTCTTCATGT	138
Qy	777	GTTAACCACTGCTTCTCTGAGCCTTGAGCCACGGTGACTGTATTACATGTTGTTATAGA	836
Db	137	GTTAACCACTGCTTCTCTGAGCCTTGAGCCACGGTGACTGTATTACATGTTGTTATAGA	78
Qy	837	AAACTGATTTTGAAGTTCGATCGTTCAGAGAGATGATTAATAATATACATTTGCT	890
Db	77	AAACTGATTTTGAAGTTCGATCGTTCAGAGAGATGATTAATAATATACATTTGCT	24

Search completed: May 31, 2005, 00:10:59
Job time : 3463.52 secs